



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 180153

TO: Patricia Duffy
Location: REM-3B05/3C18
Art Unit: 1645
Wednesday, March 01, 2006
Case Serial Number: 09/955502

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

part 12015

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STIC-Biotech/ChemLib

180153

From: Pak, Michael
Sent: Wednesday, February 22, 2006 9:37 AM
To: STIC-Biotech/ChemLib
Cc: Duffy, Patricia
Subject: FW: multiple short protein search each <100 AA long 09/955,502

Importance: High

Dear STIC,

Please search the multiple sequence search request set forth below.

Thanks,

Mike Pak

-----Original Message-----

From: Duffy, Patricia
Sent: Tuesday, February 21, 2006 4:54 PM
To: Pak, Michael
Subject: multiple short protein search each <100 AA long 09/955,502
Importance: High

Mike,

Please approve multiple short protein sequences.

All sequences used in method claims. Genus claim free of the art. All species claimed.

Thanks,

Pat d.

Dear Stic,

Please search SEQ ID NOS:2-45.

Please print out top 25 hits in each category.

Please perform both an interference and commercial database search.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Thanks.

Patricia A. Duffy, Ph.D.
Primary Patent Examiner
571-272-0855,
Remsen 3B05,
Mailbox: 3C18

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search

NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
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LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:30:02 ; Search time 19.4713 Seconds
(without alignments)
373.651 Million cell updates/sec

Title: US-09-955-502A-42

Perfect score: 467

Sequence: 1 MARWVFCVKNKEAGMKFP.....QMEGYFPGDADAVGVYPO 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

Issued Patents AA:*

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- 5: /cgm2_6/ptodata/1/1aa/RB_COMB.pep:*
- 6: /cgm2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	225.5	48.3	93	2	US-09-328-352-5456
3	221	47.3	92	2	US-09-543-681A-5443
4	207	44.3	122	2	US-09-252-991A-23355
5	182	39.0	110	2	US-09-540-236-2859
6	68.5	14.7	361	2	US-09-252-991A-25005
7	67.5	14.5	466	2	US-09-252-991A-32761
8	66	14.1	418	2	US-09-489-039A-13155
9	65.5	14.0	649	2	US-09-107-532A-4298
10	65.5	14.0	3838	2	US-09-949-016-10853
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12	64.5	13.8	361	2	US-09-955-518-21
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14	63	13.5	461	1	US-08-672-571A-3
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17	62	13.3	360	2	US-09-543-681A-7067
18	62	13.3	671	2	US-09-252-991A-18020
19	61.5	13.2	422	2	US-09-198-452A-377
20	61.5	13.2	423	2	US-09-438-185A-363
21	60.5	13.0	478	2	US-09-489-039A-7300
22	60.5	13.0	596	2	US-09-902-540-10121
23	60	12.8	621	2	US-09-489-039A-10378
24	60	12.8	2186	1	US-08-822-445-2
25	60	12.8	2186	1	US-09-396-540-2
26	59.5	12.7	315	2	US-09-461-325-297
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ALIGNMENTS

28	59.5	12.7	315	2	US-10-115-123-297	Sequence 297, App
29	59.5	12.7	346	2	US-09-808-701A-32	Sequence 32, Appl
30	59.5	12.7	420	2	US-09-902-540-16463	Sequence 16463, A
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32	59.5	12.7	431	2	US-10-012-542-146	Sequence 146, App
33	59.5	12.7	431	2	US-09-311-021-118	Sequence 178, App
34	59.5	12.7	431	2	US-10-115-123-146	Sequence 146, App
35	59.5	12.7	848	2	US-09-538-092-33	Sequence 33, App
36	59.5	12.7	977	2	US-08-335-844A-22	Sequence 22, Appl
37	59.5	12.7	977	2	US-09-123-366-22	Sequence 22, Appl
38	59	12.6	366	2	US-09-252-991A-1958	Sequence 31958, A
39	59	12.6	563	2	US-09-583-110-4195	Sequence 4195, App
40	59	12.6	577	2	US-09-107-433-3424	Sequence 3424, App
41	59	12.6	206	2	US-10-042-665A-5	Sequence 5, Appl
42	58.5	12.5	213	2	US-09-959-873B-16	Sequence 16, Appl
43	58.5	12.5	213	2	US-09-949-016-5555	Sequence 5955, App
44	58.5	12.5	284	1	US-08-061-889-2	Sequence 2, Appl
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46	58.5	12.5	284	2	US-08-623-428D-2	Sequence 2, Appl
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49	58.5	12.5	340	2	US-09-270-767-42358	Sequence 42358, A
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51	58.5	12.5	397	2	US-09-079-030-123	Sequence 123, App
52	58.5	12.5	401	2	US-09-252-991A-17272	Sequence 17272, App
53	58	12.4	303	2	US-09-543-681A-7924	Sequence 7924, App
54	58	12.4	318	2	US-09-489-039A-8369	Sequence 8369, App
55	58	12.4	331	2	US-08-849-751-4	Sequence 4, Appl
56	58	12.4	331	2	US-09-478-816-4	Sequence 4, Appl
57	58	12.4	486	2	US-08-906-743-4	Sequence 4, Appl
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59	58	12.4	563	2	US-08-906-743-2	Sequence 2, Appl
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63	57.5	12.3	163	2	US-09-198-452A-103	Sequence 103, App
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66	57.5	12.3	200	2	US-09-710-279-2390	Sequence 2390, App
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69	57.5	12.3	282	2	US-09-543-681A-7115	Sequence 4715, App
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72	57.5	12.3	890	2	US-09-583-110-4739	Sequence 4739, App
73	57	12.2	157	2	US-09-902-540-15203	Sequence 15203, A
74	57	12.2	184	2	US-10-094-944-19	Sequence 19, Appl
75	57	12.2	412	2	US-09-538-092-709	Sequence 709, App

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Berton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match	48.6%;	Score 227;	DB 2;	Length 107;
Best Local Similarity	48.9%;	Pred. No. 5.7e-24;		
Matches 43;	Conservative 16;	Mismatches 27;	Indels 2;	Gaps 2;

Dy 1 MARNYFCVKLNKEAEGMKFPPLDNLGKRIFFENYQDAWAATWTRQTMLENKRSLADP 600
| : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 17 MSRTI PCTPLQREADGDGFQLYPGELGRIRLYNEISKAEMAQWHQKTMALINERKLSTMPNP 760

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QY      61 RAREYLAAQMEQYFFGSDADA-VQGVTP 87
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Db      77 EHRKLTLEDENVQFLF-EGKDVHIEGYTP 103

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RESULT 2
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 5456000

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OR INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

ORGANISM: *Acinetobacter baumannii*
US-09-328-352-5456

Query Match	48.3%	Score 225.5	DB 2	Length 92
Best Local Similarity	44.9%	Pred. No. 7.5e-24		
Matches 40	Conservative 19	Mismatches 29		Indels 1
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QY	1	MARVVF	CVKL	NKEA	EGMK	FPL	PNEL	GKRT	FT
		:	:	:	:	:	:	:	:
Db	4	MSRQV	FCRK	YQKE	MEGL	DFAP	FGAK	GQEE	FF

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Db      |::| :|| ::| | : :|
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US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION.

1 TITLE OF INVENTION: ANALGESIC AND ANTI-INFLAMMATORY AGENTS AND METHODS
 2
 3 FILE REFERENCE: 2709.1002-001
 4
 5 CURRENT APPLICATION NUMBER: US/09/543,681A
 6
 7 CURRENT FILING DATE: 2000-04-05
 8
 9 PRIOR APPLICATION NUMBER: US 60/128,706
 10
 11 PRIOR FILING DATE: 1999-04-09

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; SEQ ID NO 5443
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; LENGTH: 93
; TYPE: PRT
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US-09-543-681A-5443	
Query Match	47.3%; Score 221;
Posterior Similarity	40.0%;
Posterior	40.0%;

Db 64 DDRKLEQEMVRFLEGHVHIDGYTP 90

RESULT 4
US-09-252-991A-23355
Sequence 23355, Application US/09252991A

? APPLICANT: Marc J. Rubenfield et al.
 ? TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ? TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-23355

Query Match	44.3%	Score 207;	DB 2;	Length 122;
Best Local Similarity	42.5%	Pred. No. 4-5e-21;		
Matches 37;	Conservative 19;	Mismatches 31;	Indels 0;	Gaps 0;

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DB 33 MSRTVMCRKYHEELPLGLDRPPYPGAKGSDIYY

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QY      61 RAREYLAQQMEQYFFGGDADAVQGYTP 87
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Db      93 EDRKFLQQEMDKFLSGEDYAKADGYTP 115

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RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No 6679910

/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
 / TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 / FILE REFERENCE: 2709.2005-001
 / CURRENT APPLICATION NUMBER: US/09/540,236
 / CURRENT FILING DATE: 2000-04-04
 / NUMBER OF SEQ ID NOS: 3840

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; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis

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Query Match	39.0%;	Score 182;
Best Local Similarity	41.7%;	Pred. No. 1
Matched	35	Concentration 14
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QY 4 MVECVKLNKEABGMKFPPLPNELGKRIFENT
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Db 24 MVEGRKYQONT.PKTLPNBPBPNAKGAETOTPT
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 :||:| |::| |||
 nb 84 KYTNEQRKELDNGEYRKPAQGYVP 107

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: March 1, 2006, 00:44:45 ; Search time 57.1494 Seconds
(without alignments)
643.383 Million cell updates/sec

Title: US-09-955-502A-42

Perfect score: 467

Sequence: 1 MARWVFCVKNLKBKBAKMKP.....QMEQYFGDADAVQGVYVQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	339	72.6	87	US-09-955-502-29	Sequence 29, Appl
5	339	72.6	87	US-09-955-502-30	Sequence 30, Appl
6	294	63.0	87	US-09-955-502-31	Sequence 31, Appl
7	290	62.1	87	US-09-955-502-32	Sequence 32, Appl
8	290	62.1	87	US-09-955-502-33	Sequence 33, Appl
9	272.5	58.4	86	US-09-955-502-34	Sequence 34, Appl
10	258	55.2	88	US-09-955-502-35	Sequence 35, Appl
11	243	52.0	87	US-09-955-502-36	Sequence 36, Appl
12	240	51.4	90	US-09-955-502-37	Sequence 37, Appl
13	235	50.3	87	US-09-955-502-38	Sequence 38, Appl
14	230	49.3	88	US-09-955-502-39	Sequence 39, Appl
15	228	48.8	87	US-09-955-502-40	Sequence 40, Appl
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17	219	46.9	87	US-09-955-502-42	Sequence 42, Appl
18	217	46.5	87	US-09-955-502-43	Sequence 43, Appl
19	213	45.6	91	US-09-955-502-44	Sequence 44, Appl
20	213	45.6	91	US-09-955-502-45	Sequence 45, Appl
21	213	45.6	91	US-09-955-502-46	Sequence 46, Appl
22	211	45.2	88	US-09-955-502-47	Sequence 47, Appl
23	211	45.2	91	US-09-955-502-48	Sequence 48, Appl
24	211	45.2	91	US-09-955-502-49	Sequence 49, Appl
25	211	45.2	91	US-09-955-502-50	Sequence 50, Appl
26	210	45.0	78	US-09-955-502-51	Sequence 51, Appl
27	207	44.3	87	US-09-955-502-52	Sequence 52, Appl

28	202	43.3	91	US-09-955-502-18	Sequence 18, Appl
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47	65.5	14.0	3830	US-10-745-237-256	Sequence 256, Appl
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54	65	13.9	465	US-10-335-977-8912	Sequence 8913, Ap
55	65	13.9	465	US-10-857-625-698	Sequence 698, Appl
56	64.5	13.8	361	US-10-857-625-698	Sequence 21, Appl
57	64.5	13.8	361	US-10-289-152-21	Sequence 22706, A
58	64.5	13.8	1501	US-10-732-923-22706	Sequence 22705, A
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60	64.5	13.8	1553	US-10-425-115-281438	Sequence 281438, A
61	64.5	13.6	954	US-10-472-928-1752	Sequence 8759, Ap
62	63.5	13.6	288	US-10-156-761-8759	Sequence 172448, A
63	63	13.5	417	US-10-437-963-172448	Sequence 68811, A
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65	62.5	13.3	360	US-10-369-493-4727	Sequence 7456, Ap
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67	62	13.3	532	US-09-815-242-11951	Sequence 66545, A
68	62	13.3	570	US-10-282-122A-66545	Sequence 67, Appl
69	62	13.3	835	US-10-087-887-67	Sequence 74, Appl
70	62	13.3	835	US-10-087-887-74	Sequence 7, Appl
71	62	13.3	835	US-10-889-340-7	Sequence 149485, A
72	62	13.3	835	US-10-424-599-149485	
73	62	13.3	835		
74	62	13.3	835		
75	62	13.3	1025		

ALIGNMENTS

RESULT 1
US-09-955-502-26
Sequence 26, Application US/09955502
Patent No. US2002072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.9/559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 26
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

US-09-955-502-26

Query Match 100.0%; Score 467; DB 3; Length 88;

Best Local Similarity 100.0%; Pred. No. 2.6e-50; Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARWFCVKLNKEAGMKPPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
Db 1 MARWFCVKLNKEAGMKPPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60

Qy 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88
Db 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88

RESULT 2

US-09-955-502-27

Sequence 27, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 27

LENGTH: 88

TYPE: PRT

ORGANISM: Neisseria meningitidis B

US-09-955-502-27

Query Match 100.0%; Score 467; DB 3; Length 88;

Best Local Similarity 100.0%; Pred. No. 2.6e-50; Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARWFCVKLNKEAGMKPPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
Db 1 MARWFCVKLNKEAGMKPPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60

Qy 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88
Db 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88

RESULT 3

US-09-955-502-28

Sequence 28, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 28

LENGTH: 88

TYPE: PRT

ORGANISM: Neisseria meningitidis A

US-09-955-502-28

Query Match 100.0%; Score 467; DB 3; Length 88;

Best Local Similarity 100.0%; Pred. No. 2.6e-50; Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARWFCVKLNKEAGMKPPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
Db 1 MARWFCVKLNKEAGMKPPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60

Qy 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88
Db 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88

RESULT 4

US-09-955-502-29

Sequence 29, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 29

LENGTH: 87

TYPE: PRT

ORGANISM: Burkholderia mallei

US-09-955-502-29

Query Match 72.6%; Score 339; DB 3; Length 87;

Best Local Similarity 67.8%; Pred. No. 2.6e-34; Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MARWFCVKLNKEAGMKPPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
Db 1 MARWFCVKLNKEAGMKPPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60

Qy 61 RAREYLAQOMEQYFFGADAVQGYVP 87
Db 61 RAREYLAQOMEQYFFGADAVQGYVP 87

RESULT 5

US-09-955-502-30

Sequence 30, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 30

LENGTH: 87

TYPE: PRT

ORGANISM: Burkholderia pseudomallei

US-09-955-502-30

Query Match 72.6%; Score 339; DB 3; Length 87;

Best Local Similarity 67.8%; Pred. No. 2.6e-34; Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:45:38 ; Search time 5.56322 Seconds
(without alignments)
235.489 Million cell updates/sec

Title: US-09-955-502A-42

Perfect score: 467

Sequence: 1 MARWVFCYKLNKBAEMKFP.....QMEGYFPGDADAVQGYVPQ 88

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 75 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	US-10-467-657-968	Sequence 968, App
2	60	12.8	1092	US-10-821-234-999	Sequence 999, App
3	58	12.4	380	US-10-525-674-28	Sequence 28, App
4	58	12.4	614	US-11-165-576-2	Sequence 2, App
5	58	12.4	614	US-11-165-576-4	Sequence 4, App
6	57.5	12.3	200	US-10-793-626-1186	Sequence 1186, App
7	57.5	12.3	200	US-10-793-626-2390	Sequence 2390, App
8	57.5	12.3	204	US-11-098-686-10498	Sequence 10498, App
9	57.5	12.3	655	US-11-098-686-10464	Sequence 10464, App
10	57	12.2	384	US-11-219-282-19	Sequence 19, App
11	57	12.2	620	US-10-131-826A-324	Sequence 324, App
12	56.5	12.1	575	US-11-098-686-10635	Sequence 10635, App
13	56.5	12.1	688	US-11-165-226-124	Sequence 124, App
14	56	12.0	1124	US-11-090-617-688	Sequence 688, App
15	56	12.0	1376	US-10-995-561-809	Sequence 809, App
16	56	12.0	1376	US-11-100-640-32	Sequence 32, App
17	55.5	11.9	403	US-11-009-658-14	Sequence 14, App
18	55.5	11.9	408	US-10-821-234-1100	Sequence 1100, App
19	55.5	11.9	449	US-11-098-686-10535	Sequence 10535, App
20	55	11.8	258	US-11-090-439-38	Sequence 38, App
21	55	11.8	261	US-10-467-657-400	Sequence 400, App
22	55	11.8	611	US-10-454-437-54	Sequence 54, App
23	55	11.8	633	US-11-193-561-13	Sequence 13, App
24	55	11.8	633	US-11-193-771-13	Sequence 13, App
25	55	11.8	633	US-11-193-769-13	Sequence 13, App

26	55	11.8	633	7	US-11-193-806-13	Sequence 13, App
27	55	11.8	633	7	US-11-193-857-13	Sequence 13, App
28	55	11.8	925	6	US-10-454-437-50	Sequence 50, App
29	55	11.8	967	7	US-11-202-268-6	Sequence 6, App
30	55	11.8	1011	7	US-11-202-268-2	Sequence 2, App
31	54.5	11.7	719	7	US-11-087-227-14	Sequence 14, App
32	54	11.6	307	6	US-10-793-626-522	Sequence 522, App
33	54	11.6	685	7	US-11-098-686-10574	Sequence 10574, App
34	54	11.6	738	7	US-11-140-625-11	Sequence 11, App
35	53.5	11.5	291	6	US-10-883-532-103	Sequence 103, App
36	53.5	11.5	310	6	US-11-055-153-7	Sequence 7, App
37	53.5	11.5	344	7	US-11-055-163-6	Sequence 6, App
38	53.5	11.5	432	6	US-10-933-115-8	Sequence 8, App
39	53.5	11.5	432	7	US-11-056-354-4	Sequence 4, App
40	53.5	11.5	440	6	US-10-933-115-2	Sequence 2, App
41	53.5	11.5	473	6	US-10-131-826A-382	Sequence 382, App
42	53	11.3	288	6	US-10-467-657-3426	Sequence 3426, App
43	53	11.3	291	7	US-11-120-308-24	Sequence 24, App
44	53	11.3	710	7	US-11-124-367A-354	Sequence 354, App
45	53	11.3	710	7	US-11-124-367A-359	Sequence 359, App
46	53	11.3	713	7	US-11-124-367A-355	Sequence 355, App
47	53	11.3	713	7	US-11-124-367A-356	Sequence 356, App
48	53	11.3	713	7	US-11-124-367A-358	Sequence 358, App
49	53	11.3	734	6	US-10-821-234-1056	Sequence 1056, App
50	53	11.3	3507	7	US-11-075-185-7	Sequence 7, App
51	52.5	11.2	197	6	US-10-966-501-296	Sequence 296, App
52	52.5	11.2	229	6	US-10-793-626-2818	Sequence 2818, App
53	52.5	11.2	335	7	US-11-072-175-245	Sequence 245, App
54	52.5	11.2	754	7	US-11-140-625-10	Sequence 10, App
55	52.5	11.2	1476	6	US-10-647-956A-4	Sequence 4, App
56	52.5	11.2	4128	7	US-10-770-726-77	Sequence 77, App
57	52	11.1	223	7	US-11-018-868-140	Sequence 140, App
58	52	11.1	381	7	US-11-024-959-418	Sequence 418, App
59	52	11.1	390	7	US-11-019-711-55	Sequence 55, App
60	52	11.1	390	7	US-11-219-282-12	Sequence 12, App
61	52	11.1	1022	7	US-11-156-084-118	Sequence 118, App
62	51.5	11.0	209	5	US-09-995-493-94	Sequence 94, App
63	51.5	11.0	396	7	US-11-202-731-2	Sequence 2, App
64	51.5	11.0	403	7	US-11-074-176-354	Sequence 354, App
65	51.5	11.0	408	7	US-11-074-176-186	Sequence 186, App
66	51.5	11.0	447	7	US-11-024-959-286	Sequence 286, App
67	51.5	11.0	479	6	US-10-821-234-871	Sequence 871, App
68	51.5	11.0	1034	7	US-11-072-512-2343	Sequence 2343, App
69	51.5	11.0	1159	6	US-10-613-744-12	Sequence 12, App
70	51.5	11.0	1159	6	US-10-957-116-9	Sequence 9, App
71	51	10.9	326	7	US-11-098-686-10173	Sequence 10173, App
72	51	10.9	387	7	US-11-219-282-20	Sequence 20, App
73	50.5	10.8	124	7	US-11-069-642-10	Sequence 10, App
74	50.5	10.8	347	6	US-10-853-807A-45	Sequence 45, App
75	50.5	10.8	352	6	US-10-878-556A-40	Sequence 40, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 100.0%; Score 467; DB 6; Length 88;
Best Local Similarity 100.0%; Pred. No. 1,7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARVFCVKLNKEAGMKFPELPNELGKRIFFENVSOEAMAWTRHQTMLINENRSLADP 60
DB 1 MARVFCVKLNKEAGMKFPELPNELGKRIFFENVSOEAMAWTRHQTMLINENRSLADP 60

QY 61 RAREYLAQOMEQYFFGADAVQGVPPQ 88
DB 61 RAREYLAQOMEQYFFGADAVQGVPPQ 88

RESULT 2

US-10-821-234-999
Sequence 999, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:

APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for diagnosis and treatment of Pre-eclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

PRIOR FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pc_seq_genes Version 1.0

SEQ ID NO 999

LENGTH: 1092

TYPE: PRT

ORGANISM: Homo sapiens

US-10-821-234-999

Query Match 12.8%; Score 60; DB 6; Length 1092;
Best Local Similarity 30.6%; Pred. No. 28;
Matches 15; Conservative 12; Mismatches 20; Indels 2; Gaps 2;

QY 31 FENVSOEAMAWT-RHQTMLINENRSLADP-RAREYLAQOMEQYFFGD 77
DB 492 FEAGAMENWGILTFREETLLYDSNTSSMADRKLVTYKIAHEILAHQWFGN 540

RESULT 3

US-10-525-674-28
Sequence 28, Application US/10525674
Publication No. US20060003425A1
GENERAL INFORMATION:

APPLICANT: Kroger, Burkhard
APPLICANT: Zelder, Oskar

APPLICANT: Kolpproge, Corinna

APPLICANT: Schroder, Hartwig

APPLICANT: Hafner, Stefan

TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing

FILE REFERENCE: 13111-00002-US

CURRENT APPLICATION NUMBER: US/10/525,674

PRIOR FILING DATE: 2005-02-24

PRIOR APPLICATION NUMBER: PCT/EP 2003/009452

PRIOR FILING DATE: 2003-08-26

PRIOR APPLICATION NUMBER: DE 102 39 073.8

PRIOR FILING DATE: 2002-08-26

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PatentIn version 3.3

SEQ ID NO 28

LENGTH: 380
TYPE: PRT
ORGANISM: Thermus thermophilus
US-10-525-674-28

Query Match 12.4%; Score 58; DB 6; Length 380;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 15; Conservative 14; Mismatches 22; Indels 6; Gaps 2;

QY 34 VSOEAMAWTRHQTMLINENR--LSLADPRAREYLAQOMEQYFFGADAVQGVPPQ 88
DB 1 MSRIALRAMEGHEALILKPPRSPISIPPKRAVLPFRREGVYTE---LGGYLPE 53

RESULT 4

US-11-165-576-2
Sequence 2, Application US/11165576
Publication No. US20060009388A1
GENERAL INFORMATION:

APPLICANT: Mi, Sha

APPLICANT: Pepinsky, R. Blake

APPLICANT: McCoy, John

TITLE OF INVENTION: Treatment of Conditions Involving Demyelination

FILE REFERENCE: 2159.046004

CURRENT APPLICATION NUMBER: US/11/165,576

PRIOR FILING DATE: 2005-06-24

PRIOR APPLICATION NUMBER: 60/680,475

PRIOR FILING DATE: 2005-05-13

PRIOR APPLICATION NUMBER: 60/628,435

PRIOR FILING DATE: 2004-11-15

PRIOR APPLICATION NUMBER: 60/617,297

PRIOR FILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: 60/582,966

PRIOR FILING DATE: 2004-06-24

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 614

TYPE: PRT

ORGANISM: Homo sapiens

US-11-165-576-2

Query Match 12.4%; Score 58; DB 7; Length 614;
Best Local Similarity 27.4%; Pred. No. 24;
Matches 17; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

QY 3 RMVFCVKLNKEA--EGMKFPELPNELGKRIFFENVSOEAMAWTRHQTMLINENRSLADP 60
DB 47 RAVLCHRKFVAVEGIPETRLDLGKNRIKTLINQDEPFASFPHLELELLENIVSAVEP 106

QY 61 RA 62
DB 107 GA 108

RESULT 5

US-11-165-576-4
Sequence 4, Application US/11165576
Publication No. US20060009388A1
GENERAL INFORMATION:

APPLICANT: Mi, Sha

APPLICANT: Pepinsky, R. Blake

APPLICANT: McCoy, John

TITLE OF INVENTION: Treatment of Conditions Involving Demyelination

FILE REFERENCE: 2159.046004

CURRENT APPLICATION NUMBER: US/11/165,576

PRIOR FILING DATE: 2005-06-24

PRIOR APPLICATION NUMBER: 60/680,475

PRIOR FILING DATE: 2005-05-13

PRIOR APPLICATION NUMBER: 60/628,435

PRIOR FILING DATE: 2004-11-15

PRIOR APPLICATION NUMBER: 60/617,297

PRIOR FILING DATE: 2004-10-07

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:49:36 / Search time 73.25 Seconds
(without alignments)
521.856 Million cell updates/sec

Title: US-09-955-502a-43

Perfect score: 471
Sequence: 1 MSRMVQVKGHEAEGLDRP.....KQMEAYFPDGAQSPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	471	100.0	87	5	ABB78176 Amino aci
2	310	65.8	87	5	ABB78175 Amino aci
3	304	64.5	87	5	ABB78174 Amino aci
4	294	62.4	88	5	ABB78171 Amino aci
5	294	62.4	88	5	ABB78172 Amino aci
6	294	62.4	88	5	ABB78173 Amino aci
7	294	62.4	88	6	ABB77219 N. gonorr
8	291	61.8	87	5	ABB78177 Amino aci
9	286	60.7	88	5	ABB78178 Amino aci
10	286	60.7	89	9	ABE41576 L. pneumo
11	286	60.7	95	9	ABE38294 L. pneumo
12	275	58.4	87	5	ABB78148 Amino aci
13	275	58.4	87	5	ABB78147 Amino aci
14	257.5	54.7	86	5	ABB78149 Amino aci
15	242	51.4	87	5	ABB78170 Amino aci
16	242	51.4	122	7	ABO74609 Pseudomon
17	237	50.3	87	5	ABB78169 Amino aci
18	225.5	47.9	92	6	ADA34169 Acinetoba
19	219	46.5	90	5	ABB78168 Amino aci
20	213	45.2	88	5	ABB78154 Amino aci
21	211	44.8	87	5	ABB78153 Amino aci
22	208.5	44.3	90	5	ABB78167 Amino aci
23	208	44.2	91	5	ABB78150 Amino aci
24	208	44.2	93	7	ADF05158 Bacterial

ALIGNMENTS

RESULT 1	ABB78176	standard; protein; 87 AA.
ID	ABB78176;	
AC	ABB78176;	
DT	29-AUG-2003 (revised)	
DT	05-NOV-2002 (first entry)	
DE	Amino acid sequence of a YggX homologue.	
XX	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
XX	hydroxyl radical; DNA damage; YggX homologue.	
OS	Acidithiobacillus ferrooxidans.	
PN	US2002072118-A1.	

25	208	44.2	107	7	ABO65445	AbO65445 Klebsiella
26	204	43.3	90	5	ABB78155	Abb78155 Amino aci
27	202	42.9	87	5	ABB78152	Abb78152 Amino aci
28	200	42.5	87	5	ABB78151	Abb78151 Amino aci
29	200	42.5	91	5	ABB78158	Abb78158 Amino aci
30	200	42.5	91	5	ABB78157	Abb78157 Amino aci
31	200	42.5	91	5	ABB78156	Abb78156 Amino aci
32	197	41.8	88	5	ABB78160	Abb78160 Amino aci
33	197	41.8	91	5	ABB78161	Abb78161 Amino aci
34	197	41.8	91	5	ABB78159	Abb78159 Amino aci
35	197	41.8	91	5	ABB78162	Abb78162 Amino aci
36	196	41.6	78	5	ABB78164	Abb78164 Amino aci
37	190	40.3	91	5	ABB78163	Abb78163 Amino aci
38	186	39.5	90	5	ABB78165	Abb78165 Amino aci
39	177	37.6	110	8	ADL05173	AdL05173 M. catarr
40	166	35.2	76	5	ABB78166	Abb78166 Amino aci
41	166	35.2	76	5	ABB78166	Abb78166 Amino aci
42	152	35.2	2285	7	ABB63057	Abb63057 Drosophila
43	152	35.2	387	4	ABO82328	ABO82328 Pseudomon
44	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
45	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
46	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
47	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
48	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
49	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
50	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
51	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
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55	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
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57	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
58	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
59	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
60	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
61	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
62	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
63	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
64	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
65	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
66	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
67	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
68	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
69	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
70	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
71	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
72	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
73	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
74	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil
75	151.1	35.2	523	4	AAU35394	AAU35394 Haemophil

```
XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX Sequence 87 AA;
SQ
Query Match 100.0%; Score 471; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSRMVQCVKLGHEAGLDPRPPYRGALGARIVQSVSKAMQGMKQMTLINEYRLSPIDP 60
DB 1 MSRMVQCVKLGHEAGLDPRPPYRGALGARIVQSVSKAMQGMKQMTLINEYRLSPIDP 60
OY 61 KSRTFLEKOMEAYFFGDQASPEGYVP 87
DB 61 KSRTFLEKOMEAYFFGDQASPEGYVP 87
RESULT 2
ABB78175
ID ABB78175 standard; protein; 87 AA.
AC ABB78175;
AT 05-NOV-2002 (first entry)
DE Amino acid sequence of a YggX homologue.
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
XX US2002072118-A1.
PN 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
```

```
PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX Sequence 87 AA;
SQ
Query Match 65.8%; Score 310; DB 5; Length 87;
Best Local Similarity 64.4%; Pred. No. 4.4e-31;
Matches 56; Conservative 10; Mismatches 21; Indels 0; Gaps 0;
OY 1 MSRMVQCVKLGHEAGLDPRPPYRGALGARIVQSVSKAMQGMKQMTLINEYRLSPIDP 60
DB 1 MARHICAKYKGEKAGLDPPPLPELGKRLYSVSKQAMQDWLQQTMLINENRLNMAPD 60
OY 61 KSRTFLEKOMEAYFFGDQASPEGYVP 87
DB 61 RARQYIMKQTKRYFFGEGADQASGYVP 87
RESULT 3
ABB78174
ID ABB78174 standard; protein; 87 AA.
AC ABB78174;
AT 05-NOV-2002 (first entry)
DE Amino acid sequence of a YggX homologue.
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
XX US2002072118-A1.
PN 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
```

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:27:00 ; Search time 10.75 Seconds
(without alignments)
778.685 Million cell updates/sec

Title: US-09-955-502a-43
Perfect score: 471
Sequence: 1 MSRMVQCVLDGHEABGLDRP.....KQMEAYFGDAQSPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	62.4	88	2 H81014	conserved hypotet
2	242	51.4	90	2 H83003	conserved hypotet
3	215	45.6	105	2 C82624	conserved hypotet
4	204	43.3	90	2 C82320	conserved hypotet
5	202	42.9	90	2 C64013	hypothetical prote
6	200	42.5	91	2 A85954	hypothetical prote
7	200	42.5	91	2 A65082	hypothetical prote
8	200	42.5	91	2 P91108	hypothetical prote
9	197	41.8	91	2 AH0879	conserved hypotet
10	186	39.5	90	2 A10116	conserved hypotet
11	166	35.2	93	2 E84994	hypothetical prote
12	71.5	15.2	383	2 F83321	hypothetical prote
13	71	15.1	523	1 T64055	GMP synthase (glut
14	71	15.1	568	2 T25162	Frlz1-1 protein
15	70	14.9	1197	2 T39613	pyruvate (flavodox
16	70	14.9	1199	2 AD2156	pyruvate-flavodox
17	69.5	14.8	501	2 T35009	probable phosphol
18	69	14.6	1263	2 T43934	DNA-directed DNA p
19	68.5	14.5	249	2 A83963	hypothetical prote
20	67.5	14.3	564	2 T49322	related to RNA-bin
21	67	14.2	915	2 A43335	transferrin-bindin
22	67	14.2	950	2 B64135	oxoglutarate dehyd
23	66	14.0	604	2 S36493	E1 protein - human
24	65.5	13.9	186	1 MMR219	19k globulin precu
25	65.5	13.9	186	2 JCA484	alpha-globulin pre
26	65.5	13.9	368	2 T31103	probable GMP synth
27	65	13.8	159	2 AD0348	probable membrane
28	65	13.8	1434	2 G71232	hypothetical prote
29	64.5	13.7	914	2 T17233	hypothetical prote

30	64.5	13.7	4273	2 C69679	polyketide synthas
31	64	13.6	205	2 AD0788	heme exporter prot
32	64	13.6	205	2 AC0960	heme exporter prot
33	64	13.6	306	2 A97249	Zn-binding lipopro
34	64	13.6	364	2 C48376	orf2 5' to phoC -
35	64	13.6	598	2 A75531	hypothetical prote
36	63.5	13.5	376	2 C82310	sulfate ABC transp
37	63.5	13.5	609	2 S36481	E1 protein - human
38	63.5	13.5	1199	2 S77082	pyruvate (flavodox
39	63.5	13.5	1243	2 TC5615	membrane-associate
40	63	13.4	265	2 T46733	citr protein (impo
41	63	13.4	443	2 T48593	hypothetical prote
42	63	13.4	468	2 F87359	leucine aminopepti
43	63	13.4	705	2 S18733	glutamin high mole
44	63	13.4	1455	2 E75199	DNA-directed DNA p
45	62.5	13.3	243	2 J01427	hypothetical 27k p
46	62.5	13.3	289	2 T46370	hypothetical prote
47	62.5	13.3	393	2 T49257	protein kinase-1lk
48	62.5	13.3	475	2 S54993	reverse transcript
49	62.5	13.3	475	2 S54994	reverse transcript
50	62.5	13.3	510	2 A96735	hypothetical prote
51	62.5	13.3	513	2 AB1921	hypothetical prote
52	62.5	13.3	605	2 S36469	E1 protein - human
53	62	13.2	316	2 C91272	hypothetical prote
54	62	13.2	316	2 C86113	hypothetical prote
55	62	13.2	503	2 AP2029	hypothetical prote
56	62	13.2	512	1 FOMVGS	gag polyprotein -
57	62	13.2	520	1 FOLJGL	gag polyprotein -
58	62	13.2	662	2 T41215	probable acetate-C
59	61	13.0	254	2 T15187	hypothetical prote
60	61	13.0	316	2 B37318	delta(2)-isopenten
61	61	13.0	430	2 E96031	hypothetical prote
62	61	13.0	450	2 S73419	signal recognition
63	61	13.0	457	1 JCA993	biphenyl dioxygena
64	61	13.0	525	1 STECGU	GMP synthase (glut
65	61	13.0	525	2 F85894	GMP synthase (glut
66	61	13.0	525	2 AD0820	GMP synthase (glut
67	61	13.0	525	2 A91050	GMP synthase (lm
68	61	13.0	535	2 AF0103	probable sulfatase
69	61	13.0	915	2 F81196	transferrin-bindin
70	60.5	12.8	359	2 T26813	hypothetical prote
71	60.5	12.8	475	2 S54996	reverse transcript
72	60.5	12.8	475	2 S54998	reverse transcript
73	60	12.7	342	2 T19021	probable inositol
74	60	12.7	352	2 D69410	cell division cont
75	60	12.7	375	2 T39364	probable galactosy

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #ext_change 05-Oct-2004
C:Species: Neisseria meningitidis
C:Accession: H81014; F81958
R:Retcelin, H.; Saunders, N.J.; Heidelberg, U.; Jeffries, A.C.; Nelson, K.B.; Bisen, J.J.
Hickey, B.K.; Haft, D.H.; Salzberg, S.D.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, B.R.; Rappoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; M01D:2017555; PMID:10710307
A:Accession: H81014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <TR>
A:Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:G7227279; PIDN
A:Experimental source: serogroup B, strain MC58
R:Parfhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:00:23 / Search time 65.75 Seconds
(without alignments)
933.551 Million cell updates/sec

Title: US-09-955-502A-43

Perfect score: 471

Sequence: 1 MSRMVQCXVKGHEAEGIDRP.....KQMEAYFGDGAQSPGAYVP 87

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

1: uniprot_05.80:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	70.3	91	2	Q4LS19_9BURK
2	319	67.7	90	1	PEPT_CHRVO
3	313	66.5	90	1	PEPT_NITRU
4	310	65.8	91	1	PEPT_BURMA
5	310	65.8	91	1	PEPT_BURPS
6	309	65.6	91	1	PEPT_RALSO
7	294	62.4	88	1	PEPT_NEIGI
8	294	62.4	88	1	PEPT_NEIMA
9	294	62.4	88	1	PEPT_NEIMA
10	291	61.8	90	1	PEPT_METCA
11	286	60.7	89	1	PEPT_LBSPA
12	286	60.7	90	1	PEPT_LBSPA
13	286	60.7	90	1	PEPT_COXBU
14	284	60.3	89	1	PEPT_LBSPU
15	275	58.4	90	1	PEPT_BORBR
16	275	58.4	90	1	PEPT_BORPA
17	275	58.4	90	1	PEPT_BORPE
18	261	55.4	91	1	PEPT_XANAC
19	255	54.1	92	1	PEPT_XANOR
20	252	53.5	92	1	PEPT_XANCP
21	252	53.5	92	2	Q4UM14_XANCP
22	249	52.5	92	2	Q4UM04_9DELIT
23	242	51.4	90	1	PEPT_PSEAB
24	238	50.5	90	1	PEPT_IDILO
25	237	50.3	90	1	PEPT_PSPBP
26	231	49.0	90	2	Q4J228_AZOVIT
27	229	48.6	90	2	Q6T7P6_PSEBTL
28	224.5	47.7	90	1	PEPT_PSEBTL
29	222	47.1	90	1	PEPT_XYLAT
30	222	47.1	90	2	Q4KJ22_PSEBTL
31	220	46.7	90	1	PEPT_VIBF1

32	219	46.5	90	1	PEPT_PSEBM
33	219	46.5	90	2	Q4ZLB3_PSEBY
34	218	46.3	90	1	PEPT_PHOIL
35	215	45.6	90	1	PEPT_XYLPA
36	213	45.2	92	1	PEPT_SHEON
37	211	44.8	90	1	PEPT_VIBVU
38	211	44.8	90	1	PEPT_VIBVU
39	211	44.8	94	1	PEPT_HABDV
40	208	44.2	90	1	PEPT_VIBPA
41	204	43.3	90	1	PEPT_VIBCH
42	203	43.1	87	1	PEPT_PRAIT
43	202	42.9	90	1	PEPT_HABIN
44	202	42.9	90	2	Q4QMD9_HAB18
45	200	42.5	90	1	PEPT_PASMU
46	200	42.5	91	1	PEPT_PASMU
47	197	41.8	90	1	PEPT_MANSU
48	195	41.4	90	1	PEPT_ERECT
49	195	41.4	90	1	PEPT_ECO57
50	195	41.4	90	1	PEPT_ECOLI
51	194	41.2	90	1	PEPT_SHIFL
52	192	40.8	90	1	PEPT_YERPS
53	192	40.8	90	1	PEPT_PHOPI
54	192	40.8	90	1	PEPT_SALCH
55	192	40.8	90	1	PEPT_SALPA
56	192	40.8	90	1	PEPT_SALTI
57	191	40.6	90	1	PEPT_SALTY
58	186	39.5	90	1	PEPT_YERPS
59	179	38.0	78	1	PEPT_BUCAP
60	172	36.5	78	1	PEPT_WIGBR
61	172	36.5	79	1	PEPT_CANBP
62	167	35.5	96	2	Q4FVJ7_9GAMW
63	166	35.2	77	1	PEPT_BUCAI
64	142	30.1	87	1	PEPT_BUCBP
65	78.5	16.7	825	1	AOXB_ALCPA
66	78.5	16.7	826	2	Q6WB60_ALCPA
67	72.5	15.4	484	2	Q6MQ14_BDEBA
68	72.5	15.4	2308	2	Q9VP17_DROBE
69	72	15.3	514	2	Q8VNU2_DESPE
70	71.5	15.2	359	2	Q4N08_THERA
71	71.5	15.2	383	2	Q910P0_PSEBS
72	71.5	15.2	1200	2	Q4NM62_9DELIT
73	71.5	15.2	1322	2	Q75HA9_ORYSA
74	71	15.1	523	1	GUAA_HABIN
75	71	15.1	523	2	Q4QNW4_HAB18

ALIGNMENTS

RESULT 1	Q4LS19_9BURK	PRELIMINARY;	PRT;	91 AA.
ID	Q4LS19_9BURK	PRELIMINARY;	PRT;	91 AA.
AC	Q4LS19;			
DT	13-SEP-2005 (TrEMBLrel. 31, Created)			
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)			
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)			
DE	Hypothetical protein.			
GN	ORFNames=Bcen242ADRAFT_3773;			
OS	Burkholderia cenocepacia HI2424.			
OC	Bacteriæ; Proteobacteria; Betaproteobacteria; Burkholderiales;			
OC	Burkholderiaceæ; Burkholderia; Burkholderia cenocepacia complex.			
OX	NCBI_TaxID=331272;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=HI2424;			
RG	US DOE Joint Genome Institute (JGI-PGF);			
RA	Copeland A., Lucas S., Lapidus A., Barry K., Deter C., Glavina T.,			
RA	Hammon N., Izserni S., Plitnick S., Richardson P.,			
RT	"Sequencing of the draft genome assembly of Burkholderia cenocepacia			
RT	HI2424.";			
RL	Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			

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RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAHL01000021; BAM18958.1; -; Genomic_DNA.
CC DR Hypochemical protein.
CC KW Hypochemical protein.
SQ SEQUENCE 91 AA; 10327 MW; 0A540A880A76E284 CRC64;

Query Match
Best local Similarity 70.3%; Score 331; DB 2; Length 91;
Matches 61; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSRMVQCVLGGHAEGLDRPPYPGALGARIYQSVSKAOGMLKHOTMLINENRSLSPDP 60
DB 1 MARMTCANLKGKAEAGLDPPPLPGLGKRIYSSVSKAOGMLKHOTMLINENRSLMADP 60

QY 61 KSRTPLEKQMEAYFPDGAQSPGEGYVP 87
DB 61 RARQYLMKQTKKFFDGDADQAGGYVP 87

RESULT 2
FETP_CHRVO
ID FETP_CHRVO STANDARD; PRT; 90 AA.
AC 07NSR4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=CV3356;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
ON NCBI_TaxId=536;
RX 11]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimarães C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade V., Aratipe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Batuas L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Broccoli M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantiñati F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Gonçalves P.R., Grangeiro T.B.,
RA Gratepaglia D., Gristad E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhão A.O., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Páixão R.F.C., Parente J.A., Pedrosa P.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Senane H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza R.R.L.,
RA Souza R.C., Steffens M.B.R., Steindl M., Teixeira S.R., Umenyi T.,
RA Vettore A.C., Waseem R., Zana A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability."
RT Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or

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CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE016922; AA061020.1; ALT_INIT; Genomic_DNA.
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; Y9GX.
CC DR Pfam; PF04362; DUF495; 1.
CC DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
CC DR ProDom; PD029191; DUF495; 1.
CC KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10095 MW; 60492ED67A9ABE78 CRC64;

Query Match
Best local Similarity 67.7%; Score 319; DB 1; Length 90;
Matches 57; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSRMVQCVLGGHAEGLDRPPYPGALGARIYQSVSKAOGMLKHOTMLINENRSLSPDP 60
DB 1 MERTVNCIKLGEAEGLDPPPLPGLGKRIYSSVSKAOGMLKHOTMLINENRSLSDA 60

QY 61 KSRTPLEKQMEAYFPDGAQSPGEGYVP 87
DB 61 RARQYLMKQTKKFFDGDADQAGGYVP 87

RESULT 3
FETP_NITEU
ID FETP_NITEU STANDARD; PRT; 90 AA.
AC 082XF2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=NE0322;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
ON NCBI_TaxId=915;
RX 11]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RX DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.B., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayaveda-Soto L.A.,
RA Acierio D.M., Hommes N.G., Whitaker M.W., App D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BX321857; CAD8423.1; -; Genomic_DNA.
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; Y9GX.
CC DR Pfam; PF04362; DUF495; 1.
CC DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
CC DR ProDom; PD029191; DUF495; 1.
CC KW Complete proteome; Iron.

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:30:02 / Search time 19.25 Seconds
(without alignments)
373.651 Million cell updates/sec

Title: US-09-955-502a-43

Perfect score: 471

Sequence: 1 MSRVQCTKLGHBABGLDRP.....KQMEAYFRDGAQSPDEGVVP 87

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

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6: /cgn2_6/ptodata/1/1aa/Backfillies1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	242	51.4	122	US-09-252-991A-23355	Sequence 23355, A
2	225.5	47.9	92	US-09-328-352-5456	Sequence 5456, Ap
3	208	44.2	93	US-09-543-681A-5443	Sequence 5443, Ap
4	208	44.2	107	US-09-489-039A-11962	Sequence 11962, A
5	177	37.6	110	US-09-540-236-2859	Sequence 2859, Ap
6	71.5	15.2	387	US-09-252-991A-31074	Sequence 31074, A
7	69	14.6	1263	US-09-446-504-6	Sequence 6, Appli
8	69	14.6	1263	US-09-712-266-6	Sequence 6, Appli
9	68	14.6	1263	US-09-091-889A-4	Sequence 4, Appli
10	68	14.4	569	US-09-543-681A-6977	Sequence 6977, Ap
11	67	14.2	320	US-09-716-128-77	Sequence 77, Appl
12	67	14.2	353	US-09-716-129-169	Sequence 169, App
13	67	14.2	915	US-08-487-890A-96	Sequence 96, Appl
14	67	14.2	915	US-08-363-124A-2	Sequence 2, Appli
15	67	14.2	915	US-08-478-435-96	Sequence 96, Appl
16	67	14.2	915	US-08-337-483-96	Sequence 96, Appl
17	67	14.2	915	US-08-478-373-96	Sequence 96, Appl
18	67	14.2	915	US-08-474-671-96	Sequence 96, Appl
19	67	14.2	915	US-08-483-577A-96	Sequence 96, Appl
20	67	14.2	915	US-08-613-009A-18	Sequence 18, Appl
21	67	14.2	915	US-08-897-438-96	Sequence 96, Appl
22	67	14.2	915	US-08-637-654-96	Sequence 96, Appl
23	67	14.2	915	US-08-640-518-96	Sequence 96, Appl
24	67	14.2	915	US-08-778-570B-24	Sequence 24, Appl
25	67	14.2	915	US-09-059-584-24	Sequence 24, Appl
26	67	14.2	917	US-08-753-750B-11	Sequence 11, Appl
27	64.5	13.7	225	US-10-104-047-3107	Sequence 3107, Ap

ALIGNMENTS

RESULT 1
US-09-252-991A-23355
Sequence 23355, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23355
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23355

Query Match	51.4%;	Score 242;	DB 2;	Length 122;
Best Local Similarity	51.7%;	Pred. No. 2.6e-24;		
Matches 45;	Conservative 13;	Mismatches 29;	Indels 0;	Gaps 0;

QY 1 MSRWVCCVTLGHEHEGIDRRPPFGAAGARLYQESYSEKMWGMLKHQTHMLINERLSPID 60
DB 33 MSRTVTRCKRKHTEELPGIDRRPPFGAKEDLYNNVSRKAMDEMQRHQTMLINERKLNNMNA 92
QY 61 KSRTFLEKQEAAYFFGDAQSPGCTVP 87
DB 93 EDRKFTLOEDMKFLSGEDYAKADGYVP 119

RESULT 2

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US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Query Match	47.9%;	Score 225.5;	DB 2;	Length 92;
Best Local Similarity	50.0%;	Pred. No. 2.8e-22;		
Matches 44;	Conservative 14;	Mismatches 29;	Indels 1;	Gaps 1;

QY 1 MSRWVCCYGLGHEALBGLDRPPYBGLAKARIYQESKEANOGMLKQHMILNFRSLPID 6
 Db 4 MSROVFCCKYKQKEMBGDLDPAPFGAQQGQFFENSVKQAMQSMLOHQTLLINRKLNVFEB 63
 QY 61 KSRTPLEKQMEAYFFGD-GAQSPEGVYP 87
 Db 64 EAKKFLBEOREKFPNUNDSVKAAGMP 91

RESULT 3

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US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
;
; LENGTH: 93
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; TYPE: PRT
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; ORGANISM: Proteus mirabilis
; US-09-543-681A-5443

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Query Match	44.2%;	Score 208;	DB 2;	Length 93;
Best Local Similarity	47.1%;	Pred. No. 6.2e-20;		
Matches 41; Conservative	13;	Mismatches 33;	Indels 0;	Gaps 0

[illegible]

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DB	64	DDRKLLEQEMVRFLFEGHDVHIDGYTP	90

RESULT 4

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US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
;
; LENGTH: 107
;
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Query Match 44.2%; Score 208; DB 2; Length 107;
Best Local Similarity 49.4%; Pred. No. 7.5e-20;
Matches 43; Conservative 10; Mismatches 34; Indels 0; Gaps 0;

QY 1 MSRRNVGVKLGHEAREGLDNPYPFGALGARIYQVDSKRAMQSMKLTQHTLINERYSLPID 60
Db 17 MSRTIFCTPLQRRADGGDFQLYFGEISGSKIIYNISIKAWAQMOKHTMLINERKLSMNP 76
QY 61 KSRITFLKQMEAYFFGDGAQSPBGYP 87
Db 77 EHRRILQENMVQFLFEGKVNIIEGYR 103

RESULT 5

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US-09-540-236-8859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2859

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QY 4 MVOCVKLGHEAGLDPRPYGALGARLYOEVSKEAMQGMKHOHMLINERYLSPIDPKXR 63
DB 24 MVRKRKTQQNLPKLNNPPFPNAGOGELDPTISAKANNAMLLETQMILINEKHLSMIDPQAK 83
QY 64 TFELEOMEAYFFPGDGAOSPEGYVP 87
DB 84 KYLINREBKFLINDNGYEKKYPAGYKP 107

RESULT

US-09-252-991A-31074
; Sequence 31074, Application US/09252991A

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: March 1, 2006, 00:44:45 ; Search time 56.5 Seconds
(without alignments)
643.383 Million cell updates/sec

Title: US-09-955-502a-43

Perfect score: 471

Sequence: 1 MSRWQCVKLGHEAEGLDLP.....KQMEAYVFGDAQSPGEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	294	62.4	88	3	US-09-955-502-26
5	294	62.4	88	3	US-09-955-502-27
6	294	62.4	88	3	US-09-955-502-28
7	291	61.8	87	3	US-09-955-502-32
8	286	60.7	88	3	US-09-955-502-33
9	275	58.4	87	3	US-09-955-502-2
10	275	58.4	87	3	US-09-955-502-3
11	257.5	54.7	86	3	US-09-955-502-4
12	242	51.4	87	3	US-09-955-502-25
13	237	50.3	87	3	US-09-955-502-24
14	219	46.5	90	3	US-09-955-502-23
15	215	45.6	89	3	US-09-955-502-22
16	213	45.2	88	3	US-09-955-502-9
17	211	44.8	87	3	US-09-955-502-8
18	208	44.2	91	3	US-09-955-502-5
19	204	43.3	90	3	US-09-955-502-10
20	202	42.9	87	3	US-09-955-502-7
21	200	42.5	87	3	US-09-955-502-6
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23	200	42.5	91	3	US-09-955-502-12
24	200	42.5	91	3	US-09-955-502-13
25	197	41.8	88	3	US-09-955-502-15
26	197	41.8	91	3	US-09-955-502-14
27	197	41.8	91	3	US-09-955-502-16

28	197.	41.8	91	3	US-09-955-502-17	Sequence 17, Appl
29	196	41.6	78	3	US-09-955-502-19	Sequence 18, Appl
30	190	40.3	91	3	US-09-955-502-18	Sequence 19, Appl
31	186	39.5	90	3	US-09-955-502-20	Sequence 20, Appl
32	166	35.2	76	3	US-09-955-502-21	Sequence 21, Appl
33	78	16.6	289	4	US-10-437-963-109722	Sequence 109722,
34	72.5	15.4	2285	6	US-11-097-143-15963	Sequence 15963, A
35	71	15.1	523	3	US-09-815-243-10987	Sequence 10987, A
36	71	15.1	523	4	US-10-282-122A-58107	Sequence 58107, A
37	71	15.1	568	4	US-10-369-493-5205	Sequence 5205, Ap
38	69	14.6	1263	3	US-09-971-309-6	Sequence 6, Appl
39	68.5	14.5	249	4	US-10-369-493-17326	Sequence 17326, A
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42	67.5	14.3	1159	4	US-10-437-963-129387	Sequence 129387,
43	67	14.2	319	4	US-10-632-983-77	Sequence 77, Appl
44	67	14.2	319	5	US-10-472-533-317	Sequence 317, App
45	67	14.2	353	4	US-10-632-983-169	Sequence 169, App
46	67	14.2	561	4	US-10-094-749-2371	Sequence 2371, Ap
47	67	14.2	907	4	US-10-467-534-82	Sequence 82, Appl
48	67	14.2	915	3	US-09-332-226-2	Sequence 2, Appl
49	67	14.2	915	3	US-10-043-344-96	Sequence 96, Appl
50	67	14.2	950	3	US-09-815-243-11271	Sequence 11271, A
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53	66.5	14.1	126	4	US-10-437-963-172448	Sequence 172448,
54	66.5	14.1	356	4	US-10-437-963-129348	Sequence 129348,
55	66.5	14.1	972	6	US-11-097-143-37266	Sequence 37266, A
56	66.5	14.1	1125	4	US-10-437-963-129383	Sequence 129383,
57	66.5	14.1	1278	4	US-10-437-963-181016	Sequence 181016,
58	66.5	14.1	1389	4	US-10-437-963-181030	Sequence 181030,
59	65.5	13.9	186	5	US-10-481-032A-214	Sequence 214, App
60	65.5	13.9	186	5	US-10-481-032A-228	Sequence 228, App
61	65.5	13.9	198	5	US-10-450-763-53459	Sequence 53459, A
62	65.5	13.9	523	4	US-10-282-122A-66959	Sequence 66959, A
63	65.5	13.9	870	4	US-10-437-963-154457	Sequence 154457,
64	65.5	13.9	1479	4	US-10-437-963-181010	Sequence 181010,
65	65	13.8	683	4	US-10-156-761-9254	Sequence 9254, Ap
66	64.5	13.7	221	4	US-10-424-599-148972	Sequence 148972,
67	64.5	13.7	225	4	US-10-104-047-3107	Sequence 3107, Ap
68	64.5	13.7	289	4	US-10-767-701-42005	Sequence 42005, A
69	64.5	13.7	328	3	US-09-867-550-1052	Sequence 1052, Ap
70	64.5	13.7	501	4	US-10-181-108-14	Sequence 14, Appl
71	64.5	13.7	501	6	US-11-079-743-14	Sequence 69, Appl
72	64.5	13.7	502	3	US-09-739-254-69	Sequence 69, Appl
73	64.5	13.7	502	3	US-09-904-615-69	Sequence 69, Appl
74	64.5	13.7	502	4	US-10-054-988-69	Sequence 69, Appl
75	64.5	13.7	575	4	US-10-425-115-234031	Sequence 234031,

ALIGNMENTS

RESULT 1
US-09-955-502-31
Sequence 31, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 87
TYPE: PRT
ORGANISM: Thiobacillus ferrooxidans

US-09-955-502-31

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Best Local Similarity 100.0%; Pred. No. 8.6e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSRWQCVKLGHEABGLDRPPYPGALGARITYOVSKEAMQGMKQHTMLINERYLSPIDP 60

Qy 61 KSRTFLEKQMEAYFFGDGAQSPGEGYVP 87
Db 61 KSRTFLEKQMEAYFFGDGAQSPGEGYVP 87

RESULT 2

US-09-955-502-29

/ Sequence 29, Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ FILE REFERENCE: 960296.97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ PRIOR FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 29
/ LENGTH: 87
/ TYPE: PRT
/ ORGANISM: Burkholderia mallei

US-09-955-502-29

Query Match 65.8%; Score 310; DB 3; Length 87;
Best Local Similarity 64.4%; Pred. No. 5.3e-30;
Matches 56; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

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Db 1 MARWTHCAKLGKEABGLDRPPYPGALGARITYOVSKEAMQGMKQHTMLINERYLSPIDP 60

Qy 61 KSRTFLEKQMEAYFFGDGAQSPGEGYVP 87
Db 61 RARQYLMQTEKCYFFGEGADQASGYVP 87

RESULT 3

US-09-955-502-30

/ Sequence 30, Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ FILE REFERENCE: 960296.97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ PRIOR FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 30
/ LENGTH: 87
/ TYPE: PRT
/ ORGANISM: Burkholderia pseudomallei

US-09-955-502-30

Query Match 65.8%; Score 310; DB 3; Length 87;

Best Local Similarity 64.4%; Pred. No. 5.3e-30;
Matches 56; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MSRWQCVKLGHEABGLDRPPYPGALGARITYOVSKEAMQGMKQHTMLINERYLSPIDP 60
Db 1 MARWTHCAKLGKEABGLDRPPYPGALGARITYOVSKEAMQGMKQHTMLINERYLSPIDP 60

Qy 61 KSRTFLEKQMEAYFFGDGAQSPGEGYVP 87
Db 61 RARQYLMQTEKCYFFGEGADQASGYVP 87

RESULT 4

US-09-955-502-26

/ Sequence 26, Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ FILE REFERENCE: 960296.97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ PRIOR FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae

US-09-955-502-26

Query Match 62.4%; Score 294; DB 3; Length 88;
Best Local Similarity 62.1%; Pred. No. 5e-28;
Matches 54; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MSRWQCVKLGHEABGLDRPPYPGALGARITYOVSKEAMQGMKQHTMLINERYLSPIDP 60
Db 1 MARWPCVKLKEABGLDRPPYPGALGARITYOVSKEAMQGMKQHTMLINERYLSPIDP 60

Qy 61 KSRTFLEKQMEAYFFGDGAQSPGEGYVP 87
Db 61 RAREYLAQMEQYFFGDGAQASGYVP 87

RESULT 5

US-09-955-502-27

/ Sequence 27, Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ FILE REFERENCE: 960296.97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ PRIOR FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Neisseria meningitidis B

US-09-955-502-27

Query Match 62.4%; Score 294; DB 3; Length 88;
Best Local Similarity 62.1%; Pred. No. 5e-28;
Matches 54; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: February 28, 2006, 23:40:14 ; Search time 18 Seconds
(without alignments)
370.025 Million cell updates/sec

Title: US-09-955-502A-43

Sequence: 1 MSRMVQCVLIGHEABGLDRP.....KQMEAYFGDGAQSPGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 318885 seqs, 76556838 residues

Total number of hits satisfying chosen parameters: 318885

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Pending Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	87	5	US-09-955-502A-31
2	471	100.0	87	5	US-09-955-502A-43
3	310	65.8	87	5	US-09-955-502A-29
4	310	65.8	87	5	US-09-955-502A-30
5	294	62.4	88	5	US-09-955-502A-26
6	294	62.4	88	5	US-09-955-502A-27
7	294	62.4	88	5	US-09-955-502A-28
8	294	62.4	88	5	US-09-955-502A-42
9	291	61.8	87	5	US-09-955-502A-32
10	286	60.7	88	5	US-09-955-502A-33
11	275	58.4	87	5	US-09-955-502A-2
12	275	58.4	87	5	US-09-955-502A-3
13	267	56.7	84	5	US-09-955-502A-44
14	257.5	54.7	86	5	US-09-955-502A-4
15	242	51.4	87	5	US-09-955-502A-25
16	242	51.4	87	5	US-09-955-502A-40
17	237	50.3	87	5	US-09-955-502A-24
18	237	50.3	87	5	US-09-955-502A-41
19	219	46.5	90	5	US-09-955-502A-23
20	215	45.6	89	5	US-09-955-502A-22
21	215	45.6	89	5	US-09-955-502A-45
22	213	45.2	88	5	US-09-955-502A-9
23	213	45.2	88	5	US-09-955-502A-39
24	211	44.8	87	5	US-09-955-502A-8
25	208	44.2	91	5	US-09-955-502A-5

26	204	43.3	90	5	US-09-955-502A-10	Sequence 10, Appl
27	202	42.9	87	5	US-09-955-502A-7	Sequence 7, Appl
28	202	42.9	87	5	US-09-955-502A-38	Sequence 38, Appl
29	200	42.5	87	5	US-09-955-502A-6	Sequence 6, Appl
30	200	42.5	91	5	US-09-955-502A-11	Sequence 11, Appl
31	200	42.5	91	5	US-09-955-502A-12	Sequence 12, Appl
32	200	42.5	91	5	US-09-955-502A-13	Sequence 13, Appl
33	200	42.5	91	5	US-09-955-502A-36	Sequence 36, Appl
34	197	41.8	91	5	US-09-955-502A-14	Sequence 14, Appl
35	197	41.8	91	5	US-09-955-502A-17	Sequence 17, Appl
36	197	41.8	91	5	US-09-955-502A-34	Sequence 34, Appl
37	197	41.8	91	5	US-09-955-502A-35	Sequence 35, Appl
38	196	41.6	91	5	US-09-955-502A-19	Sequence 19, Appl
39	190	40.3	88	5	US-09-955-502A-15	Sequence 15, Appl
40	190	40.3	91	5	US-09-955-502A-18	Sequence 18, Appl
41	190	40.3	91	5	US-09-955-502A-20	Sequence 20, Appl
42	186	39.5	90	5	US-09-955-502A-37	Sequence 37, Appl
43	186	39.5	90	5	US-09-955-502A-21	Sequence 21, Appl
44	166	35.2	76	5	US-09-955-502A-21	Sequence 21, Appl
45	78.5	16.7	825	1	PCT-US06-00964-4067	Sequence 4067, Ap
46	78.5	16.7	825	1	PCT-US06-00964-4526	Sequence 4526, Ap
47	78.5	16.7	825	7	US-11-330-403-4067	Sequence 4067, Ap
48	78.5	16.7	825	7	US-11-330-403-4526	Sequence 4526, Ap
49	78.5	16.7	826	1	PCT-US06-00964-9438	Sequence 9438, Ap
50	78.5	16.7	826	7	US-11-330-403-9438	Sequence 9438, Ap
51	67	14.2	319	7	US-11-346-470-973	Sequence 973, App
52	67	14.2	826	1	PCT-US06-00964-3081	Sequence 3081, Ap
53	67	14.2	826	7	US-11-330-403-3081	Sequence 3081, Ap
54	66.5	14.1	445	8	US-60-752-355-10338	Sequence 10338, A
55	66	14.0	387	6	US-10-461-673-14703	Sequence 14703, A
56	64.5	13.7	213	8	US-60-752-355-9611	Sequence 9611, Ap
57	64.5	13.7	328	6	US-10-461-673-11545	Sequence 11545, A
58	64.5	13.7	435	6	US-10-461-673-12437	Sequence 12437, A
59	64.5	13.7	435	6	US-10-461-673-12437	Sequence 12437, A
60	64.5	13.7	486	6	US-10-461-673-11544	Sequence 11544, A
61	64.5	13.7	501	7	US-11-342-366-1213	Sequence 1213, Ap
62	64.5	13.7	501	7	US-11-342-367-1213	Sequence 1213, Ap
63	64.5	13.7	501	7	US-60-751-420-2310	Sequence 2310, Ap
64	63.5	13.5	213	8	US-60-752-355-4453	Sequence 4453, Ap
65	63.5	13.5	213	8	US-60-752-355-26038	Sequence 26038, A
66	63.5	13.5	213	8	US-60-752-355-28542	Sequence 28542, A
67	63	13.4	863	6	US-10-953-349-3332	Sequence 3332, Ap
68	63	13.4	937	6	US-10-953-349-3331	Sequence 3331, Ap
69	63	13.4	942	6	US-10-953-349-3330	Sequence 3330, Ap
70	62.5	13.3	605	6	US-10-461-673-13961	Sequence 13961, A
71	62	13.2	418	8	US-60-752-355-20909	Sequence 20909, A
72	62	13.2	500	8	US-60-752-355-39106	Sequence 39106, A
73	62	13.2	513	8	US-60-742-219-1524	Sequence 1524, Ap
74	62	13.2	534	6	US-10-567-867-1108	Sequence 1108, Ap
75	62	13.2	634	8	US-60-752-355-32764	Sequence 32764, A

ALIGNMENTS

RESULT 1
US-09-955-502A-31
; Sequence 31, Application US/09955502A
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Grainick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296, 97559
; CURRENT APPLICATION NUMBER: US/09/955,502A
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Thiodacillus ferrooxidans
US-09-955-502A-31

Query Match	100.0%;	Score 471;	DB 5;	Length 87;
Best Local Similarity	100.0%;	Pred. No. 4e-47;		
Matches 87;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MSRWQCVKLGHEHSEGLDRPPYPGALGAR.YQGVSKSAWGMKQHTMLINERLSPIDP	60
Db	1	MSRWQCVKLGHEHSEGLDRPPYPGALGAR.YQGVSKSAWGMKQHTMLINERLSPIDP	60
Qy	61	KSRFTLEKOMEAAYFPDGASPSBSYVP	87
Db	61	KSRFTLEKOMEAAYFPDGASPSBSYVP	87

RESULT 2
US-09-955-502A-43
; Sequence 43, Application US/09955502A
; GENERAL INFORMATION.

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: APPLICANT: Downs, Diana M.
: APPLICANT: Gralnick, Jeff A.
: TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
: TITLE OF INVENTION: Oxygen-labile Proteins
: EMB REFERENCE: 960396, 97559
: CURRENT APPLICATION NUMBER: US/09/955,502A
: CURRENT FILING DATE: 2001-09-18
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 43
: LENGTH: 87
: TYPE: PR1
: ORGANISM: Thioabacillus ferrooxidans
: US-09-955-502A-43

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Query Match	100.0%;	Score 471;	DB 5;	Length 87;
Best Local Similarity	100.0%;	Pred. No. 4e-47;		
Matches 87;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	1	MSRWOCYKLGHEABEGDLPYPYFGALARIIOEVSKAMQGMXLHQTMLINERLSIDP	6
Dd	1	MSRWOCYKLGHEABEGDLPYPYFGALGRIIOEVSKEAMQGMXLHQTMLINERLSIDP	6
Oy	61	KSRTPLEKMEAYFPGDAGOSPEGYVP	87
Dd	61	KSRTPLEKMEAYFFGDAGOSPEGYVP	87

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RESULT 3
US-09-955-502A-29
; Sequence 29, Application US/09955502A
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 87
; TYPE: PRF
; ORGANISM: Burkholderia mallei
US-09-955-502A-29

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Query Match	65.8%;	Score 310;	DB 5;	Length 87;
Best Local Similarity	64.4%;	Pred. No. 1.4e-28;		
Matches	56;	Conservative	10;	Mismatches 21;
				Indels 0;
				Gaps 0;

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OY 1 MSRMVQCYLGHAEAGLDPRPPYPGALGARLYQZVSKEAWQWMLKHQTMLINBYRLSPIDP 600
      |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 MARMIHCAKLGKEAEGLDPRPPLPGELGKRLYVSVSQAWQDWMLKQQTMLINENRLNADPR 600

```

```
QY      61 KSRFTLEQM EAYFFGDQAQSPG YVP 87
        :: : | | | | | : | | |
Db      61 PARQYLKQT EKYPFEGEADQA SG YVP 87
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RESULT 4
US-09-955-502A-30
; Sequence 30, Application US/09955502A
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502A
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia pseudomallei
US-09-955-502A-30

```

Query Match	65.8%;	Score 310;	DB 5;	Length 87;
Best Local Similarity	64.4%;	Pred. No. 1.4e-28;		
Matches 56;	Conservative 10;	Mismatches 21;	Indels 0;	Gaps 0;

[illegible]

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RESULT 5
US-09-955-502A-26
; Sequence 26, Application US/09955502A
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502A
; CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 88
; TYPE: PR1
; ORGANISM: Neisseria gonorrhoeae
US-09-955-502A-26

```

Query Match	62.4%	Score 294	DB 5	Length 88
Best Local Similarity	62.1%	Pred. No. 1e-26		
Matches	54	Conservative	12	Mismatches 21; Indels 0; Gaps 0

QY	Db
1 MSRRVQCCAKLGHKEHGLDRLPPYPGALGARLYQGVSKAAQGMVKQTMTINSTRLLSPID	1 MARVVCYKLNKSRABGKKPPPLPNEGKTRFENVSGEAAWAATRHQTMTINENRLSLADP
61 KSRFTEKQMEAYFPFGDASPEGGYYP 87	61 KSRFTEKQMEAYFPFGDADAVQGYYP 87

RESULT 6
US-09-955-502A-27
; Sequence 27, Application US/09955502A
; GENERAL INFORMATION:

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:49:36 ; Search time 70.7241 Seconds
(without alignments)
521.856 Million cell updates/sec

Title: US-09-955-502A-44
Perfect score: 446
Sequence: 1 MSRVNCVXLKREAEGLDFP.....YLQOQMERFLPEDGVTEAQS 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2000s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	436	97.8	86	5	ABB78149 Amino aci
2	436	97.8	87	5	ABB78148 Amino aci
3	436	97.8	87	5	ABB78147 Amino aci
4	278	62.3	87	5	ABB78175 Amino aci
5	272	61.0	87	5	ABB78174 Amino aci
6	267	59.9	87	5	ABB78176 Amino aci
7	265	59.4	88	5	ABB78171 Amino aci
8	265	59.4	88	5	ABB78172 Amino aci
9	265	59.4	88	5	ABB78173 Amino aci
10	265	59.4	88	6	ABB77219 N. gonorr
11	252	56.5	87	5	ABB78150 Amino aci
12	242	54.3	91	5	ABB78150 Amino aci
13	238	53.4	88	5	ABB78154 Amino aci
14	237	53.1	91	5	ABB78158 Amino aci
15	237	53.1	91	5	ABB78157 Amino aci
16	237	53.1	91	5	ABB78156 Amino aci
17	235	52.7	89	9	ABB78156 Amino aci
18	235	52.7	89	9	ABB78156 Amino aci
19	234	52.5	87	5	ABB78152 Amino aci
20	231	51.8	88	5	ABB78150 Amino aci
21	231	51.8	90	5	ABB78155 Amino aci
22	231	51.8	91	5	ABB78161 Amino aci
23	231	51.8	91	5	ABB78159 Amino aci
24	231	51.8	91	5	ABB78162 Amino aci

ALIGNMENTS

25	231	51.8	91	5	ABB78163 Amino aci
26	229	51.3	87	5	ABB78151 Amino aci
27	228	51.1	93	7	ADP05158 Bacterial
28	225	50.4	107	7	ABO65445 Klebsiell
29	221	49.6	87	5	ABB78153 Amino aci
30	220.5	49.4	92	6	ADA34169 Amino aci
31	218	48.9	78	5	ABB78164 Amino aci
32	218	48.9	87	5	ABB78170 Amino aci
33	218	48.9	122	7	ABO74609 Pseudomon
34	216	48.4	88	5	ABB78178 Amino aci
35	208	46.6	90	5	ABB78165 Amino aci
36	200	44.8	87	5	ABB78169 Amino aci
37	197.5	44.3	90	5	ABB78167 Amino aci
38	196	43.9	76	5	ABB78166 Amino aci
39	196	43.9	90	5	ABB78168 Amino aci
40	153.5	34.4	110	8	ADL05173 Amino aci
41	72.5	16.3	303	9	ABM94402 Amino aci
42	71	15.9	527	6	ADB06106 Amino aci
43	71	15.9	528	6	ADB06108 Amino aci
44	70.5	15.8	308	6	ABM70179 Amino aci
45	69.5	15.6	749	5	ABB54524 Amino aci
46	69.5	15.6	1233	8	ADQ66727 Novel hum
47	69	15.5	124	9	ADX40209 Amino aci
48	67	15.0	381	5	AAO20498 Amino aci
49	67	15.0	389	4	AAO20498 Amino aci
50	66.5	14.9	664	4	ABU40908 Amino aci
51	66.5	14.9	665	7	ADP05593 Amino aci
52	66.5	14.9	680	6	ABU49707 Amino aci
53	66	14.8	229	3	AAAB1703 Amino aci
54	66	14.8	341	9	ABE40319 Amino aci
55	66	14.8	341	9	ABE36958 Amino aci
56	66	14.8	503	2	AAWB5085 Amino aci
57	66	14.8	726	7	ABO62233 Klebsiell
58	66	14.8	856	6	ABR39820 Amino aci
59	65.5	14.7	529	5	AAE26857 Amino aci
60	65.5	14.7	533	8	AAV57085 Amino aci
61	65.5	14.7	563	8	ADG12800 Amino aci
62	65.5	14.7	2291	4	ABB61876 Amino aci
63	65	14.6	124	9	ADX40214 Amino aci
64	64.5	14.5	207	6	ABM73508 Amino aci
65	64.5	14.5	207	9	ADV16859 Amino aci
66	64.5	14.5	207	9	ADW94758 Amino aci
67	64.5	14.5	503	2	AAW24140 Amino aci
68	64.5	14.5	702	8	ADR86184 Amino aci
69	64.5	14.5	1240	6	ABU29661 Amino aci
70	64.5	14.5	1242	7	ADC95614 Amino aci
71	64.5	14.5	3346	9	ABE22178 Amino aci
72	64	14.3	117	9	ADX40159 Amino aci
73	64	14.3	244	3	AAAB42492 Amino aci
74	64	14.3	272	4	AAAB36605 Amino aci
75	64	14.3	373	4	AAAB95352 Amino aci

RESULT 1
ID ABB78149 standard; protein; 86 AA.
XX ABB78149;
XX

05-NOV-2002 (first entry)

Amino acid sequence of a YggX homologue.

Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.

Bordetella bronchiseptica.

US2002072118-A1.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: February 28, 2006, 20:27:00 ; Search time 10.3793 Seconds

(without alignments)
778.685 Million cell updates/sec

Title: US-09-955-502a-44

Perfect score: 446
Sequence: 1 MSRLVNCVKLRRAKGLDFP.....YLGQOMERFLFEDGTVEAOG 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*

1: pirl:.*
2: pirl:.*
3: pirl:.*
4: pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	265	59.4	88	2	AB1014
2	237	53.1	91	2	AB5954
3	237	53.1	91	2	AB5082
4	237	53.1	91	2	F91108
5	234	52.5	90	2	C64013
6	231	51.8	90	2	C82320
7	231	51.8	91	2	AH0879
8	218	48.9	90	2	H83003
9	208	46.6	90	2	A10116
10	205	46.0	105	2	C82624
11	196	43.9	93	2	B84994
12	196	43.9	749	2	B86774
13	69.5	15.6	134	2	T37027
14	69	15.5	134	2	S19999
15	69	15.5	241	2	A52501
16	67.5	15.1	855	2	A45713
17	67	15.0	389	2	T14751
18	66.5	14.9	1177	2	AD0438
19	66.5	14.9	1177	2	AD0438
20	65.5	14.7	412	2	B59796
21	65.5	14.7	2291	1	A46147
22	65	14.6	110	2	S70211
23	65	14.6	506	2	T50211
24	65	14.6	1068	2	B73091
25	64.5	14.5	207	2	B89952
26	64.5	14.5	622	2	T38804
27	64.5	14.5	931	2	C90891
28	64.5	14.5	931	2	F85726
29	64.5	14.5	1883	2	G82875

30	64	14.3	133	2	G75385
31	63.5	14.2	393	2	T49257
32	63.5	14.2	531	2	S75607
33	63.5	14.2	714	2	S77385
34	63.5	14.2	931	2	A64903
35	63	14.1	228	2	C26599
36	63	14.1	229	1	B31775
37	63	14.1	238	1	LRR782
38	63	14.1	320	2	B11879
39	63	14.1	372	2	B81952
40	63	14.1	904	2	S45673
41	63	14.1	1966	2	T32552
42	63	14.1	2848	2	T32550
43	62.5	14.0	272	2	G96930
44	62.5	14.0	332	2	D86295
45	62.5	14.0	664	2	AG0113
46	62.5	14.0	897	2	G02529
47	62	13.9	107	2	AG1878
48	62	13.9	865	2	B44718
49	62	13.9	989	2	T46183
50	61.5	13.8	164	2	E75293
51	61.5	13.8	396	2	H84383
52	61.5	13.8	522	1	ISB15S
53	61.5	13.8	667	1	A48650
54	61.5	13.8	667	2	G91044
55	61.5	13.8	667	2	B85889
56	61.5	13.8	877	2	T03098
57	61.5	13.8	1069	2	AB1050
58	61.5	13.8	1464	2	T07050
59	61.5	13.8	2774	2	A43359
60	61.5	13.8	4644	1	A38905
61	61	13.7	143	2	D70003
62	61	13.7	260	2	AH1639
63	61	13.7	321	2	T02754
64	61	13.7	323	2	U70755
65	61	13.7	337	2	A66184
66	61	13.7	337	2	AG2423
67	61	13.7	416	2	CA7017
68	61	13.7	416	2	AF2017
69	61	13.7	431	2	T32694
70	61	13.7	439	2	A36911
71	61	13.7	567	2	B84504
72	60.5	13.6	348	2	D85212
73	60.5	13.6	388	2	T38810
74	60.5	13.6	509	2	T01344
75	60.5	13.6	713	2	S56833

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [Imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: H81014, F81958
R:Retelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, R.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizsa, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:2015755; PMID:10710307
A:Accession: H81014
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-88 <TET>
A:Cross-references: UNIPARC:UP100000C4E7F; GB:AB02552; GB:AB02098; NID:G7227279; PIDN:
A:Experimental source: serogroup B, strain MC58
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jorgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:00:23 ; Search time 63.4828 Seconds
(without alignments)
933.551 Million cell updates/sec

Title: US-09-955-502A-44

Perfect score: 446
Sequence: 1 MSRIWCVKLRKRAEGLDP.....YLQOMERFLPBDGTVEAG 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	436	97.8	90	1	FETP_BORBR
2	436	97.8	90	1	FETP_BORBP
3	436	97.8	90	1	FETP_BORBP
4	291	65.2	91	1	FETP_RALSO
5	282	63.2	91	2	QAL819_9BURK
6	278	62.3	91	1	FETP_BURMA
7	276	61.9	90	1	FETP_CHRVO
8	265	59.4	88	1	FETP_NBRGI
9	265	59.4	88	1	FETP_NBRMA
10	265	59.4	88	1	FETP_NBRMA
11	265	59.4	88	1	FETP_NBRMA
12	262	58.7	90	1	FETP_NBRMA
13	252	56.5	90	1	FETP_NBRMA
14	238	53.4	92	1	FETP_SHEON
15	237	53.1	90	1	FETP_SHEON
16	236	52.9	90	1	FETP_VIBPA
17	235	52.7	89	1	FETP_IDILO
18	235	52.7	89	1	FETP_LBSPA
19	235	52.7	89	1	FETP_LBSPA
20	234	52.5	89	1	FETP_MANSN
21	234	52.5	89	1	FETP_MANSN
22	234	52.5	89	1	FETP_MANSN
23	234	52.5	89	1	FETP_MANSN
24	232	52.0	90	1	FETP_ECOS7
25	232	52.0	90	1	FETP_ECOS7
26	232	52.0	90	1	FETP_ECOS7
27	232	52.0	90	1	FETP_ECOS7
28	232	52.0	90	1	FETP_ECOS7
29	232	52.0	90	1	FETP_ECOS7
30	232	52.0	90	1	FETP_ECOS7
31	231	51.8	90	1	FETP_ECOS7

32	230	51.6	91	1	FETP_XANNC	O6p17 xanthomonas
33	229	51.3	90	1	FETP_PASNU	O6c19 pasteurella
34	229	51.3	90	1	FETP_PHOBR	O6lmt1 photobacter
35	226	50.7	90	1	FETP_SALCH	O57k4 salmonella
36	226	50.7	90	1	FETP_SALCH	O5pm1 salmonella
37	226	50.7	90	1	FETP_SALTI	P67618 salmonella
38	226	50.7	90	1	FETP_SALTI	P67618 salmonella
39	224	50.2	90	2	Q4J228_AZOV1	P67617 salmonella
40	224	50.2	92	1	FETP_XANOR	O4J228 azotobacter
41	221.5	49.7	90	1	FETP_AC1AD	O5gy22 xanthomonas
42	221	49.6	90	1	FETP_ERMCT	O6tfb3 acinetobact
43	221	49.6	92	1	FETP_XANCP	O6g8j9 erwinia car
44	221	49.6	92	2	Q4UW14_XANCP	O6p829 xanthomonas
45	221	49.6	94	1	FETP_HARDU	Q4UW14 xanthomonas
46	218	48.9	90	1	FETP_PSBAB	O7vkb6 haemophilus
47	216	48.4	78	1	FETP_BUCAP	O8n936 pseudomonas
48	216	48.4	90	1	FETP_COXBU	O8k925 buchiera ap
49	216	48.4	90	1	FETP_YERPS	O83d06 coxiella bu
50	212	47.5	90	1	FETP_XYLPT	O66m1 yersteinia ps
51	209	46.9	79	1	FETP_CANBP	O87d06 xyloella fas
52	208	46.6	90	1	FETP_YERPE	O7vrg9 candidatus
53	205	46.0	90	1	FETP_XYLPA	O8zhet yeastina pe
54	200	44.8	90	1	FETP_PSEPK	O8pc73 xyloella fas
55	196	43.9	77	1	FETP_BUCAI	O8r419 pseudomonas
56	196	43.9	90	1	FETP_PSESM	P57618 buchiera ap
57	196	43.9	90	2	Q4ZL63_PSESY	O87u15 pseudomonas
58	192	43.0	90	2	O6T76_PSESY	O421b3 pseudomonas
59	192	43.0	90	2	Q4KJ22_PSEPS	O67f6 pseudomonas
60	189	42.4	78	1	FETP_WIGBR	O4k122 pseudomonas
61	185	41.5	92	1	Q4NMQ4_9DELT	O8d35 wigleswort
62	177	39.7	87	1	FETP_FRATT	Q4NMQ4 anaeromyxob
63	162	36.3	96	2	Q4FV77_9GAMM	O5h18 francisella
64	153	34.3	87	1	FETP_BUCBP	O4fv77 psychrobact
65	79.5	17.8	116	2	O6UF77_9HIV1	O89a44 buchiera ap
66	77	17.3	330	2	Q5DA35_SCHUA	O6uf77 human immun
67	76.5	17.2	766	2	Q4IC45_GIBZE	O5da35 echistocoma
68	76.5	17.2	2410	2	Q5A249_EBENI	O4ic45 gibberella
69	75.5	16.9	116	2	O6MS71_9HIV1	O5a249 aspergillus
70	75.5	16.9	116	2	O596M7_9HIV1	O6ms71 human immun
71	73	16.4	509	2	O5ESM1_VIBB1	O596m7 human immun
72	71	15.9	2322	2	O6UDM6_PLARA	O5esm1 vibrio fisc
73	70.5	15.8	272	2	O8KAR9_CHLRE	O6udm6 plasmodium
74	70.5	15.8	307	2	O7N770_PHOHL	O8kar9 chlorobium
75	70.5	15.8	663	2	O87GV4_VIBPA	O7n770 photorhabdu

ALIGNMENTS

RESULT 1
FETP_BORBR
ID FETP_BORBR STANDARD; PRT; 90 AA.
AC Q7WH06;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocName=BB3405;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RB50 / ATCC BAA-568;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,

RA Rabbittowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmons M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: BX640447; CAB3897.1; -; Genomic_DNA.
DR HAMAP: MF_00686; -; 1.
DR InterPro: IPR007457; YggX.
DR Pfam: PF04362; DUF495; 1.
DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR PRODOM: PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 97.8%; Score 436; DB 1; Length 90;
Best Local Similarity 98.8%; Pred. No. 9.3e-39;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSRIYVCVKLRKRAEGLDPPYPGELGTRIWQISKEAMBEWKQIOTRLVNERLNLPADA 60
DB 1 MSRIYVCVKLRKRAEGLDPPYPGELGTRIWQISKEAMBEWKQIOTRLVNERLNLPADA 60

QY 61 RARKYLQOQMERFLFEDGTVEAOG 84
DB 61 RARKYLQOQMERFLFEDGTVEAOG 84

RESULT 2
FETP BORPE STANDARD; PRT; 90 AA.
ID FETP BORPE
AC Q7W9Q2;
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BP21703;
OS *Bordetella parapertussis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; *Bordetella*.
CX NCBI_TaxID=519;

RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabbittowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmons M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: BX640428; CAB37004.1; -; Genomic_DNA.
DR HAMAP: MF_00686; -; 1.
DR InterPro: IPR007457; YggX.
DR Pfam: PF04362; DUF495; 1.
DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR PRODOM: PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 97.8%; Score 436; DB 1; Length 90;
Best Local Similarity 98.8%; Pred. No. 9.3e-39;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSRIYVCVKLRKRAEGLDPPYPGELGTRIWQISKEAMBEWKQIOTRLVNERLNLPADA 60
DB 1 MSRIYVCVKLRKRAEGLDPPYPGELGTRIWQISKEAMBEWKQIOTRLVNERLNLPADA 60

QY 61 RARKYLQOQMERFLFEDGTVEAOG 84
DB 61 RARKYLQOQMERFLFEDGTVEAOG 84

RESULT 3
FETP BORPE STANDARD; PRT; 90 AA.
ID FETP BORPE
AC Q7W9Q2;
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BP2336;
OS *Bordetella pertussis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; *Bordetella*.
CX NCBI_TaxID=520;

RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA STRAIN=Tohama 1 / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabbittowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmons M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: BX640418; CAB42609.1; -; Genomic_DNA.
DR HAMAP: MF_00686; -; 1.
DR InterPro: IPR007457; YggX.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:30:02 ; Search time 18.5862 Seconds
(Without alignments)
373.651 Million cell updates/sec

Title: US-09-955-502a-44
Perfect score: 446
Sequence: 1 MSRIIVNCVTKRKRAEGLDFP.....YIQQOMERFLPEDGTVEAQQ 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/prodata/1/1aa/7 COMB.pep:*
4: /cgn2_6/prodata/1/1aa/8 COMB.pep:*
5: /cgn2_6/prodata/1/1aa/9 COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	228	51.1	93	US-09-543-681A-5443	Sequence 5443, Ap
2	225	50.4	107	US-09-489-039A-11962	Sequence 11962, A
3	220.5	49.4	92	US-09-328-352-5456	Sequence 5456, Ap
4	218	48.9	122	US-09-252-991A-23355	Sequence 23355, A
5	153.5	34.4	110	US-09-540-236-2859	Sequence 2859, Ap
6	72.5	16.3	303	US-09-902-540-13601	Sequence 13601, A
7	67	15.0	381	US-09-949-016-9788	Sequence 9788, Ap
8	67	15.0	381	US-09-964-899-13	Sequence 13, Appl
9	66.5	14.9	665	US-09-543-681A-5878	Sequence 5878, Ap
10	66	14.8	503	US-09-058-260-26	Sequence 26, Appl
11	66	14.8	726	US-09-489-039A-8750	Sequence 8750, Ap
12	64.5	14.5	1242	US-09-107-532A-5241	Sequence 5241, Ap
13	64	14.3	1493	US-09-713-273A-20	Sequence 20, Appl
14	63.5	14.2	200	US-09-710-279-1186	Sequence 1186, Ap
15	63.5	14.2	200	US-09-710-279-2390	Sequence 2390, Ap
16	63.5	14.2	208	US-09-134-001C-3785	Sequence 3785, Ap
17	63.5	14.2	498	US-09-058-260-16	Sequence 16, Appl
18	63.5	14.2	503	US-08-781-802-2	Sequence 2, Appl
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21	63.5	14.2	503	US-08-694-078-2	Sequence 2, Appl
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25	63.5	14.2	503	US-09-058-260-28	Sequence 28, Appl
26	63.5	14.2	503	US-09-058-260-30	Sequence 30, Appl
27	63.5	14.2	666	US-09-270-767-62249	Sequence 62249, A

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29	63	14.1	581	US-09-713-273A-12	Sequence 12, Appl
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32	62	13.9	979	US-09-543-681A-5466	Sequence 5466, Ap
33	61.5	13.8	478	US-10-000-489-108	Sequence 108, Ap
34	61.5	13.8	504	US-08-441-139-18	Sequence 18, Appl
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36	61.5	13.8	518	US-09-746-390-4	Sequence 4, Appl
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55	59.5	13.3	447	US-09-902-540-13195	Sequence 13195, A
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65	58.5	13.1	318	US-10-213-452A-12	Sequence 12, Appl
66	58.5	13.1	436	US-09-107-532A-5135	Sequence 5135, Ap
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ALIGNMENTS

RESULT 1
US-09-543-681A-5443
Sequence 5443, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543, 681A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5443
LENGTH: 93
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5443

GenCore version 5.1.7
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Run on: March 1, 2006, 00:44:45 ; Search time 54.5517 Seconds
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Title: US-09-955-502a-44

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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	278	62.3	87	3	US-09-955-502-30
6	267	59.9	88	3	US-09-955-502-31
7	265	59.4	88	3	US-09-955-502-26
8	265	59.4	88	3	US-09-955-502-27
9	265	59.4	88	3	US-09-955-502-28
10	252	56.5	87	3	US-09-955-502-32
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12	238	53.4	88	3	US-09-955-502-9
13	237	53.1	91	3	US-09-955-502-11
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15	237	53.1	91	3	US-09-955-502-13
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17	231	51.8	88	3	US-09-955-502-15
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21	231	51.8	91	3	US-09-955-502-17
22	229	51.3	87	3	US-09-955-502-18
23	229	51.3	87	3	US-09-955-502-6
24	221	49.6	87	3	US-09-955-502-8
25	218	48.9	78	3	US-09-955-502-19
26	218	48.9	87	3	US-09-955-502-25
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31	196	43.9	76	3	US-09-955-502-21	Sequence 21, Appl
32	196	43.9	90	3	US-09-955-502-23	Sequence 23, Appl
33	196	43.9	90	3	US-09-955-502-23	Sequence 23, Appl
34	171	41.5	527	5	US-10-501-282-46	Sequence 189670,
35	171	41.5	528	5	US-10-501-282-48	Sequence 46, Appl
36	169	41.5	826	4	US-10-437-963-189868	Sequence 189868,
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45	168	41.5	1748	4	US-10-437-963-158726	Sequence 158726,
46	167	41.5	373	4	US-10-437-963-107538	Sequence 107538,
47	167	41.5	381	3	US-09-964-899-13	Sequence 13, Appl
48	167	41.5	381	5	US-10-975-523-13	Sequence 13, Appl
49	167	41.5	837	4	US-10-437-963-189921	Sequence 189921,
50	167	41.5	901	4	US-10-437-963-189632	Sequence 189632,
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52	166.5	14.9	664	4	US-10-282-122A-68832	Sequence 68832, A
53	166.5	14.9	680	4	US-10-282-122A-77631	Sequence 77631, A
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64	165.5	14.7	563	5	US-10-788-197-23	Sequence 23, Appl
65	165.5	14.7	563	5	US-10-754-473-23	Sequence 23, Appl
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67	165.5	14.7	2291	6	US-11-097-143-12420	Sequence 12420, A
68	165	14.6	319	5	US-10-732-923-10012	Sequence 10012, A
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75	164.5	14.5	752	4	US-10-437-963-159713	Sequence 159713,

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US-09-955-502-4
Sequence 4, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 86
TYPE: PRT
ORGANISM: Bordetella bronchiseptica

US-09-955-502-4

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Best Local Similarity 98.8%; Pred. No. 4.3e-43;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 RARKYLOQOMERFLFEDGTVEAOG 84
DB 61 RARKYLOQOMERFLFEDGTVEAOG 84

RESULT 2

US-09-955-502-2
Sequence 2, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2
LENGTH: 87
TYPE: PRT
ORGANISM: Bordetella pertussis
US-09-955-502-2

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Best Local Similarity 98.8%; Pred. No. 4.3e-43;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 RARKYLOQOMERFLFEDGTVEAOG 84
DB 61 RARKYLOQOMERFLFEDGTVEAOG 84

RESULT 3

US-09-955-502-3
Sequence 3, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3
LENGTH: 87
TYPE: PRT
ORGANISM: Bordetella parapertussis
US-09-955-502-3

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Best Local Similarity 98.8%; Pred. No. 4.3e-43;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 RARKYLOQOMERFLFEDGTVEAOG 84
DB 61 RARKYLOQOMERFLFEDGTVEAOG 84

RESULT 4

US-09-955-502-29
Sequence 29, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 29
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia mallei
US-09-955-502-29

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Best Local Similarity 56.0%; Pred. No. 1.3e-24;
Matches 47; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

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QY 61 RARKYLOQOMERFLFEDGTVEAOG 84
DB 61 RARKYLOQOMERFLFEDGTVEAOG 84

RESULT 5

US-09-955-502-30
Sequence 30, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

Query Match 62.3%; Score 278; DB 3; Length 87;
Best Local Similarity 56.0%; Pred. No. 1.3e-24;
Matches 47; Conservative 20; Mismatches 17; Indels 0; Gaps 0;

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Title: US-09-955-502a-44

Perfect score: 446
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SUMMARIES

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6	63	14.1	384	7	US-11-098-686-10752
7	61.5	13.8	478	6	US-10-689-742-184
8	61.5	13.8	832	7	US-11-098-686-10182
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25	57	12.8	2504	6	US-10-647-956A-8

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48	56	12.6	833	7	US-11-242-730-1	Sequence 1, Appl
49	56	12.6	833	7	US-11-198-746-85	Sequence 85, Appl
50	55.5	12.4	1659	7	US-11-198-794-85	Sequence 85, Appl
51	55.5	12.4	3353	7	US-11-072-175-205	Sequence 205, App
52	55	12.3	212	7	US-11-037-243-64	Sequence 64, App
53	55	12.3	212	7	US-11-044-111-6	Sequence 6, Appl
54	55	12.3	212	7	US-11-044-111-26	Sequence 26, Appl
55	55	12.3	239	7	US-11-044-111-25	Sequence 25, Appl
56	55	12.3	240	7	US-11-044-111-9	Sequence 9, Appl
57	55	12.3	519	7	US-11-099-661-10	Sequence 10, Appl
58	55	12.3	828	6	US-10-501-039-2	Sequence 2, Appl
59	55	12.3	1056	7	US-11-044-111-22	Sequence 22, Appl
60	54.5	12.2	356	7	US-11-143-986-8	Sequence 8, Appl
61	54.5	12.2	356	7	US-11-143-986-9	Sequence 9, Appl
62	54	12.1	432	6	US-10-933-115-8	Sequence 8, Appl
63	54	12.1	432	7	US-11-056-354-4	Sequence 4, Appl
64	54	12.1	440	6	US-10-933-115-2	Sequence 2, Appl
65	54	12.1	784	6	US-10-517-939-324	Sequence 324, App
66	53.5	12.0	623	7	US-11-072-512-3378	Sequence 3378, App
67	53.5	12.0	662	7	US-11-072-175-184	Sequence 184, App
68	53.5	12.0	951	7	US-11-121-438-14	Sequence 14, Appl
69	53.5	12.0	2630	7	US-11-186-721-2	Sequence 2, Appl
70	53.5	12.0	7968	7	US-11-186-731-5	Sequence 5, Appl
71	53	11.9	53	7	US-11-120-308-74	Sequence 74, Appl
72	53	11.9	216	7	US-11-156-084-244	Sequence 244, App
73	53	11.9	216	7	US-11-156-084-322	Sequence 322, App
74	53	11.9	316	7	US-11-156-084-210	Sequence 210, App
75	53	11.9	316	7	US-11-156-084-280	Sequence 280, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan9, version 1.04

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RESULT 5
US-10-793-626-2390
/ Sequence 2390, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMBERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PUS480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2390

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:49:36 ; Search time 74.9339 Seconds
(without alignments)
521.856 Million cell updates/sec

Title: US-09-955-502a-45

Perfect score: 483

Sequence: 1 MORIFCEYRQDTEGIDPV.....LNKFLPERRVAKPEGYIEPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472.5	97.8	90	5	ABB78167 Amino aci
2	246	50.9	87	5	ABB78153 Amino aci
3	238	49.3	107	7	ABO65445 Klebsiell
4	237	49.1	87	5	ABB78151 Amino aci
5	237	49.1	87	5	ABB78152 Amino aci
6	234	48.4	91	5	ABB78150 Amino aci
7	234	48.0	91	5	ABB78161 Amino aci
8	232	48.0	91	5	ABB78159 Amino aci
9	232	48.0	91	5	ABB78162 Amino aci
10	230	47.6	91	5	ABB78163 Amino aci
11	229	47.4	88	5	ABB78160 Amino aci
12	228	47.2	90	5	ABB78155 Amino aci
13	227	47.0	93	7	ADFO5158 Bacteri
14	226	46.8	91	5	ABB78158 Amino aci
15	226	46.8	91	5	ABB78157 Amino aci
16	226	46.8	91	5	ABB78156 Amino aci
17	220	45.5	78	5	ABB78164 Amino aci
18	215	44.5	87	5	ABB78176 Amino aci
19	214	44.3	89	9	ABB78178 Amino aci
20	209	43.3	89	9	ABB78176 Amino aci
21	209	43.3	89	9	ABB78178 Amino aci
22	205	42.4	87	5	ABB78148 Amino aci
23	205	42.4	87	5	ABB78147 Amino aci
24	203.5	42.1	92	6	ADA34169 Acinetoba

25	203	42.0	90	5	ABB78165 Amino aci
26	201	41.6	87	5	ABB78177 Amino aci
27	201	41.6	88	5	ABB78171 Amino aci
28	201	41.6	88	5	ABB78172 Amino aci
29	201	41.6	88	5	ABB78173 Amino aci
30	201	41.6	88	5	ABB78172 Amino aci
31	200	41.4	90	5	ABB77219 Amino aci
32	198	41.0	87	5	ABB78168 Amino aci
33	198	41.0	87	5	ABB78169 Amino aci
34	197	40.8	122	7	ABO74609 Pseudom
35	196	40.6	88	5	ABB78175 Amino aci
36	195	40.4	86	5	ABB78154 Amino aci
37	192	39.8	87	5	ABB78149 Amino aci
38	191	39.5	87	5	ABB78170 Amino aci
39	183	37.9	87	5	ABB78174 Amino aci
40	150	31.1	110	8	AD05173 Amino aci
41	71	14.7	582	8	ADY10873 Plant ful
42	67.5	14.0	272	5	ABU05512 M. tuberc
43	67	13.9	87	3	AA054259 Human pan
44	67	13.9	302	4	AAU35741 Helicobac
45	67	13.9	302	6	ABU30804 Protein e
46	67	13.9	305	7	ADM25449 Hyperther
47	66	13.7	379	4	AAV97562 Mouse Wnt
48	66	13.7	379	6	ABG71361 Mouse Wnt
49	66	13.7	379	7	ADD90585 Mouse WIF
50	66	13.7	379	7	ADD90585 Mouse WIF
51	66	13.7	379	7	ADD90583 WIF domai
52	66	13.7	379	7	ADD90581 WIF domai
53	66	13.7	379	7	ADD90579 WIF domai
54	66	13.7	379	8	ADD95945 Murine WI
55	64.5	13.4	327	3	AAH16535 Bacteriop
56	64	13.3	208	2	AAV41660 Trilicium
57	64	13.3	365	7	ADD90570 Bacteri
58	64	13.3	831	8	ADN20509 Bacteri
59	63	13.0	305	7	ADM25866 Hyperther
60	63	13.0	544	3	AAV40947 Zea may
61	62.5	12.9	219	8	ADM57215 A thailan
62	62.5	12.9	314	6	ABU44876 Protei
63	62.5	12.9	363	7	AD0555261 Rat Prote
64	62.5	12.9	389	7	ADM04329 Human pro
65	62.5	12.9	405	6	AAE32119 Human cyt
66	62.5	12.9	439	6	ABU50419 Protein e
67	62	12.8	409	8	ADT58047 Plant pol
68	62	12.8	435	4	ABG08894 Novel hum
69	62	12.8	533	2	AAE339705 Chicken p
70	62	12.8	646	3	AAV57307 P. aerugi
71	62	12.8	667	5	ABG93976 Herdicida
72	62	12.8	667	8	ADN73801 Thale cre
73	62	12.8	670	3	AAV57314 P. aerugi
74	62	12.8	686	7	ABO80650 Pseudomon
75	62	12.8			

ALIGNMENTS

RESULT 1	ABB78167	standard; protein, 90 AA.
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AC	ABB78167	
XX		
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
XX	hydroxyl radical; DNA damage; YggX homologue.	
OS	Xylella fastidiosa.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 61	

PT /note="not specified"
XX
XX US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PD 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 90 AA;
XX
Query Match 97.8%; Score 472.5; DB 5; Length 90;
Best Local Similarity 98.9%; Pred. No. 5,7e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 MORIIFCEYRDTEGLDFVYPYGEIGQKIPACIGKVGMAAMLVHQTMLINENRLSPRNP 60
DB 1 MORIIFCEYRDTEGLDFVYPYGEIGQKIPACIGKVGMAAMLVHQTMLINENRLSPRNP 60
XX
QY 61 SHRAFLBEELNKFLFERRVAKPEGYIEPD 89
DB 61 XSHRAFLBEELNKFLFERRVAKPEGYIEPD 90
XX
RESULT 2
ABB78153
ID ABB78153 standard; protein; 87 AA.
XX
AC ABB78153;
XX
DT 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
DE
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
XX US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PD 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.

PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;
XX
Query Match 50.9%; Score 246; DB 5; Length 87;
Best Local Similarity 51.2%; Pred. No. 4.1e-22;
Matches 44; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
XX
QY 1 MORIIFCEYRDTEGLDFVYPYGEIGQKIPACIGKVGMAAMLVHQTMLINENRLSPRNP 60
DB 1 MARWVFCEYLKKEABGLDFVYPYGEIGQKIPACIGKVGMAAMLVHQTMLINENRLSPRNP 60
XX
QY 61 SHRAFLBEELNKFLFERRVAKPEGYI 86
DB 61 EHROLLEAWVNFLEFGKDVHIDGYV 86
XX
RESULT 3
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
AC ABO65445;
XX
DT 29-JUL-2004 (first entry)
XX
XX Klebsiella pneumoniae polypeptide segid 11962.
DE
XX Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
OS Klebsiella pneumoniae.
XX
XX US6610836-B1.
XX
PD 26-AUG-2003.
XX
PD 27-JAN-2000; 2000US-00489039.
XX
PF 29-JAN-1999; 99US-0117747P.
XX
PR (GENO-) GENOME THERAPEUTICS CORP.
XX
PA Breton GL, Osborne M;
XX
PI WPI; 2003-895346/82.
XX
DR N-PSDB; ACH98996.
XX
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 11962; 932pp; English.
XX

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:27:00 ; Search time 10.9971 Seconds
(without alignments)
778.685 Million cell updates/sec

Title: US-09-955-502a-45

Perfect score: 483
Sequence: 1 MORIIFCEYEQRTDEGLDFV.....LNKFLFERRVAKPGYIEPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	105	2 C82624	conserved hypotet
2	243	50.3	90	2 C64013	hypothetical prote
3	232	48.0	91	2 AH0879	conserved hypotet
4	228	47.2	90	2 C82320	conserved hypotet
5	226	46.8	91	2 A65954	hypothetical prote
6	226	46.8	91	2 A65082	hypothetical prote
7	226	46.8	91	2 F91108	hypothetical prote
8	203	42.0	90	2 A10116	conserved hypotet
9	201	41.6	88	2 H81014	conserved hypotet
10	198	41.0	90	2 H83003	conserved hypotet
11	185	38.3	93	2 B84994	hypothetical prote
12	67.5	14.0	272	2 H87075	probable conserved
13	67	13.9	302	2 B4584	GTP-binding protei
14	63.5	13.1	587	2 S23312	retrovirus-related
15	63.5	13.1	1131	2 T14517	hypothetical prote
16	63	13.0	105	2 B75442	conserved hypotet
17	63	13.0	415	2 S55617	hypothetical prote
18	62.5	12.9	219	2 C96510	hypothetical prote
19	62.5	12.9	439	2 AC0491	xylose isomerase (
20	62	12.8	188	2 C86508	hypothetical prote
21	62	12.8	188	2 H72114	transcription regu
22	62	12.8	305	1 HMP5A	ornithine carbamoy
23	62	12.8	526	2 S26420	protein-tyrosine k
24	62	12.8	533	1 TVCHS	conserved hypotet
25	62	12.8	670	2 C83540	conserved hypotet
26	62	12.8	863	2 S88140	probable finger pr
27	61.5	12.7	359	2 C84963	hypothetical prote
28	61.5	12.7	445	2 T01591	hypothetical prote
29	61.5	12.7	494	2 S23315	hypothetical prote

30	61.5	12.7	729	2	G97169	protein containing
31	61.5	12.7	869	1	A47257	1-phosphatidylinos
32	61	12.6	143	2	I47053	relaxin B,C and A
33	61	12.6	301	2	G71929	GTP-binding protei
34	61	12.6	332	2	B47017	probable transcrip
35	61	12.6	332	2	AD2541	transcription init
36	61	12.6	379	2	A59180	Mnt inhibitory fac
37	60.5	12.5	440	2	AC0980	xylose isomerase (
38	60.5	12.5	1894	2	UC4980	plexin 1 precursor
39	60	12.4	243	2	AF1611	3-ketocacyl-acyl ca
40	60	12.4	318	2	C83555	hypothetical prote
41	60	12.4	360	1	F64601	conserved hypotet
42	60	12.4	878	2	G71371	probable endopepti
43	60	12.4	901	1	FAHUA3	alpha-actinin 3 -
44	60	12.4	984	2	T48216	hypothetical prote
45	59.5	12.3	761	2	AC0791	ribonucleoside-dip
46	59.5	12.3	761	2	S32629	ribonucleoside-dip
47	59.5	12.3	997	2	S33754	glutamate receptor
48	59.5	12.3	1017	2	T08553	hypothetical prote
49	59	12.2	231	2	A80725	conserved hypotet
50	59	12.2	231	2	AP3028	hypothetical prote
51	59	12.2	231	2	B98256	hypothetical prote
52	59	12.2	283	2	D72398	conserved hypotet
53	59	12.2	290	2	AC3417	DNA polymerase, ba
54	59	12.2	360	2	B71910	hypothetical prote
55	59	12.2	486	2	F98106	glutamate-tRNA lig
56	59	12.2	496	2	D83614	conserved hypotet
57	59	12.2	3587	2	I40486	surfactin syntheta
58	58.5	12.1	127	2	B72593	probable gastrin p
59	58.5	12.1	231	2	AF1838	hypothetical prote
60	58.5	12.1	323	2	H71481	hypothetical prote
61	58.5	12.1	496	2	JC5110	cyclin-dependent k
62	58.5	12.1	1327	2	T21268	hypothetical prote
63	58	12.0	194	2	I39526	hypothetical 21.6k
64	58	12.0	247	2	T27205	hypothetical prote
65	58	12.0	251	2	B50428	hypothetical prote
66	58	12.0	457	2	F64095	argininosuccinate
67	58	12.0	526	1	TVFVR	protein-tyrosine k
68	58	12.0	526	2	S15582	protein-tyrosine k
69	58	12.0	632	2	H83106	chemotactic transd
70	58	12.0	1066	2	B95037	hyaluronidase [imp
71	58	12.0	1078	2	F97907	hyaluronate lyase
72	58	12.0	1107	2	T21280	hypothetical prote
73	58	12.0	4450	2	JX0340	gramicidin S synth
74	58	12.0	4452	1	YGBSG2	gramicidin S synth
75	57.5	11.9	373	2	F70781	probable citA prot

ALIGNMENTS

RESULT 1
C82624 conserved hypothetical protein XP1908 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82624
R/anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: C82624
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-105 <Sim>
A/Cross-references: UNIPARC:UPI00000C288F; GB:AE004010; GB:AE003849; NID:G9106992; PIDN:
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briotes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Fromm

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:00:23 ; Search time 67.2615 Seconds

(without alignments)
933.551 Million cell updates/sec

Title: US-09-955-502a-45

Perfect score: 483
Sequence: 1 MQRIFCEYRQDTEGLDFV.....LNKFLFERRVAKPGGYTPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	100.0	90	1	Q9PC73 xylella fas
2	465	96.3	90	1	Q87D06 xylella fas
3	380	78.7	92	1	Q8P829 xanthomonas
4	380	78.7	92	2	Q4UM14 XANCP
5	367	76.0	91	1	Q8PJ7 xanthomonas
6	367	76.0	92	1	Q8PJ7 xanthomonas
7	247	51.1	90	1	Q8PJ7 xanthomonas
8	246	50.9	94	1	Q8PJ7 xanthomonas
9	244	50.5	90	1	Q8PJ7 xanthomonas
10	243	50.3	90	1	Q8PJ7 xanthomonas
11	243	50.3	90	1	Q8PJ7 xanthomonas
12	243	50.3	90	1	Q8PJ7 xanthomonas
13	236	48.9	91	1	Q8PJ7 xanthomonas
14	228	47.2	90	1	Q8PJ7 xanthomonas
15	227	47.0	90	1	Q8PJ7 xanthomonas
16	227	47.0	90	1	Q8PJ7 xanthomonas
17	227	47.0	90	1	Q8PJ7 xanthomonas
18	227	47.0	90	1	Q8PJ7 xanthomonas
19	225	46.6	90	1	Q8PJ7 xanthomonas
20	222	46.0	90	1	Q8PJ7 xanthomonas
21	221	45.8	90	1	Q8PJ7 xanthomonas
22	221	45.8	90	1	Q8PJ7 xanthomonas
23	221	45.8	90	1	Q8PJ7 xanthomonas
24	219	45.3	90	1	Q8PJ7 xanthomonas
25	217	44.9	90	1	Q8PJ7 xanthomonas
26	217	44.9	90	1	Q8PJ7 xanthomonas
27	217	44.9	90	1	Q8PJ7 xanthomonas
28	214	44.3	90	1	Q8PJ7 xanthomonas
29	212	43.9	91	1	Q8PJ7 xanthomonas
30	211	43.7	90	1	Q8PJ7 xanthomonas
31	211	43.7	90	1	Q8PJ7 xanthomonas

32	211	43.7	90	1	FETP_BORR	Q7WC4 bordetella
33	211	43.7	90	1	FETP_YERP	Q66M3 yersinia ps
34	209	43.3	89	1	FETP_LBGP	Q5X39 legionella
35	209	43.3	89	1	FETP_LBGP	Q5X39 legionella
36	209	43.3	90	1	FETP_VIBP	Q5E70 vibrio fusc
37	208	43.1	89	1	FETP_LBGP	Q5WC4 legionella
38	207	42.9	90	1	FETP_MEIC	Q60A7 methylococc
39	206	42.7	87	1	FETP_FRAT	Q5HJ8 francisella
40	204.5	42.3	90	1	FETP_ACID	Q6F13 acinetobact
41	204	42.2	90	1	FETP_PSEB	Q8R49 pseudomonas
42	203	42.0	90	1	FETP_YERP	Q8A07 yersinia pe
43	203	42.0	91	1	FETP_BURR	Q6Z19 burkholderi
44	203	42.0	91	1	FETP_BURR	Q6Z19 burkholderi
45	203	42.0	91	2	Q4LS19 BURK	Q4LS19 burkholderi
46	201	41.6	88	1	FETP_NEIG	Q5E53 neisseria g
47	201	41.6	88	1	FETP_NEIM	Q5E53 neisseria m
48	201	41.6	88	1	FETP_NEIM	Q5E53 neisseria m
49	200	41.4	90	1	FETP_CHRO	Q7NS4 chromobacte
50	200	41.4	90	1	FETP_NITE	Q8X12 nitrosomonas
51	200	41.4	90	1	FETP_PSEB	Q8R49 pseudomonas
52	200	41.4	90	2	Q4ZLP3 PSEB	Q4ZLP3 pseudomonas
53	198	41.0	90	2	FETP_PSEB	Q8R49 pseudomonas
54	197	40.8	90	2	Q4U228 AZOV	Q4U228 azotobacter
55	196	40.6	92	1	FETP_SHEO	Q8B06 shewanella
56	196	40.6	90	2	Q4KJ22 PSEB	Q4KJ22 pseudomonas
57	191	39.5	78	1	FETP_BUCAP	Q8K925 buchnera ap
58	190	39.3	90	2	Q6T7F6 PSEB	Q6T7F6 pseudomonas
59	185	38.3	77	1	FETP_BUCAI	Q8K925 buchnera ap
60	180	37.3	78	1	FETP_WIGR	Q8K925 buchnera ap
61	172	35.6	87	1	FETP_BUCBP	Q8K925 buchnera ap
62	168	34.8	92	2	Q4NQ4_9DEL	Q4NQ4 anaeromyxob
63	156	32.3	79	1	FETP_CANB	Q7V99 candidatus
64	154	31.9	96	2	Q4FVJ7_9GAM	Q4FVJ7 psychrobact
65	91.5	18.9	123	2	Q81Z21_BACR	Q81Z21 bacillus ce
66	75.5	15.6	635	2	Q6YB0_TOXCO	Q6YB0 toxoplasma
67	74.5	15.4	402	2	Q7NVX6_CHRO	Q7NVX6 chromobacte
68	73	15.1	174	2	Q6B658_HELPO	Q6B658 helicobacte
69	70.5	14.6	764	2	Q7UPU4_RHOBA	Q7UPU4 rhodospirill
70	70.5	14.6	764	2	Q81MC3_ORYSA	Q81MC3 oryza sativ
71	69.5	14.4	217	2	Q9DD00_AHSVA	Q9DD00 african hor
72	68.5	14.2	129	2	Q6BJ04_DBBVA	Q6BJ04 debrayomyce
73	68.5	14.2	1065	2	Q9FJ16_ARATH	Q9FJ16 arabidopsis
74	68	14.1	5141	2	Q7S6D3_NEUCR	Q7S6D3 neurospora
75	67.5	14.0	272	2	Q9ZBD7_MYCLE	Q9ZBD7 mycobacteri

ALIGNMENTS

RESULT 1				
FETP_XYLF				
ID_FETP_XYLF	STANDARD;	PRT;	90	AA.
AC_Q9PC73;				
DT_10-OCT-2003	(Rel. 42, Created)			
DT_10-OCT-2003	(Rel. 42, last sequence update)			
DT_13-SEP-2005	(Rel. 48, last annotation update)			
DE_Probable Fe(2+)	trafficking protein.			
GN_OrderedLocustNames=Xf1908;				
OS_Xylella fastidiosa.				
OC_Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;				
OC_Xanthomonadaceae; Xylella.				
OX_NCBI_TaxID=2371;				
RN_[1]				
RP_NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC_STRAIN=965C;				
RX_MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;				
RA_Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,				
RA_Alvaranga R., Alves L.M.C., Araya J.B., Bata G.S., Baptista C.S.,				
RA_Barron M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,				
RA_Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carreiro D.M., Carter H.,				
RA_Cotauro N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,				
RA_Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,				
RA_Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,				

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.U., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.B., Laigret P., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marinho C.L.,
 RA Marques M.V., Martins E.A.L., Martins B.M.F., Matukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.R.S.,
 RA Nhani A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Paschoa B.R., Pereira G.A.G., Pereira H.A.Jr., Pasquero J.B.,
 RA Paugello R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawaaki H.B.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tusharo M.H.,
 RA Vallada H., Van Sluys M.A., Verjowski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidands J., Setubal J.C.,
 RA "The genome sequence of the plant pathogen *Xylella fastidiosa*,"
 RL Nature 406:151-159(2000).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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 DR EMBL, AE004010, AAF84714.1, ALT_INIT; Genomic_DNA.
 DR HANAP, MF_00686; -, 1.
 DR InterPro: IPR007457; Y9GX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 DR Prodom: PD029191; DUF495; 1.
 KM Complete proteome; Iron.
 SQ SEQUENCE 90 AA; 10555 MW; E9BBB3BCA6D104A3 CRC64;
 Query Match 100.0%; Score 483; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.6e-47;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MQRIFCEYGRDTEGLDVPYPGELGQKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
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 DB 61 SHRAFLERLNKFLFERRVAKPEGYIEPD 89
 QY 61 SHRAFLERLNKFLFERRVAKPEGYIEPD 89
 DB 61 SHRAFLERLNKFLFERRVAKPEGYIEPD 89
 RESULT 2
 FETP_XYLF STANDARD; PRT; 90 AA.
 AC Q87D06;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 OS OrderedLocustNames=PD0883;
 GN *Xylella fastidiosa* (strain Temecula / ATCC 700964).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_Taxid=183190;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=2242131; PubMed=1253478;
 RX DOI=10.1126/JB.185.3.1018-1026.2003;
 RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
 RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

RA Taktai M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
 RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
 RA Carrier H., Carraro D.M., de Oliveira M.C., Nunes L.R., Siqueira W.J.,
 RA Coutinho L.L., Kimura E.T., Ferro R.S., Harakava R., Kuramae E.B.,
 RA Matino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.V.,
 RA Bata G.S., Bianco S.R., Brito M.S., Camnayan F.S., Celestino A.V.,
 RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
 RA Leon S.G., Oliveira A.R., Rosa V.E.Jr., Sasaki F.T., Seta J.A.D.,
 RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaro L.G.,
 RA Cliverio E.L., Simpson A.J.G., Almeida N.F.Jr., Setubal J.C.,
 RA Kitajima J.P.,
 RT "Comparative analyses of the complete genome sequences of *Pierce's*
 RT disease and citrus variegated chlorosis strains of *Xylella*
 RT *fastidiosa*,"
 RL J. Bacteriol. 185:1018-1026(2003).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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 DR EMBL, AE012556, AAO28748.1; -, Genomic_DNA.
 DR HANAP, MF_00686; -, 1.
 DR InterPro: IPR007457; Y9GX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 DR Prodom: PD029191; DUF495; 1.
 KM Complete proteome; Iron.
 SQ SEQUENCE 90 AA; 10430 MW; B5C6936496F471D CRC64;
 Query Match 96.3%; Score 465; DB 1; Length 90;
 Best Local Similarity 95.5%; Pred. No. 1.9e-45;
 Matches 85; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MQRIFCEYGRDTEGLDVPYPGELGQKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
 DB 1 MQRIFCEYGRDTEGLDVPYPGELGQKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
 QY 61 SHRAFLERLNKFLFERRVAKPEGYIEPD 89
 DB 61 SHRAFLERLNKFLFERRVAKPEGYIEPD 89
 QY 61 SHRAFLERLNKFLFERRVAKPEGYIEPD 89
 DB 61 SHRAFLERLNKFLFERRVAKPEGYIEPD 89
 RESULT 3
 FETP_XANCP STANDARD; PRT; 92 AA.
 AC Q8P829;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 OS OrderedLocustNames=XCC2419;
 GN *Xanthomonas campestris* (pv. *campestris*).
 OC Xanthomonas campestris (pv. *campestris*).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_Taxid=340;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
 RA Almeida N.F.Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
 RA Camargo L.E.A., Camarotte G., Camnayan F., Cardoso J., Chambergo F.,
 RA Clapina L.P., Claparelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
 RA El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
 RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Kishi L.T.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:30:02 ; Search time 19.6925 Seconds
(without alignments)
373.651 Million cell updates/sec

Title: US-09-955-502A-45

Perfect score: 483

Sequence: 1 MQRIFCEYRQRTGGLDFV.....LNKLFERRVAKPEGYLPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/Pcetus.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RG.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	49.3	107	2	US-09-489-039A-11962
2	227	47.0	93	2	US-09-543-681A-5443
3	203.5	42.1	92	2	US-09-328-352-5456
4	198	41.0	122	2	US-09-252-991A-23355
5	150	31.1	110	2	US-09-540-236-2859
6	62	12.8	174	2	US-09-198-452A-158
7	62	12.8	198	2	US-09-438-185A-141
8	62	12.8	645	2	US-09-328-501-1
9	62	12.8	646	5	US-09-777-710A-1
10	62	12.8	646	5	US-10-191-289A-1
11	62	12.8	670	2	US-09-328-501-15
12	62	12.8	670	2	US-09-777-710A-15
13	62	12.8	670	5	US-10-191-289A-15
14	62	12.8	686	2	US-09-252-991A-29396
15	61	12.6	333	2	US-09-107-532A-4544
16	61	12.6	461	2	US-09-107-433-2847
17	60.5	12.5	251	2	US-09-489-039A-7987
18	60	12.4	286	2	US-09-543-681A-5269
19	59.5	12.3	626	2	US-09-248-796A-27023
20	59.5	12.3	770	2	US-09-543-681A-4291
21	59	12.2	170	2	US-09-489-039A-7536
22	59	12.2	295	2	US-08-952-089A-1
23	59	12.2	295	2	US-09-690-885-1
24	59	12.2	320	2	US-09-248-796A-15469
25	59	12.2	348	1	US-08-844-153-2
26	59	12.2	480	1	US-08-962-203-2
27	59	12.2	480	2	US-09-282-125A-2

28	59	12.2	480	2	US-09-273-142-2	Sequence 2, Appli
29	58.5	12.1	185	2	US-09-270-767-36317	Sequence 36317, A
30	58.5	12.1	185	2	US-09-270-767-51534	Sequence 51534, A
31	58.5	12.1	496	2	US-09-695-795A-8	Sequence 8, Appli
32	58.5	12.1	771	1	US-08-742-753-2	Sequence 2, Appli
33	58	12.0	331	2	US-09-719-108-2	Sequence 2, Appli
34	58	12.0	640	2	US-09-252-991A-23252	Sequence 23252, A
35	58	12.0	776	2	US-09-284-180A-3	Sequence 3, Appli
36	58	12.0	2353	2	US-08-984-709A-50	Sequence 50, Appli
37	57.5	11.9	278	1	US-08-258-261B-20	Sequence 20, Appli
38	57.5	11.9	278	1	US-08-456-837-20	Sequence 20, Appli
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43	57.5	11.9	278	1	US-08-729-214-20	Sequence 20, Appli
44	57.5	11.9	278	2	US-09-028-934-20	Sequence 20, Appli
45	57.5	11.9	647	2	US-09-252-991A-32816	Sequence 32816, A
46	57	11.8	184	2	US-09-270-767-46275	Sequence 46275, A
47	57	11.8	293	2	US-09-071-035-496	Sequence 496, App
48	57	11.8	293	2	US-10-206-576-496	Sequence 496, App
49	57	11.8	316	2	US-09-071-035-494	Sequence 494, App
50	57	11.8	316	2	US-10-206-576-494	Sequence 494, App
51	57	11.8	371	2	US-09-543-681A-6429	Sequence 6429, App
52	57	11.8	379	2	US-09-907-794A-4	Sequence 4, Appli
53	57	11.8	379	2	US-09-905-125A-4	Sequence 4, Appli
54	57	11.8	379	2	US-09-902-775A-4	Sequence 4, Appli
55	57	11.8	379	2	US-09-906-700-4	Sequence 4, Appli
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63	57	11.8	379	2	US-09-902-736A-4	Sequence 4, Appli
64	57	11.8	380	2	US-09-906-722A-4	Sequence 4, Appli
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66	57	11.8	380	2	US-10-004-860-441	Sequence 441, App
67	57	11.8	484	2	US-08-913-578-2	Sequence 2, Appli
68	57	11.8	484	2	US-08-785-427-2	Sequence 2, Appli
69	56.5	11.7	321	2	US-09-107-532A-4975	Sequence 4975, App
70	56.5	11.7	357	2	US-09-489-039A-13955	Sequence 13955, A
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75	56.5	11.7	1206	2	US-09-252-991A-19632	Sequence 19632, A

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match	49.3%	Score 238;	DB 2;	Length 107;
Best Local Similarity	51.7%	Pred. No. 1e-23;		
Matches	46;	Conservative	12;	Mismatches 31;
			Indels	0;
			Gaps	0;

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Oy      1 MORITFCEYEBRDTGCLDFFVYPGELGOKIFACTIGKVGMAAMLVHQTMILINENRISPRNP   60
        | | | | : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      17 MSRTI FCTPLQREADGQDFQLTPGELGRIYNYSISKAAWQWQHKTMTLINEKKLSMMPN    76
```

QY 61 SHRAFLBEELNKFLFERRVAKPEGIYRPD 89
|||:::|||||:
Db 77 EHRKLLQEMVQFLFEGKDVHIEGYTPE 105

RESULT 2
US-09-543-681A-5443

Query Match	47.0%	Score 227	DB 2:	Length 93;
Best Local Similarity	47.2%	Pred. No. 2.5e-22;		
Matches 42; Conservative	14;	Mismatches 33;	Indels 0;	Gaps 0;

Qy 1 MORIICEYEQRDTEGLDFVPIYGEELGOKIPACIGKVGMAAMLVHQMTLINENRUSPRNP 60
| | | | : : : | | | | | : : | | | | : : |
Db 4 MSRTIFCTPLANKADGDLFQLYGELGKRIIPNEISKEANGQMAQMTLINENKNTMNP 63

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Oy      61 SHRAFLBEELNKFLPERVAKEGYIEPD 89
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Db      64 DDRKLLGEQMVRFLEFGHDVHTIDGYTPE 92

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RESULT 3
US-09-328-352-5456
; Sequence 5456: Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: prt
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Query Match	42.1%	Score 203.5	DB 2	Length 92
Best Local Similarity	46.5%	Pred. No. 3.2e-19		
Matches 40	Conservative	11	Mismatches 34	Indels 1
				Gaps 1

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QY      1 MQRIFCEYEYRDTEGLDFVPYPGSLGQKIPACIGKVGMAMLVHQTMLINENRLSPNP    60GG
        |::|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      4 MSRQVFCCKKYQKMEGLDAPPPGAAGQGEFFENVSKQAQWEMLQHQTLLINEKRLANFEP    63
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61 SHRAFLBBLNKFL-FERRVAKPEGY 85

Db 64 BAKKLEBQREKFFNNDESVEKAEGW 89

RESULT 4
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A

Query Match	41.0%	Score 198	DB 2	Length 122
Best Local Similarity	42.0%	Pred. No. 2.5e-18		
Matches 37; Conservative	13	Mismatches 38	Indels 0	Gaps 0

DQ 1 MGRIFCEYEGRDTEGIDFVPPYGBELCQKIFACIGKVCAAMLVHQMTLINENRLSPRP 600
| : | | | | | : : : | | | | | : |
DB 33 MSRTWCRKYHBELPGIDRPPYPGAKEBDIYNNVSRAKADWDQKHQTMLINERRLNMGNA 922

Oy 61 SHRAFLLEBLINKFLPERRVAKEEGYIEP 88
| | | : : : |
Db 93 EDRKFLQEQMDKFLSGEDYAKADGYVP 120

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RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: prt
; ORGANISM: M.catarrhalis
US-09-540-236-2859

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Query Match	31.1%	Score 150	DB 2	Length 110
Best Local Similarity	40.2%	Pred. No. 5e-12		
Matches 33	Conservative 10	Mismatches 39	Indels 0	Gaps 0

Oy

4 IIFCEYERDTEGLDFVVPYGELGQIKIACIGKVGWAAMLVHQTMLINENRLSPRNSHR 63
::| | : | | | | | | | :

Db

24 MVFCRKQQNLKLPPNPFPNAKGQEIDTISAKANMANMLQTMLINEKHLSMIDIQAk 80
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OY      64 AFLEBELNKFLFERRVAKPEGY 85
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Db      84 KYLNEQREKFLDNGDYEKPAY 105

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RESULT 6
US-09-198-452A-158
; Sequence 158, Application US/09198452A

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:44:45 ; Search time 57.7989 Seconds

(without alignments)
643.383 Million cell updates/sec

Title: US-09-955-502A-45

Perfect score: 483

Sequence: 1 MORIIFCYEQRDTGDLFV.....LNKFLFERRVAKPGYIEPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_AA_Main:

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	483	100.0	89 3 US-09-955-502-22	Sequence 22, Appl
2	246	50.9	87 3 US-09-955-502-8	Sequence 8, Appl
3	237	49.1	87 3 US-09-955-502-6	Sequence 7, Appl
4	237	49.1	87 3 US-09-955-502-7	Sequence 5, Appl
5	234	48.4	91 3 US-09-955-502-5	Sequence 14, Appl
6	232	48.0	91 3 US-09-955-502-14	Sequence 16, Appl
7	232	48.0	91 3 US-09-955-502-16	Sequence 17, Appl
8	232	48.0	91 3 US-09-955-502-17	Sequence 18, Appl
9	230	47.6	91 3 US-09-955-502-15	Sequence 15, Appl
10	229	47.4	90 3 US-09-955-502-18	Sequence 11, Appl
11	228	47.2	90 3 US-09-955-502-10	Sequence 12, Appl
12	226	46.8	91 3 US-09-955-502-11	Sequence 13, Appl
13	226	46.8	91 3 US-09-955-502-12	Sequence 19, Appl
14	226	46.8	91 3 US-09-955-502-13	Sequence 13, Appl
15	220	45.5	78 3 US-09-955-502-19	Sequence 31, Appl
16	215	44.5	87 3 US-09-955-502-31	Sequence 33, Appl
17	214	44.3	88 3 US-09-955-502-33	Sequence 2, Appl
18	205	42.4	87 3 US-09-955-502-2	Sequence 20, Appl
19	205	42.4	87 3 US-09-955-502-3	Sequence 32, Appl
20	203	42.0	90 3 US-09-955-502-20	Sequence 26, Appl
21	201	41.6	87 3 US-09-955-502-32	Sequence 27, Appl
22	201	41.6	88 3 US-09-955-502-26	Sequence 28, Appl
23	201	41.6	88 3 US-09-955-502-27	Sequence 24, Appl
24	201	41.6	88 3 US-09-955-502-28	Sequence 29, Appl
25	200	41.4	90 3 US-09-955-502-23	
26	198	41.0	87 3 US-09-955-502-24	
27	197	40.8	87 3 US-09-955-502-29	

28	197	40.8	87 3 US-09-955-502-30	Sequence 30, Appl
29	196	40.6	88 3 US-09-955-502-9	Sequence 9, Appl
30	195	40.4	86 3 US-09-955-502-4	Sequence 4, Appl
31	192	39.8	87 3 US-09-955-502-25	Sequence 25, Appl
32	183	37.9	76 3 US-09-955-502-21	Sequence 22, Appl
33	71	14.7	580 4 US-10-425-115-224020	Sequence 22, Appl
34	71	14.7	582 4 US-10-425-114-66688	Sequence 66688, A
35	70.5	14.6	764 4 US-10-437-963-104787	Sequence 104787, A
36	67.5	14.0	272 4 US-10-080-170-163	Sequence 163, App
37	67.5	14.0	272 4 US-10-080-170-163	Sequence 163, App
38	67.5	14.0	272 4 US-10-468-356-163	Sequence 163, App
39	67	13.9	87 3 US-09-928-297-711	Sequence 711, App
40	67	13.9	115 4 US-10-425-115-337472	Sequence 337472, A
41	67	13.9	302 3 US-09-815-242-11334	Sequence 11334, A
42	67	13.9	302 4 US-10-282-122A-58728	Sequence 58728, A
43	66	13.7	379 4 US-10-013-310-7	Sequence 7, Appl
44	66	13.7	379 4 US-10-682-230-7	Sequence 7, Appl
45	66	13.7	379 5 US-10-745-110-2	Sequence 2, Appl
46	66	13.7	379 5 US-10-507-343-2	Sequence 2, Appl
47	66	13.7	379 5 US-10-507-343-15	Sequence 15, Appl
48	66	13.7	379 5 US-10-507-343-17	Sequence 19, Appl
49	66	13.7	379 5 US-10-507-343-19	Sequence 21, Appl
50	66	13.7	379 5 US-10-507-343-21	Sequence 21, Appl
51	66	13.7	593 4 US-10-424-599-213920	Sequence 213920, A
52	65	13.5	87 4 US-10-425-115-362001	Sequence 362001, A
53	65	13.5	578 4 US-10-437-963-107904	Sequence 107904, A
54	64.5	13.4	73 4 US-10-424-599-262025	Sequence 262025, A
55	64.5	13.4	287 4 US-10-437-963-148594	Sequence 148594, A
56	64.5	13.4	327 3 US-09-727-892-81	Sequence 81, Appl
57	64	13.3	112 4 US-10-437-963-131206	Sequence 131206, A
58	64	13.3	365 5 US-10-507-343-6	Sequence 6, Appl
59	64	13.3	658 4 US-10-156-761-14350	Sequence 14350, A
60	64	13.3	831 4 US-10-359-493-3162	Sequence 3162, App
61	63.5	13.1	154 4 US-10-335-977-6532	Sequence 6532, App
62	63.5	13.1	155 4 US-10-335-977-6531	Sequence 6531, App
63	63.5	13.1	288 4 US-10-437-963-163689	Sequence 163689, A
64	63.5	13.1	446 5 US-10-732-923-5208	Sequence 5208, App
65	63.5	13.1	314 4 US-10-732-923-11149	Sequence 11149, A
66	62.5	12.9	314 4 US-10-282-122A-72800	Sequence 72800, A
67	62.5	12.9	375 5 US-10-732-923-11589	Sequence 11589, A
68	62.5	12.9	389 4 US-10-108-260A-3014	Sequence 3014, App
69	62.5	12.9	405 4 US-10-473-574-17	Sequence 17, Appl
70	62.5	12.9	439 4 US-10-282-122A-78343	Sequence 78343, App
71	62	12.8	174 4 US-10-289-762-158	Sequence 158, App
72	62	12.8	409 5 US-10-739-930-8124	Sequence 8124, App
73	62	12.8	435 5 US-10-450-763-39253	Sequence 39253, A
74	62	12.8	453 5 US-10-732-923-13651	Sequence 13651, A
75	62	12.8	478 4 US-10-424-599-260720	Sequence 260720, A

ALIGNMENTS

RESULT 1
US-09-955-502-22
Sequence 22, Application US/09955502
Patent No. US20020672118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 22
LENGTH: 89
TYPE: PRT
ORGANISM: Xylella fastidiosa

US-09-955-502-22

Query Match 100.0%; Score 483; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.8e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORIIFCEYBORDTEGLDPVYPGELGQKIFACIGKVGMAAMLVHQTMLINENRLSPRP 60
Db 1 MARIVFCEYKQSSBGLDPOLYPGELGKRIFFDSISKQAMKEMKKQTMVNEKCLNMNNA 60

Qy 61 SHRAFLBEEINKFLFERRVAKPEGYI 89
Db 61 SHRAFLBEEINKFLFERRVAKPEGYI 89

RESULT 2

US-09-955-502-8
Sequence 8, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 87
TYPE: PRT
ORGANISM: Haemophilus ducreyi
US-09-955-502-8

Query Match 50.9%; Score 246; DB 3; Length 87;
Best Local Similarity 51.2%; Pred. No. 3.7e-22;
Matches 44; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MORIIFCEYBORDTEGLDPVYPGELGQKIFACIGKVGMAAMLVHQTMLINENRLSPRP 60
Db 1 MARIVFCEYKQSSBGLDPOLYPGELGKRIFFDSISKQAMKEMKKQTMVNEKCLNMNNA 60

Qy 61 SHRAFLBEEINKFLFERRVAKPEGYI 86
Db 61 SHRAFLBEEINKFLFERRVAKPEGYI 86

RESULT 3

US-09-955-502-6
Sequence 6, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 87
TYPE: PRT
ORGANISM: Pasteurella multocida
US-09-955-502-6

Query Match 49.1%; Score 237; DB 3; Length 87;

Best Local Similarity 50.0%; Pred. No. 4.7e-21;
Matches 43; Conservative 15; Mismatches 28; Indels 0; Gaps 0;

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Db 1 MARIVFCEYKQSSBGLDPOLYPGELGKRIFFDSISKQAMKEMKKQTMVNEKCLNMNNA 60

Qy 61 SHRAFLBEEINKFLFERRVAKPEGYI 86
Db 61 SHRAFLBEEINKFLFERRVAKPEGYI 86

RESULT 4

US-09-955-502-7
Sequence 7, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 87
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-09-955-502-7

Query Match 49.1%; Score 237; DB 3; Length 87;
Best Local Similarity 48.8%; Pred. No. 4.7e-21;
Matches 42; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MORIIFCEYBORDTEGLDPVYPGELGQKIFACIGKVGMAAMLVHQTMLINENRLSPRP 60
Db 1 MARIVFCEYKQSSBGLDPOLYPGELGKRIFFDSISKQAMKEMKKQTMVNEKCLNMNNA 60

Qy 61 SHRAFLBEEINKFLFERRVAKPEGYI 86
Db 61 SHRAFLBEEINKFLFERRVAKPEGYI 86

RESULT 5

US-09-955-502-5
Sequence 5, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 91
TYPE: PRT
ORGANISM: Actinobacillus actinomycetemcomitans
US-09-955-502-5

Query Match 48.4%; Score 234; DB 3; Length 91;
Best Local Similarity 48.3%; Pred. No. 1.2e-20;
Matches 43; Conservative 15; Mismatches 31; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:45:38 ; Search time 5.62644 Seconds
(without alignments)
235.489 Million cell updates/sec

Title: US-09-955-502A-45

Perfect score: 483

Sequence: 1 MORITFCYRQRTGDLFV.....LNKLFFRRVAKPGYIEPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	66	13.7	379	US-11-136-619-22	Sequence 23, Appl
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4	61	12.6	335	US-11-136-619-30	Sequence 30, Appl
5	61	12.6	379	US-11-136-619-2	Sequence 2, Appl
6	58	12.0	351	US-11-136-619-14	Sequence 14, Appl
7	58	12.0	376	US-10-925-970-3	Sequence 3, Appl
8	57	11.8	378	US-11-129-143-49	Sequence 49, Appl
9	57	11.8	379	US-10-131-826A-308	Sequence 308, App
10	56	11.6	372	US-11-143-980-37	Sequence 37, Appl
11	56	11.6	533	US-11-230-995-3	Sequence 3, Appl
12	56	11.6	536	US-10-821-231C-1	Sequence 1, Appl
13	55.5	11.5	430	US-11-126-313-35	Sequence 35, Appl
14	55.5	11.5	430	US-11-126-313-36	Sequence 36, Appl
15	55.5	11.5	496	US-10-770-726-72	Sequence 72, Appl
16	55.5	11.5	2080	US-11-124-367A-364	Sequence 364, App
17	55.5	11.5	2542	US-11-124-367A-363	Sequence 363, App
18	55	11.4	774	US-11-242-730-7	Sequence 7, Appl
19	54.5	11.3	124	US-11-072-512-3487	Sequence 3487, Ap
20	54.5	11.3	636	US-10-516-587-2	Sequence 2, Appl
21	54	11.2	205	US-11-054-281-12	Sequence 12, Appl
22	54	11.2	364	US-11-054-281-70	Sequence 70, Appl
23	54	11.2	374	US-11-054-281-68	Sequence 68, Appl
24	54	11.2	394	US-11-054-281-66	Sequence 66, Appl
25	54	11.2	394	US-11-054-281-67	Sequence 67, Appl

26	54	11.2	418	US-11-244-219-2	Sequence 2, Appl
27	54	11.2	1225	US-11-102-476-2	Sequence 2, Appl
28	54	11.2	1424	US-11-102-476-4	Sequence 4, Appl
29	54	11.2	1889	US-11-102-476-46	Sequence 46, Appl
30	53.5	11.1	774	US-11-077-886-34	Sequence 34, Appl
31	53.5	11.1	774	US-11-242-730-6	Sequence 6, Appl
32	53.5	11.1	787	US-11-154-227-110	Sequence 110, App
33	53.5	11.1	2504	US-10-647-956A-8	Sequence 8, Appl
34	53	11.0	378	US-11-072-512-3698	Sequence 3698, Ap
35	53	11.0	471	US-11-098-686-11229	Sequence 11229, A
36	53	11.0	1207	US-10-755-092-7	Sequence 7, Appl
37	52.5	10.9	148	US-11-072-512-3547	Sequence 3547, Ap
38	52.5	10.9	200	US-11-176-830-710	Sequence 710, App
39	52.5	10.9	296	US-10-467-657-1198	Sequence 3198, Ap
40	52.5	10.9	498	US-10-510-947-9	Sequence 9, Appl
41	52.5	10.9	528	US-10-511-558-255	Sequence 255, App
42	52.5	10.9	685	US-11-098-686-10574	Sequence 10574, A
43	52	10.8	181	US-11-000-463-890	Sequence 890, App
44	52	10.8	182	US-11-000-463-418	Sequence 418, App
45	52	10.8	235	US-11-098-686-11270	Sequence 11270, A
46	52	10.8	271	US-10-857-780-19	Sequence 19, Appl
47	52	10.8	271	US-11-107-028-25	Sequence 25, Appl
48	52	10.8	309	US-10-873-528-156	Sequence 156, App
49	52	10.8	486	US-10-821-234-1063	Sequence 1063, Ap
50	52	10.8	516	US-11-080-991-2	Sequence 2, Appl
51	52	10.8	575	US-11-072-512-3622	Sequence 3622, Ap
52	51.5	10.7	417	US-11-098-686-10533	Sequence 10533, A
53	51.5	10.7	844	US-11-097-463-4	Sequence 4, Appl
54	51.5	10.7	1508	US-11-043-889-47	Sequence 47, Appl
55	51	10.6	245	US-11-072-512-2600	Sequence 2600, Ap
56	51	10.6	474	US-10-986-501-249	Sequence 249, App
57	51	10.6	496	US-11-069-642-20	Sequence 20, Appl
58	51	10.6	818	US-11-144-985-13	Sequence 13, Appl
59	51	10.6	1020	US-11-144-985-3	Sequence 3, Appl
60	51	10.6	1340	US-11-070-575-6	Sequence 6, Appl
61	51	10.6	1344	US-11-091-643-20	Sequence 20, Appl
62	51	10.6	1822	US-11-169-041-193	Sequence 193, App
63	51	10.6	5712	US-11-143-980-47	Sequence 47, Appl
64	50.5	10.5	200	US-11-176-830-122	Sequence 122, App
65	50.5	10.5	290	US-10-793-626-1892	Sequence 1892, App
66	50.5	10.5	303	US-10-793-626-1140	Sequence 1140, Ap
67	50.5	10.5	304	US-10-055-877-173	Sequence 173, App
68	50.5	10.5	359	US-10-793-626-2742	Sequence 2742, Ap
69	50.5	10.5	525	US-10-763-712A-108	Sequence 108, App
70	50.5	10.5	554	US-10-467-657-8240	Sequence 8240, Ap
71	50	10.4	193	US-10-467-657-2700	Sequence 2700, App
72	50	10.4	200	US-11-176-830-726	Sequence 726, App
73	50	10.4	270	US-10-988-476-2	Sequence 2, Appl
74	50	10.4	500	US-11-098-686-10274	Sequence 10274, A
75	49.5	10.2	184	US-11-177-860-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 41.6%; Score 201; DB 6; Length 88;
Best Local Similarity 41.9%; Pred. No. 1,7e-18;
Matches 36; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 MORIIFCYEORDIEGLDFVYPYBGLGQKIFACIGKV-GMAAMLVHQMTLINENRLSPRNP 60
DB 1 MARVIFCYCKLKEAGMKFPELPELGRIFENVSQEMAAWTRQMTLINENRLSLADP 60

OY 61 SHRAFLBEELNKFLFERRVAK-PEGYIEP 86
DB 61 RAREYLAQOMEQYFFGADAVQGTIV 86

RESULT 2

US-11-136-619-22
Sequence 22, Application US/11136619
Publication No. US20050288226A1

GENERAL INFORMATION:
APPLICANT: You, Liang
APPLICANT: He, Biao
APPLICANT: Xu, Zhihong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: METHODS FOR TREATING AND DIAGNOSING CANCER WITH WNT INHIBITORY
TITLE OF INVENTION: FACTOR-1 (WIF-1)
FILE REFERENCE: 023070-148711US
CURRENT APPLICATION NUMBER: US/11/136,619
CURRENT FILING DATE: 2005-05-23
PRIOR APPLICATION NUMBER: US 60/664,241
PRIOR FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: US 60/573,197
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3

SEQ ID NO 22
LENGTH: 379
TYPE: PRT
ORGANISM: Mus musculus
US-11-136-619-22

Query Match 13.7%; Score 66; DB 7; Length 379;
Best Local Similarity 28.6%; Pred. No. 1.1;
Matches 24; Conservative 13; Mismatches 35; Indels 12; Gaps 3;

OY 17 LDFVYPBGLGQKIFACIGKV-GMAAMLVHQMTLINENRLSPRNP 68
DB 124 LGTVPHKASVYQVGFPCIGKQDGVAAFEVNVIVNBSGNITLTPQNAIFFKTCQQAACP 183

OY 69 ---ELNKFLFERRVAK-PEGYIEP 88
DB 184 GGCRRNGFCNERRVCECPDGFYGP 207

RESULT 3
US-11-136-619-23
Sequence 23, Application US/11136619
Publication No. US20050288226A1

GENERAL INFORMATION:
APPLICANT: You, Liang
APPLICANT: He, Biao
APPLICANT: Xu, Zhihong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: METHODS FOR TREATING AND DIAGNOSING CANCER WITH WNT INHIBITORY
TITLE OF INVENTION: FACTOR-1 (WIF-1)
FILE REFERENCE: 023070-148711US
CURRENT APPLICATION NUMBER: US/11/136,619
CURRENT FILING DATE: 2005-05-23
PRIOR APPLICATION NUMBER: US 60/664,241

PRIOR FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: US 60/573,197
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23
LENGTH: 379
TYPE: PRT
ORGANISM: Rattus rattus
US-11-136-619-23

Query Match 13.3%; Score 64; DB 7; Length 379;
Best Local Similarity 28.6%; Pred. No. 2;
Matches 24; Conservative 13; Mismatches 35; Indels 12; Gaps 3;

OY 17 LDFVYPBGLGQKIFACIGKV-GMAAMLVHQMTLINENRLSPRNP 68
DB 124 LGTVPHKASVYQVGFPCIGKQDGVAAFEVNVIVNBSGNITLTPQNAIFFKTCQQAACP 183

OY 69 ---ELNKFLFERRVAK-PEGYIEP 88
DB 184 GGCRRNGFCNERRVCECPDGFYGP 207

RESULT 4

US-11-136-619-30
Sequence 30, Application US/11136619
Publication No. US20050288226A1

GENERAL INFORMATION:
APPLICANT: You, Liang
APPLICANT: He, Biao
APPLICANT: Xu, Zhihong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: METHODS FOR TREATING AND DIAGNOSING CANCER WITH WNT INHIBITORY
TITLE OF INVENTION: FACTOR-1 (WIF-1)
FILE REFERENCE: 023070-148711US
CURRENT APPLICATION NUMBER: US/11/136,619
CURRENT FILING DATE: 2005-05-23
PRIOR APPLICATION NUMBER: US 60/664,241
PRIOR FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: US 60/573,197
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3

SEQ ID NO 30
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-11-136-619-30

Query Match 12.6%; Score 61; DB 7; Length 335;
Best Local Similarity 27.4%; Pred. No. 4;
Matches 23; Conservative 14; Mismatches 35; Indels 12; Gaps 3;

OY 17 LDFVYPBGLGQKIFACIGKV-GMAAMLVHQMTLINENRLSPRNP 68
DB 96 LGTVPHKASVYQVGFPCIGKQDGVAAFEVNVIVNBSGNITLTPQNAIFFKTCQQAACP 155

OY 73 -----FLFERRVAK-PEGYIEP 88
DB 156 GGCRRNGFCNERRVCECPDGFHGP 179

RESULT 5

US-11-136-619-2
Sequence 2, Application US/11136619
Publication No. US20050288226A1

GENERAL INFORMATION:
APPLICANT: You, Liang
APPLICANT: He, Biao
APPLICANT: Xu, Zhihong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: METHODS FOR TREATING AND DIAGNOSING CANCER WITH WNT INHIBITORY

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.76888 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502a-37

Perfect score: 473
Sequence: 1 MSRTIFCTFLKMDARQDFQ.....VNFLEGGDVHAGYPPSK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:
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3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	41.9	88	US-10-467-657-968	Sequence 968, App
2	65	13.7	2101	US-10-857-780-23	Sequence 220, App
3	64.5	13.6	242	US-11-022-562-220	Sequence 21, App
4	62.5	13.2	259	US-11-179-977-21	Sequence 5358, App
5	62.5	13.2	273	US-10-467-657-5358	Sequence 317, App
6	62	13.1	593	US-11-194-246-317	Sequence 2694, App
7	61	12.9	922	US-11-072-512-2694	Sequence 903, App
8	61	12.9	1614	US-10-821-234-903	Sequence 7704, App
9	60.5	12.8	548	US-10-467-657-7704	Sequence 3814, App
10	60	12.7	571	US-11-072-512-3814	Sequence 17, App
11	58.5	12.4	1432	US-10-510-386-218	Sequence 340, App
12	57.5	12.2	980	US-11-052-554A-17	Sequence 341, App
13	57	12.1	940	US-10-491-096-190	Sequence 3313, App
14	57	12.1	1504	US-11-019-711-98	Sequence 486, App
15	56.5	11.9	136	US-10-485-517-261	
16	56.5	11.9	506	US-11-099-691-5	
17	56.5	11.9	563	US-11-072-512-3625	
18	56.5	11.9	893	US-11-072-512-3504	
19	56.5	11.9	1976	US-11-069-834-52	
20	56.5	11.9	1976	US-11-069-834-54	
21	56	11.8	1678	US-11-124-367A-340	
22	56	11.8	1678	US-11-124-367A-341	
23	55.5	11.7	305	US-11-156-084-178	
24	55.5	11.7	381	US-11-072-512-3313	
25	55.5	11.7	401	US-10-131-826A-486	

26	55	11.6	109	US-11-049-536-504	Sequence 504, App
27	55	11.6	189	US-11-071-262-1	Sequence 1, App
28	55	11.6	251	US-11-054-515-1496	Sequence 1496, App
29	55	11.6	253	US-11-054-515-1249	Sequence 1249, App
30	55	11.6	432	US-10-821-223-1463	Sequence 1463, App
31	55	11.6	499	US-10-793-626-1484	Sequence 1484, App
32	55	11.6	1705	US-11-143-984A-37	Sequence 37, App
33	54.5	11.5	124	US-11-072-512-2018	Sequence 2018, App
34	54.5	11.5	310	US-10-467-657-6318	Sequence 6318, App
35	54.5	11.5	206	US-10-055-877-195	Sequence 195, App
36	54.5	11.5	577	US-11-072-175-187	Sequence 187, App
37	54.5	11.5	601	US-10-944-272-3	Sequence 3, App
38	54.5	11.5	601	US-11-096-191-720	Sequence 720, App
39	54.5	11.5	876	US-11-077-550-82	Sequence 82, App
40	54.5	11.5	876	US-11-077-550-106	Sequence 106, App
41	54.5	11.5	1786	US-11-077-550-108	Sequence 108, App
42	54.5	11.5	1786	US-11-196-400-3	Sequence 3, App
43	54	11.4	248	US-11-024-959-401	Sequence 401, App
44	54	11.4	480	US-10-510-386-12	Sequence 12, App
45	54	11.4	574	US-10-763-712A-6	Sequence 6426, App
46	54	11.4	626	US-10-467-657-6426	Sequence 7618, App
47	54	11.4	626	US-10-467-657-7618	Sequence 10257, App
48	54	11.4	1011	US-11-098-666-10257	Sequence 1658, App
49	53.5	11.3	177	US-10-467-657-1658	Sequence 832, App
50	53.5	11.3	206	US-10-793-626-832	Sequence 417, App
51	53.5	11.3	273	US-09-978-360A-417	Sequence 10812, App
52	53.5	11.3	229	US-11-098-666-10812	Sequence 2186, App
53	53.5	11.3	508	US-11-072-512-2186	Sequence 232, App
54	53.5	11.3	690	US-11-052-554A-232	Sequence 214, App
55	53.5	11.3	702	US-10-510-386-214	Sequence 678, App
56	53.5	11.3	1813	US-10-495-083-10	Sequence 1610, App
57	53	11.2	271	US-10-793-626-678	Sequence 1555, App
58	53	11.2	2335	US-10-821-234-1610	Sequence 2760, App
59	52.5	11.1	264	US-10-821-234-1555	Sequence 9, App
60	52.5	11.1	319	US-10-793-626-2760	Sequence 1203, App
61	52.5	11.1	388	US-11-046-668-9	Sequence 10, App
62	52.5	11.1	398	US-11-046-668-9	Sequence 46, App
63	52.5	11.1	886	US-10-821-234-1329	Sequence 410, App
64	52	11.0	241	US-11-072-512-2203	Sequence 333, App
65	52	11.0	296	US-11-087-227-10	Sequence 3845, App
66	52	11.0	384	US-11-219-282-19	Sequence 1432, App
67	52	11.0	395	US-11-009-658-46	Sequence 84, App
68	52	11.0	456	US-11-069-642-8	
69	52	11.0	497	US-10-454-437-410	
70	52	11.0	588	US-11-053-554A-339	
71	52	11.0	599	US-11-109-187A-3	
72	52	11.0	600	US-11-072-512-3845	
73	52	11.0	1145	US-10-793-626-1432	
74	52	11.0	1613	US-11-108-528-84	
75	52	11.0	1613	US-11-108-528-86	

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWinn9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 41.9%; Score 198; DB 6; Length 88;
Best Local Similarity 44.3%; Pred. No. 1,3e-15;
Matches 39; Conservative 16; Mismatches 31; Indels 2; Gaps 2;

QY 1 MSRTFCTFLKDAERODPOLYGEIGRIYNEISKEAMSWITKQMLINEKLSMNTI 60
DB 1 MARWVFCYKLNKAEAGMKFPLPNEIGKRIFFENVSQZAAWATRHQTLINENRLSLDP 60

QY 61 EDRKLLEQMVNPLF-EGQDVHIAGTYP 87
DB 61 RAREYLAQOQMEQYFFGDGADA-VQGYVP 87

RESULT 2
US-10-857-780-23
Sequence 23, Application US/10857780
Publication No. US20050272043A1

GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 2101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-857-780-23

Query Match 13.7%; Score 65; DB 6; Length 2101;
Best Local Similarity 36.0%; Pred. No. 44;
Matches 18; Conservative 14; Mismatches 10; Indels 8; Gaps 4;

QY 32 NRISKE--AWSQWTKQTMLINEKLSMNIEDRLLEQEMVNFLEQO 78
DB 342 NEIETHSHKATQEMLEKQAL--EKLSAA-LQDKCLBEK--NEILOOK 386

RESULT 3
US-11-022-562-220
Sequence 220, Application US/11022562
Publication No. US2005029742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DPN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718

PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 220
LENGTH: 242
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-11-022-562-220

Query Match 13.6%; Score 64.5; DB 7; Length 242;
Best Local Similarity 27.2%; Pred. No. 3.8;
Matches 25; Conservative 19; Mismatches 31; Indels 17; Gaps 4;

QY 1 MSRTFCTFLKDAERODPOLY----PGSIGRIYNEISKEAMSWITKQMLINEKLS 56
DB 1 MAETBALSKREDPRMOKSVFIIAGAGTCRVLLKILE----QGLPSKVTILGRRKLT 56

QY 57 MNIEDRLLEQEMVNF-----LFEQDV 80
DB 57 -FDEEAYKNVNVQEVVDFEKLDDVSAFQGHV 87

RESULT 4
US-11-179-977-21
Sequence 21, Application US/11179977
Publication No. US20050249789A1

GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
FILE REFERENCE: GC511-PCT
CURRENT APPLICATION NUMBER: US/11/179,977
CURRENT FILING DATE: 2005-07-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 259
TYPE: PRT
ORGANISM: Bacillus
US-11-179-977-21

Query Match 13.2%; Score 62.5; DB 7; Length 259;
Best Local Similarity 28.8%; Pred. No. 6.9;
Matches 21; Conservative 13; Mismatches 36; Indels 3; Gaps 2;

QY 13 DAERDPPOLYGEIGRIYNEISKEAMSWITKQMLINEKLSMNIEDRLLEQEMV 72
DB 159 EADQND-SLYVRKVSVRWYRELKLTISAMVTEAFL--KVLVWQAGDKLVKTMVI 215

QY 73 FLFEGQDVHIAGY 85
DB 216 KWFNGVASHNKAY 228

RESULT 5
US-10-467-657-5358
Sequence 5358, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIAGNI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 5358
LENGTH: 273

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Title: US-09-955-502a-38

Perfect score: 461

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Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	87	5	ABB78152 Amino aci
2	435	94.4	87	5	ABB78151 Amino aci
3	434	94.1	87	5	ABB78150 Amino aci
4	425	92.2	87	5	ABB78153 Amino aci
5	387	83.9	91	5	ABB78158 Amino aci
6	387	83.9	91	5	ABB78157 Amino aci
7	387	83.9	91	5	ABB78156 Amino aci
8	386	83.7	90	5	ABB78155 Amino aci
9	385	83.5	88	5	ABB78160 Amino aci
10	385	83.5	91	5	ABB78161 Amino aci
11	385	83.5	91	5	ABB78159 Amino aci
12	385	83.5	91	5	ABB78162 Amino aci
13	378	80.7	91	5	ABB78163 Amino aci
14	372	80.7	107	7	ABO65445 Klebsiell
15	371	80.5	93	7	ADP05158 Bacteri
16	363	78.7	90	5	ABB78165 Amino aci
17	356	77.2	88	5	ABB78154 Amino aci
18	325	70.5	76	5	ABB78164 Amino aci
19	256	55.5	87	5	ABB78166 Amino aci
20	256	55.5	87	5	ABB78147 Amino aci
21	241	52.3	87	5	ABB78148 Amino aci
22	238.5	51.7	86	5	ABB78149 Amino aci
23	236	51.2	87	5	ABB78170 Amino aci

25	236	51.2	122	7	ABO74609	Abb74609 Pseudomon
26	235.5	51.1	89	9	AEBA1576	Aeb41576 L. pneumo
27	235.5	51.1	95	9	AEBA38294	Aeb38294 L. pneumo
28	235	51.0	87	5	ABB78174	Abb78174 Amino aci
29	230	49.9	90	5	ABB78168	Abb78168 Amino aci
30	229	49.7	87	5	ABB78169	Abb78169 Amino aci
31	227.5	49.3	90	5	ABB78167	Abb78167 Amino aci
32	227	49.2	88	5	ABB78171	Abb78171 Amino aci
33	227	49.2	88	5	ABB78172	Abb78172 Amino aci
34	227	49.2	88	5	ABB78173	Abb78173 Amino aci
35	227	49.2	88	5	ABB77219	Abb77219 N. gonorr
36	224	48.6	87	5	ABB78177	Abb78177 Amino aci
37	224	48.6	88	5	ABB78178	Abb78178 Amino aci
38	214.5	46.5	92	6	ADA34169	Ada34169 Acinetoba
39	202	43.8	87	5	ABB78176	Abb78176 Amino aci
40	144	31.2	110	8	ADL05173	Adl05173 M. catarr
41	76.5	16.6	591	2	AAV41141	Aay41141 Mouse mam
42	76.5	16.6	860	2	AAV41140	Aay41140 Mouse mam
43	76.5	16.6	1755	2	AAV41139	Aay41139 Mouse mam
44	73	15.8	975	5	ABP66068	Abp66068 Bifidobac
45	73	15.8	1144	8	ADS44344	AdS44344 Bacteri
46	72	15.6	506	3	AAV74371	Aay74371 Neisseria
47	71	15.4	503	4	ABG16577	Abg16577 Novel hum
48	71	15.4	883	8	ADN47233	Adn47233 Thermoco
49	70.5	15.3	723	7	ADB85144	AdB85144 Rat calci
50	70.5	15.3	723	8	AD181552	Ad181552 Rat epilch
51	70.5	15.3	723	8	AD181556	Ad181556 Rat calci
52	70.5	15.3	949	6	ABU40639	Abu40639 Protein e
53	70.5	15.3	959	7	ADP06594	Adp06594 Bacteri
54	69.5	15.1	227	3	AAg38052	Aag38052 Arabidops
55	69.5	15.1	593	4	ABG19947	Abg19947 Novel hum
56	69	15.0	484	8	ADM90985	Adm90985 Human pha
57	69	15.0	507	6	ABU40210	Abu40210 Protein e
58	68.5	14.9	218	3	AAg45909	Aag45909 Arabidops
59	68.5	14.9	234	3	AAg45908	Aag45908 Arabidops
60	68	14.8	257	3	AAg31203	Aag31203 Arabidops
61	68	14.8	297	3	AAg31202	Aag31202 Arabidops
62	68	14.8	324	3	AAg31201	Aag31201 Arabidops
63	67.5	14.6	283	8	ADY12704	Ady12704 Plant ful
64	67	14.5	474	7	ABO75727	AbO75727 Pseudomon
65	67	14.5	507	3	AAV74372	Aay74372 Neisseria
66	67	14.5	507	3	AAV74373	Aay74373 Neisseria
67	67	14.5	546	6	ABU38097	Abu38097 Protein e
68	67	14.5	1399	8	ADR75314	Adr75314 Bovine ac
69	67	14.5	1401	8	ADR75290	Adr75290 Bovine ac
70	66.5	14.4	330	4	AAU35726	Aau35726 Helicobac
71	66.5	14.4	330	6	ABU30763	Abu30763 Protein e
72	66.5	14.4	487	8	ADN01595	Adn01595 Enterobac
73	66.5	14.4	730	8	AD181550	Ad181550 Rabbit ep
74	66.5	14.4	765	6	ADA20715	Ada20715 Artichoke
75	66.5	14.4	818	6	ADA20725	Ada20725 Artichoke

ALIGNMENTS

RESULT 1	ABB78152	standard; protein; 87 AA.
ID	ABB78152	
XX	ABB78152;	
AC	05-NOV-2002	(first entry)
DT		
XX		
DE		Amino acid sequence of a YggX homologue.
XX		Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW		hydroxyl radical; DNA damage; YggX homologue.
XX		
OS		Haemophilus influenzae.
XX		
PN		US2002072118-A1.

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX
PI Downs D, Gralnicks JA;
XX
XX WPI; 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from *Salmonella*
CC *enterica* serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX
XX SQ Sequence 87 AA;

Query Match 100.0%; Score 461; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.8e-47;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARTVFCYELKKEAEGDLPOLYPGELGKRIIPDSVSKQAWGEMIKKQTMVNEKKLMMNNA 60
DB 1 MARTVFCYELKKEAEGDLPOLYPGELGKRIIPDSVSKQAWGEMIKKQTMVNEKKLMMNNA 60

OY 61 EHRKLEQEMVNFLEFGKDVHIEGYVP 87
DB 61 EHRKLEQEMVNFLEFGKDVHIEGYVP 87

RESULT 2
ABB78151
ID ABB78151 standard; protein; 87 AA.
XX
XX ABB78151;

AC 05-NOV-2002 (first entry)
XX
XX

DE Amino acid sequence of a YgX homologue.
XX
XX

KW Superoxide damage; cell; YgX; *Salmonella enterica* serovar Typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
XX
XX Pasteurella multocida.
XX
XX

OS US2002072118-A1.
XX
XX
XX 13-JUN-2002.
XX
XX

PF 18-SEP-2001; 2001US-00955502.
XX
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX

PA (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnicks JA;
XX
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from *Salmonella*
CC *enterica* serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX
XX SQ Sequence 87 AA;

Query Match 94.4%; Score 435; DB 5; Length 87;
Best Local Similarity 92.0%; Pred. No. 1.2e-43;
Matches 80; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 1 MARTVFCYELKKEAEGDLPOLYPGELGKRIIPDSVSKQAWGEMIKKQTMVNEKKLMMNNA 60
DB 1 MARTVFCYELKKEAEGDLPOLYPGELGKRIIPDSVSKQAWGEMIKKQTMVNEKKLMMNNA 60

OY 61 EHRKLEQEMVNFLEFGKDVHIEGYVP 87
DB 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87

RESULT 3
ABB78150
ID ABB78150 standard; protein; 91 AA.
XX
XX ABB78150;

AC 05-NOV-2002 (first entry)
XX
XX

DE Amino acid sequence of a YgX homologue.
XX
XX

KW Superoxide damage; cell; YgX; *Salmonella enterica* serovar Typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
XX
XX Unidentified.
XX
XX

OS US2002072118-A1.
XX
XX
XX 13-JUN-2002.
XX
XX

PF 18-SEP-2001; 2001US-00955502.
XX
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX

PA (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnicks JA;
XX
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 / Search time 9.41601 Seconds
(without alignments)
889,003 Million cell updates/sec

Title: US-09-955-502a-38

Perfect score: 461
Sequence: 1 MARVPCRYLKKRAGLDLFDQ.....QEMVFLPEKGVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	90	2	C64013 hypothetical prote
2	387	83.9	91	2	A85954 hypothetical prote
3	387	83.9	91	2	A85082 hypothetical prote
4	387	83.9	91	2	F91108 hypothetical prote
5	386	83.7	90	2	C82320 conserved hypothet
6	385	83.5	91	2	AH0879 conserved hypothet
7	363	78.7	90	2	AT0116 conserved hypothet
8	256	55.5	93	2	B84994 conserved hypothet
9	237	51.4	105	2	C82624 conserved hypothet
10	236	51.2	90	2	H83003 conserved hypothet
11	227	49.2	88	2	H81014 conserved hypothet
12	227	49.2	88	2	H81014 conserved hypothet
13	73	15.8	1024	2	T41415 gag polypeptid -
14	72.5	15.7	353	1	F0MVC8 gag polypeptid -
15	68.5	14.9	1206	2	B36507 gag polypeptid -
16	68	14.8	324	2	T05429 hypothetical prote
17	68	14.8	555	2	C96667 unknown protei
18	68	14.8	583	2	T48365 hypothetical prote
19	68	14.8	593	2	C64097 hypothetical prote
20	67.5	14.6	1119	2	T18491 ORF MSV202 hypothe
21	67	14.5	328	2	T28363 ORF MSV202 hypothe
22	67	14.5	485	2	A84043 chromosome replica
23	67	14.5	507	2	A83105 fumarate hydratase
24	67	14.5	507	2	C81063 fumarate hydratase
25	67	14.5	546	2	A81807 kecol-acid reducto
26	66.5	14.4	330	1	B64561 hypothetical prote
27	66.5	14.4	394	2	B70206 DNA ligase (ATP)
28	66.5	14.4	487	1	LQBP34 hypothetical prote
29	66	14.3	258	2	S58159

30	66	14.3	548	2	A54510	63K antigen - nema
31	65.5	14.2	152	2	B70423	transcription regu
32	65.5	14.2	300	2	F84178	hypothetical prote
33	65.5	14.2	348	2	H70337	conserved hypothet
34	65.5	14.2	723	2	JC7795	epithelial calcium
35	65.5	14.2	1787	2	G57222	hypothetical prote
36	65	14.1	166	2	C95944	probable acetyltra
37	65	14.1	182	2	C69416	hypothetical prote
38	65	14.1	330	2	G91204	hypothetical prote
39	65	14.1	367	2	A86051	hypothetical prote
40	65	14.1	392	2	H80174	hypothetical prote
41	65	14.1	548	2	A28209	60K filarial anti
42	65	14.1	558	2	B97026	probable Fe-S oxid
43	65	14.1	558	2	A85296	hypothetical prote
44	65	14.1	559	2	T05786	hypothetical prote
45	65	14.1	604	2	F84081	isomerase fucil (B
46	64.5	14.0	165	2	A81382	shikimate kinase
47	64.5	14.0	480	2	S38134	WD-40 repeat prote
48	64.5	14.0	1526	2	AC2239	spectrin beta-H ch
49	64.5	14.0	1645	2	A37792	repeat organellar
50	64.5	14.0	1939	2	T18372	probable bopb prot
51	64	13.9	342	2	T13113	ribosomal protein
52	64	13.9	553	2	G70115	methylenetetrahydr
53	64	13.9	641	2	T38659	glycosyltransferas
54	64	13.9	720	2	JC5131	kinesin-related pr
55	64	13.9	742	1	S58691	hypothetical prote
56	64	13.9	946	2	T11488	tetracyclodipicol
57	63.5	13.8	236	2	F89866	hypothetical prote
58	63.5	13.8	996	2	A71080	conserved hypothet
59	63.5	13.8	1008	2	H72310	protein MUC5B, trach
60	63.5	13.8	1321	2	JB0352	protein C05B4.8 [i
61	63	13.7	225	2	C88939	hypothetical prote
62	63	13.7	241	2	T27636	probable WRKY-type
63	63	13.7	271	2	A84643	gene 2 protein - p
64	63	13.7	274	2	S04610	probable RNA nucle
65	63	13.7	372	2	B81350	hypothetical prote
66	63	13.7	501	2	A84784	hypothetical prote
67	63	13.7	1209	2	T46027	hypothetical prote
68	63	13.7	1262	2	T33074	hypothetical prote
69	63	13.7	2672	2	A48126	translation activa
70	62.5	13.6	91	2	H90521	hypothetical prote
71	62.5	13.6	308	2	B71697	probable proteinas
72	62.5	13.6	577	1	A41289	moesin - human
73	62.5	13.6	853	2	S74609	hypothetical prote
74	62.5	13.6	1101	2	G70951	probable ATP-depen
75	62.5	13.6	1150	2	G89881	pyruvate carboxyla

ALIGNMENTS

RESULT 1
C64013 hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)
C1Species: Haemophilus influenzae
C1Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C1Accession: C64013
R1Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A1Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A1Reference number: A64000; MUID:95350630; PMID:7542800
A1Accession: C64013
A1Status: nucleic acid sequence not shown; translation not shown
A1Molecule type: DNA
A1Residues: 1-90 <TIGR>
A1Cross-references: UNIPROT:P44048; UNIPARC:UP1000013B0M4; GB:U22760; GB:L42023; NID:q15
C1Superfamily: Fe(II) trafficking protein Y9gx

Query Match 100.0%; Score 461; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.2638 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502a-38
Perfect score: 461
Sequence: 1 MKRTVFCRYLKKEAGLDFO.....QEMVNFPEGKVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	90	1	FETP_HAEIN
2	461	100.0	90	2	Q4QMD9_HAEI8
3	439	95.2	91	1	FETP_MANSW
4	435	94.4	90	1	FETP_PASWU
5	425	92.2	94	1	FETP_HAEIU
6	389	84.4	90	1	FETP_VIBPA
7	387	83.9	90	1	FETP_VIBVU
8	387	83.9	90	1	FETP_VIBVY
9	386	83.7	90	1	FETP_VIBCH
10	382	82.9	90	1	FETP_ECOU5
11	382	82.9	90	1	FETP_ECOU1
12	382	82.9	90	1	FETP_SHIFL
13	380	82.4	90	1	FETP_SALCP
14	380	82.4	90	1	FETP_SALPA
15	380	82.4	90	1	FETP_SALTI
16	380	82.4	90	1	FETP_SALTY
17	379	82.2	90	1	FETP_PHOPR
18	378	82.0	90	1	FETP_ECOL6
19	371	80.5	90	1	FETP_YERPE
20	363	78.7	90	1	FETP_YERPE
21	361	78.3	90	1	FETP_VIBF1
22	356	77.2	92	1	FETP_SHRON
23	353	76.6	90	1	FETP_ERWCT
24	348	75.5	90	1	FETP_ERWCT
25	330	71.6	90	1	FETP_ERWCT
26	256	55.5	90	1	FETP_BUCAI
27	256	55.5	90	1	FETP_BORBR
28	256	55.5	90	1	FETP_BORBR
29	256	55.5	90	1	FETP_BORBR
30	244	52.9	91	1	FETP_XANNC
31	243	52.7	90	1	FETP_NITSU

32	241	52.3	90	1	FETP_XYLFT	087d06 xylella fas
33	241	52.3	91	1	FETP_BURMA	062iun burkholderi
34	241	52.3	91	1	FETP_BURPS	063e14 burkholderi
35	239.5	52.0	89	1	FETP_LEGPL	05wvc4 legionella
36	239	51.8	92	1	FETP_XANOR	05gy22 xanthomonas
37	237	51.4	90	1	FETP_XYLPA	05pc73 xylella fas
38	236	51.2	90	1	FETP_PSEAR	05nu36 pseudomonas
39	236	51.2	90	2	Q4J228_AZCVI	04j228 azotobacter
40	235.5	51.1	89	1	FETP_LEGPA	05x3x9 legionella
41	235.5	51.1	89	1	FETP_LEGPA	05x3x9 legionella
42	235	51.0	92	1	FETP_XANCP	08p829 xanthomonas
43	235	51.0	92	2	Q4UW14_XANCP	04uw14 xanthomonas
44	232	50.3	91	1	FETP_RALSO	08y010 ralsstonia s
45	231	50.1	91	2	Q4LS19_9BURK	04ls19 burkholderi
46	230	49.9	78	1	FETP_WIGBR	08d3cs wigglewort
47	230	49.9	90	1	FETP_PSEEM	08ufes pseudomonas
48	230	49.9	90	2	Q6T7F6_PSEFL	06t7f6 pseudomonas
49	230	49.9	90	2	Q4ZLP3_PSEBX	04zlp3 pseudomonas
50	229	49.7	90	1	FETP_PSEBK	088r49 pseudomonas
51	227	49.2	88	1	FETP_NEIG1	05f553 neisseria g
52	227	49.2	88	1	FETP_NEIMA	089a44 buchera ap
53	227	49.2	88	1	FETP_NEIMB	07nsr4 chromobacte
54	224	48.6	90	1	FETP_COXRU	08t925 buchera ap
55	224	48.6	90	1	FETP_METCA	06tfd3 acinetobact
56	221	47.9	90	2	Q4KJ72_PSEFS	04kj72 pseudomonas
57	214	46.4	87	1	FETP_BUCBP	089a44 buchera ap
58	214	46.4	90	1	FETP_CHRYO	07nsr4 chromobacte
59	212	46.0	78	1	FETP_BUCAP	08t925 buchera ap
60	211.5	45.9	90	1	FETP_ACICD	06tfd3 acinetobact
61	209	45.3	79	1	FETP_CANBF	07vrg9 candidatus
62	192	41.6	87	1	FETP_FRATF	05nhj8 francisella
63	154	33.4	92	2	Q4NQ04_9DELT	04nq04 anaeromyxob
64	146	31.7	96	2	Q4FVJ7_9GAMW	04fvj7 psychrobact
65	77.5	16.8	416	2	Q89XZ1_BRAJA	089kz1 bradyrhizob
66	76.5	16.6	187	2	Q9HB77_HUMAN	09hb77 homo sapien
67	76.5	16.6	218	2	Q7SPV9_9BETR	07spv9 human betar
68	76.5	16.6	281	2	Q6PG71_MOUSE	06pg71 mus musculu
69	76.5	16.6	372	2	Q85648_9BETR	085648 mouse mamma
70	76.5	16.6	452	2	Q7SPV8_9BETR	07spv8 human betar
71	76.5	16.6	590	1	GAG_MMTVB	P10258 mouse mamma
72	76.5	16.6	590	1	GAG_MMTVC	P11284 mouse mamma
73	76.5	16.6	591	2	Q83391_9BETR	083391 mouse mamma
74	76.5	16.6	591	2	Q91ZT6_9BETR	091zt6 exogenous m
75	76.5	16.6	591	2	Q91ZU1_9BETR	091zui endogenous m

ALIGNMENTS

RESULT 1	ID	FETP_HAEIN	STANDARD	PRT	90 AA.
AC	P44048				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	Probable Pe(2+) trafficking protein.				
GN	OrderedLocustNames=H10760;				
OS	Haemophilus influenzae.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;				
OC	Pasteurellaceae; Haemophilus.				
OX	NCBI_TaxID=727;				
RN					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC	STRAIN=RD / KW20 / ATCC 51907;				
RX	MBDLINE=95350630; PubMed=7542800;				
RA	Flaeschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,				
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,				
RA	McKenney K., Sutton G.C., Fitzhugh W., Fields C.A., Gocayne J.D.,				
RA	Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,				
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,				
RA	Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,				
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,				

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RL Science 269:496-512(1995).
 RN [2]
 RP IDENTIFICATION BY MASS SPECTROMETRY.
 RX MEDLINE=20137488; PubMed=10675023;
 RX DOI=10.1002/(SICI)1522-2683(20000101)21:2<411::AID-ELPS411>3.3.CO;2-W;
 RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
 RA Gray C., Fountoulakis M.;
 RT "Two-dimensional map of the proteome of Haemophilus influenzae";
 RL Electrophoresis 21:411-429(2000).
 CC -I- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
 CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: U32760; AAC22419.1; -; Genomic_DNA.
 CC DR PIR: G64013; G64013.
 CC DR SMR: P44048; 1-87.
 CC DR TIGR: H10760; -;
 CC DR HAMAP: MF_00686; -; 1.
 CC DR InterPro: IPR007457; Y9GX.
 CC DR Pfam: PF04362; DUF495; 1.
 CC DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 CC DR ProDom: PD029191; DUF495; 1.
 CC KW Complete proteome; Iron.
 CC SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF737B93B CRC64;
 QY Query Match 100.0%; Score 461; DB 1; Length 90;
 Db Best Local Similarity 100.0%; Pred. No. 1,8e-39;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARYFCBYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMIKQTMLVNEKKLMNNA 60
 Db 1 MARYFCBYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMIKQTMLVNEKKLMNNA 60
 QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87
 Db 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87
 RESULT 2
 Q4QMD9_HAE18 PRELIMINARY; PRT; 90 AA.
 ID Q4QMD9_HAE18 PRELIMINARY; PRT; 90 AA.
 AC Q4QMD9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein
 GN OrderedLocustNames=NT10920;
 OS Haemophilus influenzae (strain 86-028NP).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=281310;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15968074; DOI=10.1126/JB.187.13.4627-4636.2005;
 RA Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
 RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakalatz L.O.,
 RA Munson R.S., Jr.;
 RT "Genomic sequence of an otitis media isolate of nontypeable
 RT Haemophilus influenzae: comparative study with H. influenzae serotype
 RT d, strain KW20.";
 RL J. Bacteriol. 187:4627-4636(2005).
 DR EMBL: CP000057; AAX87808.1; -; Genomic_DNA.

DR InterPro: IPR007457; Y9GX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 DR ProDom: PD029191; DUF495; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF737B93B CRC64;
 QY Query Match 100.0%; Score 461; DB 2; Length 90;
 Db Best Local Similarity 100.0%; Pred. No. 1,8e-39;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MARYFCBYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMIKQTMLVNEKKLMNNA 60
 QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87
 Db 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87
 RESULT 3
 PFTP_MANSM STANDARD; PRT; 91 AA.
 ID PFTP_MANSM STANDARD; PRT; 91 AA.
 AC Q6SVT7;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 GN OrderedLocustNames=MS0316;
 OS Mannheimia succiniciproducens (strain MBE155E).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OX NCBI_TaxID=221988;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15378067; DOI=10.1038/nbt1010;
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
 RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
 RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
 RT succiniciproducens.";
 RL Nat. Biotechnol. 22:1275-1281(2004).
 CC -I- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
 CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AE016827; AAU36923.1; -; Genomic_DNA.
 CC DR SMR: Q6SVT7; 1-88.
 CC DR HAMAP: MF_00686; -; 1.
 CC DR InterPro: IPR007457; Y9GX.
 CC DR Pfam: PF04362; DUF495; 1.
 CC DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 CC DR ProDom: PD029191; DUF495; 1.
 CC KW Complete proteome; Iron.
 CC SQ SEQUENCE 91 AA; 10801 MW; 8190E2DA0B35AACC CRC64;
 QY Query Match 95.2%; Score 439; DB 1; Length 91;
 Db Best Local Similarity 90.8%; Pred. No. 3.3e-37;
 Matches 79; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MARYFCBYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMIKQTMLVNEKKLMNNA 60
 QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87
 Db 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.4589 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502a-38

Perfect score: 461

Sequence: 1 MARYFCXYLKKEABGLDFO.....QEMVNFLEFGKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/1aa/6 COMB.pep:.*
3: /cgn2_6/prodata/1/1aa/H COMB.pep:.*
4: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep:.*
5: /cgn2_6/prodata/1/1aa/RE COMB.pep:.*
6: /cgn2_6/prodata/1/1aa/Backfilest1.pep:.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	372	80.7	107	US-09-489-039A-11962	Sequence 11962, A
2	371	80.5	93	US-09-543-681A-5443	Sequence 5443, Ap
3	236	51.2	122	US-09-252-991A-23355	Sequence 23355, A
4	214.5	46.5	92	US-09-328-352-5456	Sequence 5456, Ap
5	144	31.2	110	US-09-540-236-2859	Sequence 2859, Ap
6	76.5	16.6	591	US-09-370-368-8	Sequence 8, Appli
7	70.5	15.3	959	US-09-543-681A-6879	Sequence 6879, Ap
8	67.5	14.6	271	US-09-248-796A-19265	Sequence 19265, A
9	67	14.5	474	US-09-252-991A-24473	Sequence 24473, A
10	67	14.5	1401	US-09-750-590A-2	Sequence 2, Appli
11	66	14.3	548	US-09-167-299-3	Sequence 2547, Ap
12	65.5	14.2	623	US-10-104-047-2547	Sequence 5836, Ap
13	65	14.1	292	US-09-328-352-5836	Sequence 17800, A
14	65	14.1	482	US-09-248-796A-17800	Sequence 10, Appl
15	64.5	14.0	415	US-08-602-010A-10	Sequence 10, Appl
16	64.5	14.0	415	US-08-680-726A-10	Sequence 10, Appl
17	64.5	14.0	415	US-09-092-409-10	Sequence 46792, A
18	64.5	14.0	683	US-09-270-767-46792	Sequence 7862, Ap
19	64	13.9	217	US-09-543-681A-7862	Sequence 6519, Ap
20	64	13.9	633	US-09-328-352-6519	Sequence 4, Appli
21	64	13.9	800	US-09-298-924-4	Sequence 1, Appli
22	64	13.9	720	US-08-840-236-1	Sequence 1, Appli
23	64	13.9	720	US-08-505-448A-1	Sequence 44373, A
24	63.5	13.8	586	US-09-270-767-44373	Sequence 6, Appli
25	62.5	13.6	177	US-08-647-960-6	Sequence 2, Appli
26	62.5	13.6	2285	US-09-308-375-2	Sequence 2, Appli
27	62.5	13.6	2285	US-09-932-183A-2	Sequence 2, Appli

28	62	13.4	337	2	US-09-270-767-41746	Sequence 41746, A
29	62	13.4	455	2	US-09-270-767-45790	Sequence 45790, A
30	62	13.4	550	2	US-09-107-532A-7201	Sequence 7201, Ap
31	62	13.4	674	2	US-08-961-083-200	Sequence 200, App
32	62	13.4	674	2	US-09-536-784-200	Sequence 200, App
33	62	13.4	674	2	US-09-765-271-200	Sequence 200, App
34	62	13.4	674	2	US-09-765-272A-200	Sequence 200, App
35	62	13.4	817	1	US-08-381-931B-2	Sequence 2, Appli
36	61.5	13.3	734	1	US-09-442-055-2	Sequence 13, Appl
37	61	13.2	191	1	US-08-468-576B-13	Sequence 13, Appl
38	61	13.2	191	2	US-08-468-576B-13	Sequence 13, Appl
39	61	13.2	191	2	US-08-468-576B-13	Sequence 13, Appl
40	61	13.2	359	1	US-09-092-770-6	Sequence 6, Appli
41	61	13.2	359	2	US-09-222-851-6	Sequence 6, Appli
42	61	13.2	359	2	US-10-265-062-6	Sequence 6, Appli
43	61	13.2	404	1	US-09-092-770-3	Sequence 3, Appli
44	61	13.2	404	2	US-09-222-851-3	Sequence 3, Appli
45	61	13.2	404	2	US-10-265-062-3	Sequence 3, Appli
46	61	13.2	407	2	US-09-949-016-11184	Sequence 11184, A
47	61	13.2	625	2	US-09-949-016-8485	Sequence 8485, Ap
48	61	13.2	625	2	US-09-949-016-8810	Sequence 8810, Ap
49	60.5	13.1	279	2	US-09-198-452A-221	Sequence 221, App
50	60.5	13.1	279	2	US-09-438-185A-205	Sequence 205, App
51	60.5	13.1	438	2	US-09-198-452A-985	Sequence 985, App
52	60.5	13.1	496	2	US-09-800-170-20	Sequence 20, Appl
53	60.5	13.1	547	2	US-09-438-185A-914	Sequence 914, App
54	60.5	13.1	720	2	US-09-583-110-2940	Sequence 2940, Ap
55	60.5	13.1	720	2	US-09-107-433-4193	Sequence 4193, Ap
56	60.5	13.1	782	2	US-09-710-279-2352	Sequence 2352, Ap
57	60.5	13.1	794	2	US-09-134-001C-4310	Sequence 4310, Ap
58	60	13.0	243	2	US-09-270-767-31727	Sequence 31727, A
59	60	13.0	243	2	US-09-270-767-46944	Sequence 46944, A
60	60	13.0	280	2	US-09-323-998E-37	Sequence 37, Appl
61	60	13.0	319	2	US-09-710-279-2760	Sequence 2760, Ap
62	60	13.0	443	2	US-09-134-001C-3183	Sequence 3183, Ap
63	60	13.0	465	2	US-09-769-787-164	Sequence 164, App
64	60	13.0	1248	1	US-09-080-897-12	Sequence 12, Appli
65	60	13.0	1248	2	US-09-323-735-2	Sequence 2, Appli
66	60	13.0	1315	2	US-08-899-595-3	Sequence 3, Appli
67	60	13.0	2101	1	US-08-466-390-4	Sequence 4, Appli
68	60	13.0	2101	1	US-08-470-950-4	Sequence 4, Appli
69	60	13.0	2101	1	US-08-467-781-4	Sequence 4, Appli
70	60	13.0	2101	1	US-08-195-487-4	Sequence 4, Appli
71	60	13.0	2101	1	US-08-483-924-4	Sequence 1, Appli
72	60	13.0	2101	2	US-09-452-294-1	Sequence 32, Appli
73	60	13.0	2101	2	US-09-296-662-32	Sequence 32, Appli
74	60	13.0	2101	4	PCT-US93-06160-4	Sequence 7646, Ap
75	60	13.0	2107	2	US-09-949-016-7646	

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610835
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: PNEUMONIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709, 2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/09489, 039A
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:34:35 ; Search time 54.4363 Seconds
(without alignments)
667.774 Million cell updates/sec

Title: US-09-955-502a-38

Perfect score: 461

Sequence: 1 MARVFCRYLKKAEGLDFQ.....QEMVNFLEKGVHIGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	461	100.0	87	US-09-955-502-7	Sequence 7, Appli
2	435	94.4	87	US-09-955-502-6	Sequence 6, Appli
3	434	94.1	87	US-09-955-502-5	Sequence 5, Appli
4	425	92.2	87	US-09-955-502-8	Sequence 8, Appli
5	387	83.9	91	US-09-955-502-11	Sequence 11, Appli
6	387	83.9	91	US-09-955-502-12	Sequence 12, Appli
7	387	83.9	91	US-09-955-502-13	Sequence 13, Appli
8	386	83.7	90	US-09-955-502-10	Sequence 10, Appli
9	385	83.5	88	US-09-955-502-15	Sequence 15, Appli
10	385	83.5	91	US-09-955-502-14	Sequence 14, Appli
11	385	83.5	91	US-09-955-502-16	Sequence 16, Appli
12	385	83.5	91	US-09-955-502-17	Sequence 17, Appli
13	378	82.0	91	US-09-955-502-18	Sequence 18, Appli
14	363	78.7	90	US-09-955-502-20	Sequence 20, Appli
15	356	77.2	88	US-09-955-502-9	Sequence 9, Appli
16	325	70.5	78	US-09-955-502-19	Sequence 19, Appli
17	256	55.5	76	US-09-955-502-21	Sequence 21, Appli
18	256	55.5	87	US-09-955-502-2	Sequence 2, Appli
19	256	55.5	87	US-09-955-502-3	Sequence 3, Appli
20	241	52.3	87	US-09-955-502-29	Sequence 29, Appli
21	241	52.3	87	US-09-955-502-30	Sequence 30, Appli
22	238.5	51.7	86	US-09-955-502-4	Sequence 4, Appli
23	237	51.4	89	US-09-955-502-22	Sequence 22, Appli
24	236	51.2	87	US-09-955-502-25	Sequence 25, Appli
25	230	49.9	90	US-09-955-502-23	Sequence 23, Appli
26	229	49.7	87	US-09-955-502-24	Sequence 24, Appli
27	227	49.2	88	US-09-955-502-26	Sequence 26, Appli

28	227	49.2	88	3	US-09-955-502-27	Sequence 27, Appli
29	227	49.2	88	3	US-09-955-502-28	Sequence 28, Appli
30	224	48.6	87	3	US-09-955-502-32	Sequence 32, Appli
31	224	48.6	88	3	US-09-955-502-33	Sequence 33, Appli
32	202	43.8	87	3	US-09-955-502-31	Sequence 31, Appli
33	76.5	16.6	591	3	US-09-827-822-8	Sequence 8, Appli
34	71	15.8	1144	4	US-10-369-493-22774	Sequence 22774, A
35	70.5	15.3	503	5	US-10-450-763-46936	Sequence 46936, A
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37	70.5	15.3	723	4	US-10-231-913-139	Sequence 139, App
38	70.5	15.3	723	4	US-10-231-913-140	Sequence 140, App
39	70.5	15.3	723	4	US-10-342-844-22	Sequence 22, Appli
40	70.5	15.3	723	4	US-10-342-844-26	Sequence 26, Appli
41	70.5	15.3	926	4	US-10-282-122A-68563	Sequence 68563, A
42	70	15.2	249	4	US-10-424-599-246645	Sequence 246645, A
43	70	15.2	1261	4	US-10-437-963-189166	Sequence 189166, A
44	69.5	15.1	593	5	US-10-450-763-50306	Sequence 50306, A
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47	67.5	14.6	283	4	US-10-425-114-68519	Sequence 68519, A
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52	66.5	14.4	330	4	US-10-282-122A-58687	Sequence 58687, A
53	66.5	14.4	730	4	US-10-231-913-141	Sequence 141, App
54	66.5	14.4	730	4	US-10-342-844-20	Sequence 20, Appli
55	66.5	14.4	765	4	US-10-078-770-84	Sequence 84, Appli
56	66.5	14.4	818	4	US-10-078-770-94	Sequence 94, Appli
57	66.5	14.4	1809	4	US-10-437-963-195972	Sequence 195972, A
58	65.5	14.2	463	4	US-10-156-761-12981	Sequence 12981, A
59	65.5	14.2	623	4	US-10-104-047-2547	Sequence 2547, Ap
60	65	14.1	451	4	US-10-263-929-173	Sequence 173, App
61	64.5	14.0	278	4	US-10-767-701-43849	Sequence 43849, A
62	64.5	14.0	292	4	US-10-425-114-64383	Sequence 64383, A
63	64.5	14.0	292	4	US-10-425-115-24985	Sequence 24985, A
64	64.5	14.0	320	4	US-10-282-122A-46765	Sequence 46765, A
65	64.5	14.0	415	4	US-10-156-275-10	Sequence 10, Appli
66	64.5	14.0	497	5	US-10-917-602A-57	Sequence 57, Appli
67	64.5	14.0	507	4	US-10-282-122A-69887	Sequence 69887, A
68	64.5	14.0	527	4	US-10-425-115-353344	Sequence 353344, A
69	64.5	14.0	527	5	US-10-917-602A-47	Sequence 47, Appli
70	64.5	14.0	579	4	US-10-360-849A-21	Sequence 21, Appli
71	64.5	14.0	579	4	US-10-360-849A-24	Sequence 24, Appli
72	64.5	14.0	1939	5	US-10-732-923-3340	Sequence 3340, Ap
73	64.5	14.0	4097	6	US-11-097-143-237	Sequence 237, App
74	64	13.9	553	4	US-10-282-122A-47026	Sequence 47026, A
75	64	13.9	553	5	US-10-732-923-18350	Sequence 18350, A

ALIGNMENTS

RESULT 1
US-09-955-502-7
Sequence 7, Appli
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960236.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 87
TYPE: PRT
ORGANISM: Haemophilus Influenzae

US-09-955-502-7

Query Match 100.0%; Score 461; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 4,4e-44;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARVFCGYLKKKAEGLDLPOLYPGELGKRIFDSVSKQAWGEMIKKQTMVNEKKLNMNNA 60
Db 1 MARVFCGYLKKKAEGLDLPOLYPGELGKRIFDSVSKQAWGEMIKKQTMVNEKKLNMNNA 60

Qy 61 EHRKLLBOEMVNFLEFGKDVHIEGYVP 87
Db 61 EHRKLLBOEMVNFLEFGKDVHIEGYVP 87

RESULT 2
US-09-955-502-6

; Sequence 6, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296,97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 87

; TYPE: PRT

; ORGANISM: Pasteurella multocida

US-09-955-502-6

Query Match 94.4%; Score 435; DB 3; Length 87;
Best Local Similarity 92.0%; Pred. No. 3.7e-41;
Matches 80; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MARVFCGYLKKKAEGLDLPOLYPGELGKRIFDSVSKQAWGEMIKKQTMVNEKKLNMNNA 60
Db 1 MARVFCGYLKKKAEGLDLPOLYPGELGKRIFDSVSKQAWGEMIKKQTMVNEKKLNMNNA 60

Qy 61 EHRKLLBOEMVNFLEFGKDVHIEGYVP 87
Db 61 EHRKLLBOEMVNFLEFGKDVHIEGYVP 87

RESULT 3
US-09-955-502-5

; Sequence 5, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296,97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Actinobacillus actinomycetemcomitans

US-09-955-502-5

Query Match 94.1%; Score 434; DB 3; Length 91;

Best Local Similarity 93.1%; Pred. No. 5.1e-41;
Matches 81; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MARVFCGYLKKKAEGLDLPOLYPGELGKRIFDSVSKQAWGEMIKKQTMVNEKKLNMNNA 60
Db 1 MARVFCGYLKKKAEGLDLPOLYPGELGKRIFDSVSKQAWGEMIKKQTMVNEKKLNMNNA 60

Qy 61 EHRKLLBOEMVNFLEFGKDVHIEGYVP 87
Db 61 EHRKLLBOEMVNFLEFGKDVHIEGYVP 87

RESULT 4
US-09-955-502-8

; Sequence 8, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296,97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 87

; TYPE: PRT

; ORGANISM: Haemophilus ducreyi

US-09-955-502-8

Query Match 92.2%; Score 425; DB 3; Length 87;
Best Local Similarity 90.8%; Pred. No. 5e-40;
Matches 79; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MARVFCGYLKKKAEGLDLPOLYPGELGKRIFDSVSKQAWGEMIKKQTMVNEKKLNMNNA 60

Qy 61 EHRKLLBOEMVNFLEFGKDVHIEGYVP 87
Db 61 EHRKLLBOEMVNFLEFGKDVHIEGYVP 87

RESULT 5
US-09-955-502-11

; Sequence 11, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296,97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Baccherichia coli K-12 MG1655

US-09-955-502-11

Query Match 83.9%; Score 387; DB 3; Length 91;
Best Local Similarity 78.2%; Pred. No. 1e-35;
Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.60992 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-38

Perfect score: 461
Sequence: 1 MARVFCBYLKKRAGLDLFDQ.....QEMNLFEGKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_AA_New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
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6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	49.2	88	US-10-467-657-968	Sequence 968, App
2	68	14.8	593	US-11-194-246-317	Sequence 317, App
3	66.5	14.4	765	US-11-120-308-84	Sequence 84, App
4	66.5	14.4	818	US-11-120-308-94	Sequence 94, App
5	65.5	14.2	623	US-11-072-512-2547	Sequence 2547, App
6	62.5	13.6	577	US-11-072-175-187	Sequence 187, App
7	61	13.2	342	US-11-156-084-25	Sequence 25, App
8	61	13.2	342	US-11-156-084-44	Sequence 44, App
9	61	13.2	359	US-11-087-227-8	Sequence 8, App
10	61	13.2	359	US-11-192-450-6	Sequence 6, App
11	61	13.2	369	US-11-156-084-45	Sequence 45, App
12	61	13.2	404	US-11-087-227-6	Sequence 6, App
13	61	13.2	404	US-11-192-450-3	Sequence 3, App
14	61	13.2	619	US-11-156-084-24	Sequence 24, App
15	60.5	13.1	285	US-10-467-657-232	Sequence 222, App
16	60.5	13.1	285	US-10-467-657-8230	Sequence 8230, App
17	60.5	13.1	496	US-11-069-642-20	Sequence 20, App
18	60.5	13.1	319	US-10-793-626-2352	Sequence 2352, App
19	60	13.0	319	US-10-793-626-2760	Sequence 2760, App
20	60	13.0	465	US-10-873-528-164	Sequence 164, App
21	60	13.0	2101	US-10-453-372-658	Sequence 23, App
22	59	12.8	834	US-10-453-372-658	Sequence 658, App
23	59	12.8	1734	US-11-192-967-6	Sequence 6, App
24	59	12.8	1734	US-11-192-967-6	Sequence 6, App
25	58.5	12.7	253	US-10-724-598-28	Sequence 28, App

26	58.5	12.7	466	US-10-524-647-114	Sequence 114, App
27	58.5	12.7	466	US-10-524-972-102	Sequence 102, App
28	58.5	12.7	729	US-10-511-538-101	Sequence 101, App
29	58.5	12.7	774	US-11-070-627-7	Sequence 7, App
30	58	12.6	296	US-11-087-227-10	Sequence 10, App
31	58	12.6	452	US-10-467-962B-14	Sequence 14, App
32	57.5	12.5	305	US-11-156-084-178	Sequence 178, App
33	57.5	12.5	635	US-11-098-686-10433	Sequence 10433, App
34	57.5	12.5	650	US-10-467-657-1948	Sequence 1948, App
35	57	12.4	336	US-10-453-372-658	Sequence 640, App
36	57	12.4	391	US-11-207-626A-16	Sequence 16, App
37	57	12.4	391	US-11-207-626A-27	Sequence 27, App
38	57	12.4	695	US-10-453-372-658	Sequence 648, App
39	57	12.4	700	US-10-995-561-922	Sequence 922, App
40	57	12.4	700	US-10-995-561-922	Sequence 924, App
41	57	12.4	775	US-10-995-561-924	Sequence 924, App
42	57	12.4	793	US-10-453-372-656	Sequence 925, App
43	57	12.4	793	US-10-995-561-925	Sequence 925, App
44	57	12.4	804	US-10-453-372-650	Sequence 950, App
45	57	12.4	857	US-10-453-372-652	Sequence 654, App
46	57	12.4	905	US-10-453-372-652	Sequence 652, App
47	57	12.4	905	US-10-453-372-652	Sequence 654, App
48	57	12.4	905	US-10-453-372-652	Sequence 654, App
49	57	12.4	905	US-10-453-372-652	Sequence 654, App
50	57	12.4	963	US-10-995-561-923	Sequence 664, App
51	57	12.4	1012	US-10-453-372-660	Sequence 923, App
52	56.5	12.3	349	US-10-821-234-1387	Sequence 660, App
53	56.5	12.3	411	US-11-072-512-3452	Sequence 646, App
54	56.5	12.3	1766	US-11-072-185-10	Sequence 1367, App
55	55.5	12.0	250	US-11-098-686-11014	Sequence 3452, App
56	55.5	12.0	268	US-10-995-561-718	Sequence 10, App
57	55.5	12.0	299	US-11-156-084-288	Sequence 11014, App
58	55.5	12.0	301	US-11-055-882-1062	Sequence 718, App
59	55.5	12.0	355	US-10-995-561-720	Sequence 288, App
60	55.5	12.0	739	US-10-131-826A-478	Sequence 1062, App
61	55	11.9	266	US-09-995-433-6	Sequence 720, App
62	55	11.9	279	US-11-098-686-10812	Sequence 478, App
63	55	11.9	504	US-11-072-512-3467	Sequence 6, App
64	55	11.9	560	US-11-131-479-16	Sequence 10812, App
65	54.5	11.8	242	US-11-022-562-220	Sequence 16, App
66	54.5	11.8	1299	US-10-821-234-1145	Sequence 220, App
67	54	11.7	139	US-10-793-626-1310	Sequence 1145, App
68	54	11.7	175	US-09-978-360A-762	Sequence 1310, App
69	54	11.7	175	US-10-821-234-1522	Sequence 762, App
70	54	11.7	175	US-11-072-175-206	Sequence 1522, App
71	54	11.7	177	US-10-467-657-1658	Sequence 206, App
72	54	11.7	254	US-11-072-512-3198	Sequence 1658, App
73	54	11.7	403	US-11-192-450-4	Sequence 3198, App
74	54	11.7	603	US-10-770-726-75	Sequence 4, App
75	54	11.7	1122	US-10-467-657-6112	Sequence 75, App
					Sequence 6112, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: PIZZANI Maria Rita
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

;; PRIOR FILING DATE: 1999-07-12
;; PRIOR APPLICATION NUMBER: 60/153,534
;; PRIOR FILING DATE: 1999-09-13

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; LENGTH: 818  
; TYPE: PRT  
; ORGANISM: Helianthus tuberosus  
trc-11-1320-309-84
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Query Match	14.4%	Score 66.5;	DB 7;	Length 818;
Best Local Similarity	25.0%;	Pred. No. 8;		
Matches 18;	Conservative 14;	Mismatches 17;	Indels 23;	Gaps 4

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 71.531 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502a-39

Perfect score: 466
Sequence: 1 MARYNCVHLNKADGLDFQ.....QNTSPLFGKQVEIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 433378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	466	100.0	88	5	ABB78154 Amino aci
2	356	76.4	87	5	ABB78152 Amino aci
3	347	74.5	90	5	ABB78155 Amino aci
4	346	74.2	93	7	ADf05158 Bacterial
5	345	74.0	87	5	ABB78151 Amino aci
6	344	73.8	91	5	ABB78150 Amino aci
7	336	72.1	87	5	ABB78153 Amino aci
8	336	72.1	88	5	ABB78160 Amino aci
9	336	72.1	91	5	ABB78161 Amino aci
10	336	72.1	91	5	ABB78159 Amino aci
11	336	72.1	91	5	ABB78162 Amino aci
12	332	71.2	91	5	ABB78158 Amino aci
13	332	71.2	91	5	ABB78157 Amino aci
14	332	71.2	91	5	ABB78156 Amino aci
15	327	70.2	107	7	ABO65445 Amino aci
16	326	70.0	91	5	ABB78163 Amino aci
17	308	66.1	90	5	ABB78165 Amino aci
18	292	62.7	78	5	ABB78164 Amino aci
19	256	54.9	87	5	ABB78148 Amino aci
20	256	54.9	87	5	ABB78147 Amino aci
21	242	53.0	86	5	ABB78149 Amino aci
22	237	50.9	87	5	ABB78169 Amino aci
23	235	50.4	87	5	ABB78170 Amino aci
24	235	50.4	122	7	ABO74609 Pseudomon

25	230	49.4	88	5	ABB78171 Amino aci
26	230	49.4	88	5	ABB78172 Amino aci
27	230	49.4	88	5	ABB78173 Amino aci
28	230	49.4	88	6	ABP77219 N. gonorr
29	228	48.9	90	5	ABB78168 Amino aci
30	226	48.5	87	5	ABB78175 Amino aci
31	220	47.2	87	5	ABB78174 Amino aci
32	216	46.4	76	5	ABB78166 Amino aci
33	215	46.1	87	5	ABB78177 Amino aci
34	213	45.7	87	5	ABB78176 Amino aci
35	211.5	45.4	89	9	ABR41576 Amino aci
36	211.5	45.4	95	9	ABR38294 Amino aci
37	205	44.0	88	5	ABB78178 Amino aci
38	200.5	43.0	92	6	ADA34169 Amino aci
39	186.5	40.0	90	5	ABB78167 Amino aci
40	130	27.9	110	8	ADL05173 Amino aci
41	77.5	16.6	2364	5	ABP65068 Hypoxia-i
42	77.5	16.6	2364	8	ABM80299 Tumour-as
43	77.5	16.6	2364	9	AD270337 Human pro
44	75.5	16.2	1120	2	AAW81642 Mouse elf
45	75.5	16.2	1630	2	ADJ70625 Human hea
46	75.5	16.2	2154	2	AAW81639 Mouse elf
47	75.5	16.2	2154	7	ADP74491 Murine el
48	75.5	16.2	2154	8	ADQ88363 Mouse elf
49	75.5	16.2	2154	9	AD285101 Full-leng
50	68.5	14.7	352	7	ADB80553 Ovarian c
51	68	14.6	315	7	ADP83528 C. reinha
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61	68	14.6	404	4	AAV72462 Human cyc
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63	68	14.6	404	7	ADP46687 Human cyc
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65	68	14.6	404	8	ADN05983 Antiproti
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75	66	14.2	269	8	ADP81258 Protein o
			307	5	ABB90271 Human pol

ALIGNMENTS

RESULT 1	ABB78154	standard; protein; 88 AA.
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AC	ABB78154	
XX	05-NOV-2002	(first entry)
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX		
OS	Unidentified.	
XX		
PN	US2002072118-A1.	
XX		

PD	13-JUN-2002.
XX	
EF	18-SEP-2001; 2001US-00955502.
XX	
PR	22-SEP-2000; 2000US-0234588P.
XX	
PA	(DOWN/) DOWNS D.
PA	((GRAL)) GRALNICK J A.
XX	
PI	Downs D, Gralnick JA;
XX	
DR	WPI; 2002-589476/63.
XX	
PT	Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT	cell, comprises engineering the cell to produce more YggX protein, a
XX	
PT	protein identified from <i>Salmonella enterica</i> Serovar Typhimurium.
XX	
PS	Example; Fig 1A; 16pp; English.
XX	
CC	The specification describes a method for reducing superoxide damage to a
CC	cell. The method comprises engineering the cell to produce more than the
CC	native amount of YggX protein (a protein identified from <i>Salmonella</i>
CC	<i>enterica</i> serovar Typhimurium) or its homolog, where the cells are
CC	rendered more resistant to superoxide damage. YggX reduces the oxidation
CC	of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC	clusters. The resulting decrease in free-iron levels generates fewer
CC	hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC	reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC	cell. ABB78147-78 represent YggX homologues
XX	
SQ	Sequence 88 AA;

Query Match	100.0%;	Score 466;	DB 5;	Length 88;
Best Local Similarity	100.0%;	Pred. No. 4.8e-49;		
Matches	88;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps	0;			
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Db	1	MARTVAVCHANKRADGLDFOLYPGDLGKRIFPNISKEAWGLWOKQYMLINEKLNMMNV	60	
Qy	61	DDRKFLEAQTSTFLFEGKDVIEIGFVPE	88	
Db	61	DDRKFLEAQTSTFLFEGKDVIEIGFVPE	88	
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AB878152				
ID	AB878152	standard; protein; 87 AA.		
XX				
AC	AB878152;			
XX				
DT	05-NOV-2002	(first entry)		
XX				
DE		Amino acid sequence of a YggX homologue.		
XX				
KW		Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;		
XX		hydroxyl radical; DNA damage; YggX homologue.		
XX				
OS		Haemophilus influenzae.		
XX				
PN	US2002072118-A1.			
XX				
PD	13-JUN-2002.			
XX				
PF	18-SEP-2001; 2001US-00955502.			
XX				
PR	22-SEP-2000; 2000US-0234588P.			
XX				
PA	(DOWN/)	DOWNS D.		
XX				
PA	(GRAL/)	GRALNICK J A.		
XX				
PI	Downs D, Gralnick JA;			
XX				

DR WP1, 2002-599476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more yggx protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Yggx protein (a protein identified from *Salmonella*
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. Yggx reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer for
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, Yeast, mammalian or plant
CC cell. ABB9147-78 represent yggx homologues

XX
CC
SQ Sequence 87 AA;

Query Match 76.4%; Score 356; DB 5; Length 87;
Best Local Similarity 74.7%; Pred. No. 1.4e-35;
Matches 65; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 MARTNCTHLNKKEDAGDLPOLYPPGDLGRIPDNISKEAMGLMOKQOTLINRKKLNNMNV 60
DB 1 MARYTFCYLYKKKEAGDLPOLYPPGDLGRIPDNISKEAMGLMOKQOTLINRKKLNNMNA 60
QY 61 DDKRFLBAQMTSFLFEGKDVIEGFVP 87
DB 61 EHRKLLDEGMNVFLFEGKDVIEGFVP 87

RESULT 3
 ID ABB78155 standard; protein; 90 AA.
 XX ABB78155;
 AC ABB78155;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.
 XX
 KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.
 XX
 XX *Vibrio cholerae*.
 OS
 XX
 PN US002072118-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 / Search time 9.52424 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502a-39

Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QWTSPLFGKQVEIRGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	356	76.4	90	2	C64013
2	347	74.5	90	2	C82320
3	336	72.1	91	2	AH0879
4	332	71.2	91	2	A85954
5	332	71.2	91	2	A65082
6	332	71.2	91	2	P91108
7	308	66.1	90	2	A10116
8	235	50.4	90	2	H83003
9	230	49.4	88	2	H81014
10	216	46.4	93	2	E84994
11	196	42.1	105	2	C82624
12	77.5	16.6	2364	1	A44159
13	75.5	16.2	1252	2	A47213
14	70	15.0	936	2	H71728
15	68.5	14.7	412	2	S62538
16	67.5	14.5	568	2	T25047
17	67.5	14.5	1111	2	T23047
18	67	14.4	928	2	C97728
19	66.5	14.3	260	2	H82925
20	66.5	14.3	689	2	P83902
21	66.5	14.3	1123	2	T30880
22	66.5	14.3	1176	2	S40899
23	66	14.2	384	2	F64438
24	65.5	14.1	1021	2	AC2202
25	65	13.9	300	2	T15690
26	65	13.9	380	2	T18509
27	65	13.9	651	2	G68177
28	64.5	13.8	577	1	S39804
29	64.5	13.8	1119	2	T18491

30	64	13.7	365	2	C83885	hypothetical prote
31	64	13.7	578	2	T11659	hypothetical prote
32	64	13.7	964	2	T32482	hypothetical prote
33	63.5	13.6	310	2	C64370	modification methy
34	63.5	13.6	1333	2	S65812	RNA-directed DNA p
35	63.5	13.6	1492	2	T14652	protein U - Yersin
36	63.5	13.6	1545	2	T14966	phage lambda-relat
37	63	13.5	151	2	S72243	dynein heavy chain
38	63	13.5	151	2	S72243	dynein heavy chain
39	63	13.5	408	2	H64513	hypothetical prote
40	63	13.5	507	2	C81063	hypothetical prote
41	63	13.5	546	2	A81807	hypothetical prote
42	63	13.5	793	2	C72219	hypothetical prote
43	63	13.5	1638	2	D87749	DNA mismatch repair
44	63	13.5	1638	2	D87749	protein unc-73b (i
45	62.5	13.4	368	2	C71961	guanine nucleotide
46	62.5	13.4	432	2	C97258	hypothetical prote
47	62.5	13.4	481	2	T14300	sugar-binding peri
48	62.5	13.4	516	2	A96753	hypothetical prote
49	62	13.3	150	2	S72244	probable threonine
50	62	13.3	169	2	P80560	dynein heavy chain
51	62	13.3	171	2	P80558	phytochrome - wild
52	62	13.3	179	2	B11274	phytochrome - wild
53	62	13.3	486	2	B46341	probable translati
54	62	13.3	593	2	C64097	helper component p
55	62	13.3	679	2	E80560	probable soluble I
56	62	13.3	972	2	S35521	hypothetical prote
57	62	13.3	1006	2	T00050	DNA topoisomerase
58	61.5	13.2	118	2	I15515	hypothetical prote
59	61.5	13.2	237	2	A71082	dynein-like protei
60	61.5	13.2	265	2	T46013	hypothetical prote
61	61.5	13.2	423	2	H84566	hypothetical prote
62	61.5	13.2	504	2	C64398	probable RING zinc
63	61.5	13.2	583	1	A41129	hypothetical prote
64	61.5	13.2	583	1	A46127	radixin - mouse
65	61.5	13.2	583	1	S39805	radixin - pig
66	61.5	13.2	813	2	D64527	hypothetical prote
67	61.5	13.2	905	1	A27410	nucleotide diphosp
68	61.5	13.2	1017	2	D90550	vaasa-like (myocla
69	61.5	13.2	1922	2	T00637	hypothetical prote
70	61	13.1	151	2	S72239	dynein heavy chain
71	61	13.1	188	2	I70176	dynein-like protei
72	61	13.1	477	2	G69760	beta-glucosidase h
73	61	13.1	486	2	A46341	helper component p
74	61	13.1	583	2	T48365	hypothetical prote
75	61	13.1	847	2	G95843	conserved hypochet

ALIGNMENTS

RESULT 1

C64013 hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)

CSpecies: Haemophilus influenzae

CDate: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

CAccession: C64013

R.Fritschmann, R.D., Adams, M.D., White, O., Clayton, R.A., Kirkness, E.F., Kerlavage, A

, Gocayne, J.D., Scott, J., Shirley, R., Liu, L.I., Glodek, A., Kelley, J.M., Weidman, J

, D.M., Brandon, R.C., Fine, L.D., Fritchman, J.L., Fuhrmann, J.L., Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Guelm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: C64013

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-90 <TIGR>

A:Cross-references: UNIPROT:P44048; UNIPARC:UPI000013804; GB:U32760; GB:I42023; NID:G15

C:Superfamily: Fe(II) trafficking protein Y99x

Query Match 76.4%; Score 356; DB 2; Length 90;
Best Local Similarity 74.7%; Pred. No. 1.9e-30;

Matches	65, Conservative	11, Mismatches	11, Indels	0, Gaps	0, Indels
Qy	1	MARTTNCYHLKKEADGDLFOLYPGDIKGRIFDNI	SKKAMGLMOKKQTM	INKEKLTANNPV	60
Db	1	MARTVPCYHLKKEAGDLFOLYPGELSKRIIDSVSKQAMGMIKKQTM	LVNKEKLTANNNA	60	
Qy	61	DDRKFLKQMTSFLFEGDVELEGVVP	87		
Db	61	EHKKLLQDMVFLFEGDVHLEGVVP	87		

```

RESULT 2
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogroup
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Species: Vibrio cholerae
C/Accession: C82320
R/Hesseldberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charlson, D.; Ermolaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Selzer, E
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nucleotide 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <RBI>
A/Cross-references: UNIPARC:UPI0000C2CCF; GB:AE004132; GB:AE003852; NID:93654871, PMID
A/Experimental source: serogroup O1, strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0451
A/Map position: 1

```

[illegible]

RESULT 3
 AH0879
 conserved hypothetical protein SRY3266 [imported] - *Salmonella enterica* subsp. *enterica*
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi
 A>Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AH0879
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
 , S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero
 A:Reference number: AB0502; M0ID:21534947; PMID:11677608
 A:Accession: AH0879
 A:status: preliminary
 A:molecule type: DNA
 A:Residues: 1-91 <PAR>
 A:Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:gi6504189;
 C:genetics:
 A:gene: SRY3266
 C:Superfamily: fe(II) trafficking protein YggX

Query Match	72.1%;	Score 336;	DB 2;	Length 91;
Best Local Similarity	68.2%;	Pred. No. 2.4e-28;		
Matches	60;	Conservative	13;	Mismatches 15;
				Indels 0;
				Gaps 0

```

QY 1 MARVVNVHLINKKADGIDLPOLYGGDGGKRI PDNISKEAAGLWOKOTYMLINKEKLLMNAV 60
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 1 MSRIIPETTYLGRDAEGDPLYPGELGSKRIYNEISDWAQAQKHQOTYMLINKEKLLMNAV 60
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 DDKRKLDAOMTSPLESGKQVEIRGFPVE 88
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 EHRKLLDEQWVSFLFEGDVAHIGQYTP 88
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 4
 A85954
 Hypothetical protein Y9gX [imported] - *Escherichia coli* (strain O157:H7, substrain EDL933)
 C:Species: *Escherichia coli*
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
 C:Accession: A85954
 R:Perna, N.T., Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grodzicki, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Agodaca,
 Nature 409, 523-533, 2001
 A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: A85954
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-91 <STO>
 A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:G12517511; P
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Y9gX
 C:Superfamily: fe(II) trafficking protein Y9gX

[illegible]

RESULT 5
A65082
hypothetical protein b2962 - *Escherichia coli* (strain K-12)
C.Species: *Escherichia coli*
C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C.Accession: A65082
R.Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
.A.; Rose, D.J.; Mau, B.; Shaq, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of *Escherichia coli* K-12.
A.Reference number: A64720; MUID:97426617; PMID:9278503
A.Accession: A65082
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 191. <BLAT>
A.Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:G
A.Experimental source: strain K-12, substrain M61655
C.Superfamily: fe(II) trafficking protein YggX

[illegible]

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.991 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502a-39

Perfect score: 466

Sequence: 1 MARTNCVHLNKADGLDFQ.....QNTSFLFGKQVLEIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	466	100.0	92	1	Q8BX6 shewanella
2	362	77.7	90	1	Q8DC5 vibrio vuln
3	362	77.7	90	1	Q6IM7 vibrio vuln
4	361	77.5	91	1	Q5E70 vibrio fasc
5	360	77.3	90	1	Q6IM7 vibrio fasc
6	359	77.0	90	1	Q6IM7 vibrio fasc
7	356	76.4	90	1	Q4QMD9 haemophilus
8	347	74.5	90	2	Q4QMD9 haemophilus
9	347	74.5	90	1	Q8715 vibrio para
10	346	74.2	90	1	Q8715 vibrio para
11	345	74.0	90	1	Q5GY58 pasteurilla
12	341	73.2	90	1	Q5GY58 pasteurilla
13	338	72.5	90	1	Q68J9 erwinia car
14	336	72.1	94	1	Q7YK6 haemophilus
15	331	71.0	90	1	Q57K04 salmoneilla
16	331	71.0	90	1	Q57K04 salmoneilla
17	331	71.0	90	1	Q57K04 salmoneilla
18	331	71.0	90	1	Q57K04 salmoneilla
19	330	70.8	90	1	Q67617 salmoneilla
20	327	70.2	90	1	Q8FE19 escherichia
21	327	70.2	90	1	Q8FE19 escherichia
22	327	70.2	90	1	Q8FE19 escherichia
23	322	69.1	90	1	Q8FE19 escherichia
24	316	67.8	90	1	Q8FE19 escherichia
25	308	66.1	90	1	Q8FE19 escherichia
26	257	55.2	90	1	Q8FE19 escherichia
27	256	54.9	90	1	Q8FE19 escherichia
28	256	54.9	90	1	Q8FE19 escherichia
29	256	54.9	90	1	Q8FE19 escherichia
30	240	51.5	90	2	Q4U228 azotobacter
31	237	50.9	90	1	Q88R49 pseudomonas

32	236	50.6	91	1	FETP_RALSO	Q8Y010 ralstonia s
33	235	50.4	90	1	FETP_PSEAR	Q8Y010 pseudomonas
34	230	49.4	88	1	FETP_NEIGL	Q5E553 neisseria g
35	230	49.4	88	1	FETP_NEIMA	Q5E553 neisseria m
36	230	49.4	88	1	FETP_NEIMA	Q5E553 neisseria m
37	229	49.1	90	2	Q4KJ2_PSEFS	Q4KJ2 pseudomonas
38	228	48.9	90	2	FETP_PSESM	Q8Y010 pseudomonas
39	228	48.9	90	2	Q4L1P3_PSESY	Q4L1P3 pseudomonas
40	227	48.7	91	2	Q4LS19_9BURK	Q4LS19 burkholderi
41	226	48.5	91	1	FETP_BURRA	Q62109 burkholderi
42	226	48.5	91	1	FETP_BURPS	Q62109 burkholderi
43	224	48.1	90	1	FETP_CHRYO	Q63E14 burkholderi
44	224	48.1	90	2	Q6T7F6_PSEFL	Q7N874 chromobacte
45	216	46.4	77	1	FETP_BUCAL	Q57616 pseudomonas
46	215.5	46.2	89	1	FETP_LEGPA	Q57616 pseudomonas
47	215	46.1	78	1	FETP_WIGER	Q57616 pseudomonas
48	215	46.1	90	1	FETP_WIGER	Q57616 pseudomonas
49	213	45.7	91	1	FETP_WIGER	Q57616 pseudomonas
50	211.5	45.4	89	1	FETP_WIGER	Q57616 pseudomonas
51	211.5	45.4	89	1	FETP_WIGER	Q57616 pseudomonas
52	208	44.6	79	1	FETP_XANOR	Q57616 pseudomonas
53	206	44.2	92	1	FETP_XANOR	Q57616 pseudomonas
54	205	44.0	90	1	FETP_XANOR	Q57616 pseudomonas
55	203	43.6	92	1	FETP_XANCP	Q57616 pseudomonas
56	203	43.6	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
57	199	42.7	78	1	FETP_BUCAP	Q8F925 buchiera ap
58	197.5	42.4	90	1	FETP_XANCP	Q8F925 buchiera ap
59	196	42.1	90	1	FETP_XANCP	Q8F925 buchiera ap
60	196	42.1	90	1	FETP_XANCP	Q8F925 buchiera ap
61	185	39.7	87	1	FETP_XANCP	Q8F925 buchiera ap
62	181	38.8	87	1	FETP_XANCP	Q8F925 buchiera ap
63	148.5	31.9	92	2	Q4NM04_9DELT	Q4NM04 anaeromyxob
64	131	28.1	96	2	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
65	92	19.7	507	2	Q4Y197_PLABE	Q4Y197 plasmidium
66	92	19.7	1132	2	Q4Z715_PLABE	Q4Z715 plasmidium
67	81	17.4	1096	2	Q7RTB1_PLAYO	Q7RTB1 plasmidium
68	77.5	16.6	2155	2	Q8IX99_HUMAN	Q8IX99 homo sapien
69	77.5	16.6	2364	1	SPTB2_HUMAN	Q01082 homo sapien
70	76.5	16.4	546	2	Q4MPZ8_BACCE	Q4MPZ8 bacillus ce
71	75.5	16.2	2154	2	Q5QWJ7_MOUSE	Q5QWJ7 mus musculu
72	75.5	16.2	2154	2	Q5QWJ7_MOUSE	Q5QWJ7 mus musculu
73	75.5	16.2	2314	2	Q53R99_HUMAN	Q53R99 homo sapien
74	75.5	16.2	2363	2	Q55QJ8_MOUSE	Q55QJ8 mus musculu
75	75.5	16.2	2377	2	Q55ER3_HUMAN	Q55ER3 homo sapien

ALIGNMENTS

RESULT 1	ID	FETP_SHEON	STANDARD;	PRT;	92 AA.
AC	Q8BX6				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	Probable Fe(2+) trafficking protein.				
GN	OrderedLocNames=SO3369;				
OS	Shewanella oneidensis.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;				
OC	Shewanellaceae; Shewanella.				
OX	NCBI_TaxID=70863;				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC	STRAIN=MR-1;				
RC	MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;				
RA	Heidelberg J.F., Paulsen I.T., Nelson K.B., Gallos E.J., Nelson W.C.,				
RA	Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,				
RA	Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.W.,				
RA	Brinkac L.M., Daugherty S.C., Deboy R.T., Dodson R.U., Durkin A.S.,				
RA	Halt D.H., Kolonyak J.F., Madupu R., Peterson J.D., Umayam L.A.,				
RA	White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impriali M.,				
RA	Lee K., Berry K.J., Lee C., Mueller J., Knouri H.M., Gill J.,				

```

RA Uterback T.R., McDonald L.A., Feldlyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis";
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB015774; AAN56367.1; -; Genomic_DNA.
DR TIGR; SO3369; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YgX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 92 AA; 10742 MW; 3116B2B95289B86.CRC64;

Query Match 100.0%; Score 466; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARTVNCVHLNKADGLDLPOLYPGDLGKRIIPDNISKEAWGLMOKQTMLINEKLNMMNV 60
OY 61 DDRKFLAQMSTPLFEGKDVIEGFPVE 88
DB 61 DDRKFLAQMSTPLFEGKDVIEGFPVE 88

RESULT 2
FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q8DCG5;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS OrderedLocustNames=VV11514;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6";
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB016801; AAO09940.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.

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DR Pfam; PF04362; DUF495; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7BA0CB75840A255C.CRC64;

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Best Local Similarity 77.0%; Pred. No. 2.1e-31;
Matches 67; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

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OY 61 DDRKFLAQMSTPLFEGKDVIEGFPV 87
DB 61 EHRKLETEMVNFLEFGKDVHIEGYTP 87

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AC Q7MH14;
DT 05-JUN-2004 (Rel. 44, Created)
DT 05-JUN-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS OrderedLocustNames=VY2885;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC PubMed=1465965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen";
RL Genome Res. 13:2577-2587(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BA000037; BAC95649.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YgX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7BA0CB75840A255C.CRC64;

Query Match 77.7%; Score 362; DB 1; Length 90;
Best Local Similarity 77.0%; Pred. No. 2.1e-31;
Matches 67; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 1 MARTVNCVHLNKADGLDLPOLYPGDLGKRIIPDNISKEAWGLMOKQTMLINEKLNMMNV 60
DB 1 MSRTVFCARLNKADGLDLPOLYPGDLGKRIIPDNISKEAWGLMOKQTMLINEKLNMMNDP 60
OY 61 DDRKFLAQMSTPLFEGKDVIEGFPV 87
DB 61 EHRKLETEMVNFLEFGKDVHIEGYTP 87

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.6595 Seconds
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Title: US-09-955-502a-39

Perfect score: 466

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	346	74.2	93	US-09-543-681A-5443	Sequence 5443, Ap
2	327	70.2	107	US-09-489-039A-11962	Sequence 11962, A
3	235	50.4	122	US-09-252-991A-23355	Sequence 23355, A
4	200.5	43.0	92	US-09-328-352-5456	Sequence 5456, Ap
5	130	27.9	110	US-09-540-236-2859	Sequence 2859, Ap
6	77.5	16.6	2364	US-09-538-092-1243	Sequence 1243, Ap
7	75.5	16.2	2154	US-08-841-349-4	Sequence 4, Appli
8	75.5	16.2	2154	US-09-431-184A-4	Sequence 4, Appli
9	68	14.6	359	US-09-092-770-6	Sequence 6, Appli
10	68	14.6	359	US-09-222-851-6	Sequence 6, Appli
11	68	14.6	359	US-10-265-062-6	Sequence 6, Appli
12	68	14.6	404	US-09-092-770-3	Sequence 3, Appli
13	68	14.6	404	US-09-222-851-3	Sequence 3, Appli
14	68	14.6	404	US-10-265-062-3	Sequence 3, Appli
15	68	14.6	407	US-09-949-016-11184	Sequence 11184, A
16	64	13.7	373	US-09-071-035-116	Sequence 116, App
17	64	13.7	373	US-10-206-576-114	Sequence 114, App
18	64	13.7	406	US-09-071-035-114	Sequence 114, App
19	64	13.7	406	US-10-206-576-114	Sequence 114, App
20	64	13.7	557	US-09-134-000C-4354	Sequence 4354, Ap
21	63	13.5	369	US-09-906-779-5	Sequence 5, Appli
22	62.5	13.4	182	US-09-248-796A-17806	Sequence 17806, A
23	62.5	13.4	278	US-09-567-003C-23	Sequence 23, Appli
24	62	13.3	309	US-09-248-796A-14939	Sequence 14939, A
25	62	13.3	525	US-09-540-236-2250	Sequence 2250, Ap
26	62	13.3	911	US-09-949-002-425	Sequence 425, App
27	62	13.3	1006	US-09-023-905A-12	Sequence 12, Appli

28	62	13.3	1006	US-09-949-002-361	Sequence 361, App
29	61.5	13.2	583	US-09-538-092-1071	Sequence 1071, Ap
30	61.5	13.2	688	US-09-113-750A-3	Sequence 3, Appli
31	61.5	13.2	1143	US-09-949-016-6137	Sequence 6137, Ap
32	61.5	13.2	3878	US-09-914-259-11	Sequence 11, Appli
33	61	13.1	139	US-09-710-279-1310	Sequence 1310, Ap
34	61	13.1	168	US-09-134-001C-5599	Sequence 5599, Ap
35	61	13.1	184	US-09-325-932A-66	Sequence 66, Appli
36	61	13.1	403	US-09-092-770-4	Sequence 4, Appli
37	61	13.1	403	US-09-222-851-4	Sequence 4, Appli
38	61	13.1	403	US-10-265-062-4	Sequence 4, Appli
39	61	13.1	901	US-09-134-001C-5351	Sequence 5351, Ap
40	61	13.1	1078	US-09-583-110-4036	Sequence 4036, Ap
41	61	13.1	1080	US-09-107-433-4843	Sequence 4843, Ap
42	61	13.1	1295	US-09-328-352-6045	Sequence 6045, Ap
43	60.5	13.0	526	US-09-071-035-84	Sequence 84, Appli
44	60.5	13.0	526	US-10-206-576-84	Sequence 84, Appli
45	60.5	13.0	546	US-09-071-035-82	Sequence 82, Appli
46	60.5	13.0	546	US-10-206-576-82	Sequence 82, Appli
47	60.5	13.0	586	US-09-040-755A-1	Sequence 1, Appli
48	60	12.9	301	US-09-107-532A-4953	Sequence 4953, Ap
49	59.5	12.8	92	US-09-513-999C-5393	Sequence 5393, Ap
50	59.5	12.8	191	US-09-270-767-33624	Sequence 33624, A
51	59.5	12.8	191	US-09-270-767-48841	Sequence 48841, A
52	59.5	12.8	305	US-09-248-796A-18731	Sequence 18731, A
53	59.5	12.8	380	US-09-902-540-15247	Sequence 15247, A
54	59.5	12.8	1078	US-09-949-016-11185	Sequence 11185, A
55	59.5	12.8	1085	US-08-431-080-28	Sequence 28, Appli
56	59.5	12.8	1085	US-08-938-534-28	Sequence 28, Appli
57	59.5	12.8	1085	US-09-345-294-28	Sequence 28, Appli
58	59	12.7	66	US-09-107-532A-4003	Sequence 4003, Ap
59	59	12.7	336	US-09-252-991A-28882	Sequence 28882, A
60	59	12.7	376	US-09-248-796A-14887	Sequence 14887, A
61	59	12.7	579	US-09-949-016-10483	Sequence 10483, A
62	59	12.7	580	US-09-248-796A-25118	Sequence 25118, A
63	59	12.7	750	US-10-104-047-2432	Sequence 2432, Ap
64	59	12.7	793	US-08-468-558-5	Sequence 5, Appli
65	59	12.7	793	US-08-676-444-5	Sequence 5, Appli
66	59	12.7	982	US-09-023-905A-7	Sequence 7, Appli
67	58.5	12.6	301	US-09-543-681A-8264	Sequence 8264, Ap
68	58.5	12.6	342	US-09-107-532A-5496	Sequence 5496, Ap
69	58.5	12.6	548	US-09-167-299-3	Sequence 3, Appli
70	58.5	12.6	867	US-10-104-047-3052	Sequence 3052, Ap
71	58	12.4	170	US-10-101-464A-617	Sequence 617, App
72	58	12.4	228	US-09-328-352-7306	Sequence 7306, Ap
73	58	12.4	245	US-09-902-540-11576	Sequence 11576, A
74	58	12.4	296	US-09-100-804-12	Sequence 12, Appli
75	58	12.4	336	US-09-848-294-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/128, 706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Best Local Similarity 73.6%; Pred. No. 2.4e-38;
Matches 64; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

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DB 4 MSRTIFCTFLNKADGLDPOLYPGDLGKRIIPDNISKEAWGLMOKKQTMLINEKLNMMNV 63

QY 61 DDRKFLAQMSTFLPEGKQVEIEGFVP 87
DB 64 DDRKFLAQMSTFLPEGKQVEIEGFVP 90

RESULT 2
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PR1
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 70.2%; Score 327; DB 2; Length 107;
Best Local Similarity 69.0%; Pred. No. 1e-35;
Matches 60; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

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DB 17 MSRTIFCTFLNKADGLDPOLYPGDLGKRIIPDNISKEAWGLMOKKQTMLINEKLNMMNV 76

QY 61 DDRKFLAQMSTFLPEGKQVEIEGFVP 87
DB 77 EHRKFLAQMSTFLPEGKQVEIEGFVP 103

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PR1
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Best Local Similarity 52.3%; Pred. No. 2.1e-23;
Matches 46; Conservative 18; Mismatches 22; Indels 2; Gaps 2;

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QY 61 DDRKFLAQMSTFLPEGKQVEIEGFVP 87
DB 93 EDRKFLAQMSTFLPEGKQVEIEGFVP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-039A
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PR1
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Best Local Similarity 46.1%; Pred. No. 5.7e-19;
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DB 4 MSRTVNCVHLNKADGLDPOLYPGDLGKRIIPDNISKEAWGLMOKKQTMLINEKLNMMNV 63

QY 61 DDRKFLAQMSTFLPEGKQVEIEGFVP 88
DB 64 EHRKFLAQMSTFLPEGKQVEIEGFVP 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PR1
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 27.9%; Score 130; DB 2; Length 110;
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DB 42 FPNAGQRIIPDNISKEAWGLMOKKQTMLINEKLNMMNVDDRKFLAQMSTFLPEGKQVEIEGFVP 101

QY 82 IEQFVP 87
DB 102 PAGYFP 107

RESULT 6
US-09-538-092-1243
; Sequence 1243, Application US/09538092

GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-09-955-502a-39

Perfect score: 466
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Total number of hits satisfying chosen parameters: 1867569

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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	345	74.0	87	US-09-955-502-6	Sequence 6, Appl
5	344	73.8	91	US-09-955-502-5	Sequence 5, Appl
6	336	72.1	88	US-09-955-502-8	Sequence 8, Appl
7	336	72.1	87	US-09-955-502-15	Sequence 15, Appl
8	336	72.1	91	US-09-955-502-14	Sequence 14, Appl
9	336	72.1	91	US-09-955-502-16	Sequence 16, Appl
10	336	72.1	91	US-09-955-502-17	Sequence 17, Appl
11	332	71.2	91	US-09-955-502-11	Sequence 11, Appl
12	332	71.2	91	US-09-955-502-12	Sequence 12, Appl
13	332	71.2	91	US-09-955-502-13	Sequence 13, Appl
14	326	70.0	91	US-09-955-502-18	Sequence 18, Appl
15	308	66.1	90	US-09-955-502-20	Sequence 20, Appl
16	292	62.7	78	US-09-955-502-19	Sequence 19, Appl
17	256	54.9	87	US-09-955-502-2	Sequence 2, Appl
18	256	54.9	86	US-09-955-502-3	Sequence 3, Appl
19	242.5	52.0	86	US-09-955-502-4	Sequence 4, Appl
20	237	50.9	87	US-09-955-502-24	Sequence 24, Appl
21	235	50.4	88	US-09-955-502-25	Sequence 25, Appl
22	230	49.4	88	US-09-955-502-26	Sequence 26, Appl
23	230	49.4	88	US-09-955-502-27	Sequence 27, Appl
24	230	49.4	88	US-09-955-502-28	Sequence 28, Appl
25	228	48.9	90	US-09-955-502-23	Sequence 23, Appl
26	226	48.5	87	US-09-955-502-29	Sequence 29, Appl
27	226	48.5	87	US-09-955-502-30	Sequence 30, Appl

ALIGNMENTS

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30	213	45.7	87	3	US-09-955-502-31	Sequence 31, Appl
31	205	44.0	88	3	US-09-955-502-33	Sequence 33, Appl
32	196	42.1	89	3	US-09-955-502-22	Sequence 22, Appl
33	77.5	16.6	2364	4	US-10-170-385-15	Sequence 15, Appl
34	75.5	16.2	1630	4	US-10-408-765A-2431	Sequence 2431, Ap
35	75.5	16.2	2154	4	US-10-695-994-4	Sequence 4, Appl
36	75.5	16.2	2154	5	US-10-805-684-150	Sequence 150, App
37	69	14.8	921	5	US-10-733-923-3305	Sequence 3305, Ap
38	68	14.6	315	5	US-10-510-628-4	Sequence 4, Appl
39	68	14.6	359	4	US-10-265-062-6	Sequence 6, Appl
40	68	14.6	359	4	US-10-755-889-324	Sequence 324, App
41	68	14.6	374	5	US-10-732-923-2938	Sequence 2938, Ap
42	68	14.6	404	4	US-10-265-062-3	Sequence 3, Appl
43	68	14.6	404	5	US-10-733-923-2939	Sequence 2939, Ap
44	68	14.6	737	5	US-10-510-628-2	Sequence 2, Appl
45	66.5	14.3	689	4	US-10-369-493-17280	Sequence 17280, A
46	66	14.2	307	4	US-10-264-237-2647	Sequence 2647, Ap
47	66	14.2	316	4	US-10-094-749-2195	Sequence 2195, Ap
48	66	14.2	321	4	US-10-308-279-58	Sequence 58, Appl
49	66	14.2	321	4	US-10-126-103-126	Sequence 126, App
50	66	14.2	321	4	US-10-431-036-126	Sequence 126, App
51	66	14.2	321	5	US-10-719-993-655	Sequence 655, App
52	66	14.2	321	5	US-10-719-993-656	Sequence 656, App
53	66	14.2	321	5	US-10-974-440-57	Sequence 57, App
54	66	14.2	344	4	US-10-050-704-281	Sequence 281, App
55	66	14.2	344	4	US-10-798-512-281	Sequence 281, App
56	66	14.2	348	4	US-10-050-704-129	Sequence 129, App
57	66	14.2	348	4	US-10-798-512-129	Sequence 129, App
58	66	14.2	355	4	US-10-424-599-264222	Sequence 264222, A
59	66	14.2	395	5	US-10-501-282-5848	Sequence 5848, Ap
60	65.5	14.1	85	4	US-10-425-115-325713	Sequence 325713, A
61	65.5	14.1	364	4	US-10-282-122A-63394	Sequence 63394, A
62	65.5	14.1	806	4	US-10-264-049-2841	Sequence 2841, Ap
63	65	13.9	305	4	US-10-296-115-1407	Sequence 1407, Ap
64	65	13.9	477	4	US-10-369-493-8852	Sequence 8852, Ap
65	65	13.9	483	5	US-10-732-923-19695	Sequence 19695, A
66	65	13.9	505	4	US-10-250-613-5	Sequence 5, Appl
67	65	13.9	687	5	US-10-370-715B-538	Sequence 538, App
68	64.5	13.8	357	4	US-10-424-599-153968	Sequence 153968, A
69	64.5	13.8	357	4	US-10-424-599-153969	Sequence 153969, A
70	64.5	13.8	393	4	US-10-282-122A-48667	Sequence 48667, A
71	64.5	13.8	593	5	US-10-450-763-50306	Sequence 50306, A
72	64.5	13.8	946	4	US-10-437-963-173299	Sequence 173299, A
73	64	13.7	81	4	US-10-050-704-278	Sequence 278, App
74	64	13.7	81	4	US-10-798-512-278	Sequence 278, App
75	64	13.7	311	4	US-10-363-829-442	Sequence 442, App

RESULT 1
US-09-955-502-9
Sequence 9, Application US/09955502
Patent No. US2002007218A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 9
LENGTH: 88
TYPE: PRT
ORGANISM: Shewanella putrefaciens

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.66291 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502a-39

Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLFGKDVIEIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications_AA_New:*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.dep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	49.4	88	US-10-467-657-968	Sequence 968, App
2	68	14.6	359	US-11-087-227-8	Sequence 8, Appl
3	68	14.6	404	US-11-192-450-6	Sequence 6, Appl
4	68	14.6	404	US-11-087-227-6	Sequence 6, Appl
5	68	14.6	404	US-11-192-450-3	Sequence 3, Appl
6	62	13.3	593	US-11-194-246-317	Sequence 317, App
7	61	13.1	139	US-10-793-626-1310	Sequence 1310, Ap
8	61	13.1	403	US-11-192-450-4	Sequence 4, Appl
9	60	12.9	296	US-11-087-227-10	Sequence 10, Appl
10	59.5	12.8	577	US-11-072-175-187	Sequence 187, App
11	59	12.7	750	US-11-072-512-2432	Sequence 2432, Ap
12	58.5	12.6	867	US-11-072-512-3052	Sequence 3052, Ap
13	57.5	12.3	468	US-11-167-273-1	Sequence 1, Appl
14	56	12.0	539	US-10-793-626-888	Sequence 888, App
15	55.5	11.9	312	US-10-793-626-1210	Sequence 1210, Ap
16	55	11.8	266	US-09-995-493-6	Sequence 6, Appl
17	55	11.8	731	US-10-613-744-10	Sequence 10, Appl
18	54.5	11.7	588	US-10-793-626-3328	Sequence 3328, Ap
19	54.5	11.7	1432	US-11-098-686-10739	Sequence 218, App
20	54	11.6	125	US-10-498-026-83	Sequence 83, Appl
21	54	11.6	205	US-11-156-084-274	Sequence 274, App
22	54	11.6	304	US-11-019-711-198	Sequence 198, App
23	54	11.6	391	US-10-623-155-110	Sequence 110, App
24	54	11.6	391	US-11-019-711-63	Sequence 63, Appl

26	54	11.6	400	6	US-10-623-155-112	Sequence 112, App
27	54	11.6	400	7	US-11-019-711-12	Sequence 12, Appl
28	54	11.6	400	7	US-11-019-711-14	Sequence 14, Appl
29	54	11.6	466	6	US-10-524-647-114	Sequence 114, App
30	54	11.6	466	6	US-10-524-972-102	Sequence 102, App
31	54	11.6	508	7	US-11-072-512-2186	Sequence 2186, App
32	54	11.6	648	6	US-10-467-657-2802	Sequence 2802, Ap
33	54	11.6	829	6	US-10-909-769-26	Sequence 26, Appl
34	53.5	11.5	267	7	US-11-052-554A-219	Sequence 219, App
35	53.5	11.5	326	6	US-10-485-517-306	Sequence 306, App
36	53.5	11.5	340	7	US-11-165-226-128	Sequence 128, App
37	53.5	11.5	734	6	US-10-995-561-770	Sequence 770, App
38	53.5	11.5	756	6	US-11-074-176-202	Sequence 202, App
39	53.5	11.5	765	7	US-11-120-308-84	Sequence 84, Appl
40	53.5	11.5	782	6	US-10-793-626-2352	Sequence 2352, Ap
41	53.5	11.5	817	7	US-11-120-308-94	Sequence 94, Appl
42	53	11.4	178	6	US-10-467-657-1658	Sequence 1658, Ap
43	53	11.4	259	7	US-11-180-418-4	Sequence 4, Appl
44	53	11.4	269	7	US-11-180-418-3	Sequence 3, Appl
45	53	11.4	308	7	US-11-180-418-2	Sequence 2, Appl
46	53	11.4	391	7	US-11-019-711-61	Sequence 61, Appl
47	53	11.4	400	7	US-11-019-711-10	Sequence 10, Appl
48	53	11.4	607	7	US-11-096-051-14	Sequence 14, Appl
49	53	11.4	1558	6	US-10-329-258-14	Sequence 14, Appl
50	53	11.4	2376	7	US-11-096-051-4	Sequence 4, Appl
51	53	11.4	2715	7	US-11-096-051-2	Sequence 2, Appl
52	53	11.4	2715	7	US-11-113-424-51	Sequence 51, Appl
53	53	11.4	2721	7	US-11-096-051-10	Sequence 10, Appl
54	53	11.4	2722	7	US-11-096-051-8	Sequence 8, Appl
55	52.5	11.3	1125	6	US-10-467-657-6112	Sequence 6112, Ap
56	52	11.2	325	7	US-11-074-176-368	Sequence 368, App
57	52	11.2	359	6	US-10-055-877-265	Sequence 265, App
58	52	11.2	359	7	US-11-080-091-1	Sequence 1, Appl
59	52	11.2	359	7	US-11-116-939-15	Sequence 15, Appl
60	52	11.2	359	7	US-11-087-177-23	Sequence 23, Appl
61	52	11.2	359	7	US-11-087-177-25	Sequence 25, Appl
62	52	11.2	359	7	US-11-087-177-29	Sequence 29, Appl
63	52	11.2	364	7	US-11-087-177-31	Sequence 31, Appl
64	52	11.2	364	7	US-11-087-177-33	Sequence 33, Appl
65	52	11.2	365	7	US-11-087-177-27	Sequence 27, Appl
66	52	11.2	386	7	US-11-072-512-2777	Sequence 2777, Ap
67	52	11.2	405	7	US-11-072-512-3581	Sequence 3581, Ap
68	52	11.2	588	7	US-11-052-554A-339	Sequence 339, App
69	52	11.2	640	6	US-10-467-657-4930	Sequence 4930, App
70	52	11.2	694	7	US-11-072-512-2469	Sequence 2469, Ap
71	52	11.2	717	6	US-10-793-626-3022	Sequence 3022, Ap
72	52	11.2	842	6	US-10-909-769-82	Sequence 82, Appl
73	52	11.2	893	7	US-11-072-512-3504	Sequence 3504, Ap
74	51.5	11.1	206	7	US-11-124-367A-316	Sequence 316, App
75	51.5	11.1	319	7	US-11-055-822-334	Sequence 334, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: MONACI Elisabetta
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 49.4%; Score 230; DB 6; Length 88;
Best Local Similarity 49.4%; Pred. No. 9.2e-20;
Matches 44; Conservative 19; Mismatches 24; Indels 2; Gaps 2;

QY 1 MARTVNCVHLNKEADGLFQLYPGDLGKRIFDNISKEAWGLMOKKQTMLINEKLNMMNV 60
DB 1 MARWFCVKNLKEAGMKFPLPNEIGKRIFENVSQAWAATRTQTMLINEENRSLADP 60

QY 61 DDRKFLKLAQMTSFLF-EKGDVIEEGFVPE 88
DB 61 RAREYLAQOMEQYFFGDGADA-VQGYVPQ 88

RESULT 2
US-11-087-227-8
Sequence 8, Application US/11087227
Publication No. US20050260566A1

GENERAL INFORMATION:
APPLICANT: Fischer, Timothy J.
APPLICANT: Malinowski, Douglas P.
APPLICANT: Taylor, Adrian J.
APPLICANT: Parker, Margaret R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
FILE REFERENCE: 046143/287139
CURRENT APPLICATION NUMBER: US/11/087,227
CURRENT FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: 60/556,495
PRIOR FILING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 359
TYPE: PRT
ORGANISM: Homo sapiens
US-11-087-227-8

Query Match 14.6%; Score 68; DB 7; Length 359;
Best Local Similarity 27.6%; Pred. No. 1.8;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

QY 11 NKEADGLDFQLYPGDLGKRIFDN-----ISKAWGLMOKKQTMLINEKLNMMNV 60
DB 76 HKEIGTSDFSRFTYRFRKULFINPSPLPDLISWGCSEKVLMLMKESRYVHDKHFEVLHS 135

QY 61 DDRKFLKLAQMTSFLFPE 76
DB 136 D-----LEPQMRSLILD 147

RESULT 3
US-11-192-450-6
Sequence 6, Application US/11192450
Publication No. US20050282150A1
GENERAL INFORMATION:
APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: Novel Cyclin B Genes and Proteins
FILE REFERENCE: A-524
CURRENT APPLICATION NUMBER: US/11/192,450
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: US/10/265,062
PRIOR FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/09/442,919
PRIOR FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 09/222,851

PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/092,770
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 6
LENGTH: 359
TYPE: PRT
ORGANISM: Human
US-11-192-450-6

Query Match 14.6%; Score 68; DB 7; Length 359;
Best Local Similarity 27.6%; Pred. No. 1.8;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

QY 11 NKEADGLDFQLYPGDLGKRIFDN-----ISKAWGLMOKKQTMLINEKLNMMNV 60
DB 76 HKEIGTSDFSRFTYRFRKULFINPSPLPDLISWGCSEKVLMLMKESRYVHDKHFEVLHS 135

QY 61 DDRKFLKLAQMTSFLFPE 76
DB 136 D-----LEPQMRSLILD 147

RESULT 4
US-11-087-227-6
Sequence 6, Application US/11087227
Publication No. US20050260566A1

GENERAL INFORMATION:
APPLICANT: Fischer, Timothy J.
APPLICANT: Malinowski, Douglas P.
APPLICANT: Taylor, Adrian J.
APPLICANT: Parker, Margaret R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
FILE REFERENCE: 046143/287139
CURRENT APPLICATION NUMBER: US/11/087,227
CURRENT FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: 60/556,495
PRIOR FILING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 404
TYPE: PRT
ORGANISM: Homo sapiens
US-11-087-227-6

Query Match 14.6%; Score 68; DB 7; Length 404;
Best Local Similarity 27.6%; Pred. No. 2.1;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

QY 11 NKEADGLDFQLYPGDLGKRIFDN-----ISKAWGLMOKKQTMLINEKLNMMNV 60
DB 76 HKEIGTSDFSRFTYRFRKULFINPSPLPDLISWGCSEKVLMLMKESRYVHDKHFEVLHS 135

QY 61 DDRKFLKLAQMTSFLFPE 76
DB 136 D-----LEPQMRSLILD 147

RESULT 5
US-11-192-450-3
Sequence 3, Application US/11192450
Publication No. US20050282150A1
GENERAL INFORMATION:
APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: Novel Cyclin B Genes and Proteins
FILE REFERENCE: A-524
CURRENT APPLICATION NUMBER: US/11/192,450
CURRENT FILING DATE: 2005-07-28

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 70.7181 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-40
Perfect score: 477
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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- 8: geneexp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	400	83.9	87	5	ABB78169 Amino aci
5	262.5	55.0	92	6	ADA34169 Acinetoba
6	242	50.7	87	5	ABB78176 Amino aci
7	241	50.5	89	9	ABE41576 L. pneumo
8	241	50.5	95	9	ABE38294 L. pneumo
9	240	50.3	87	5	ABB78148 Amino aci
10	240	50.3	87	5	ABB78147 Amino aci
11	236	49.5	87	5	ABB78152 Amino aci
12	235	49.3	87	5	ABB78157 Amino aci
13	235	49.3	88	5	ABB78154 Amino aci
14	235	49.3	110	8	ADL05173 M. catarr
15	233	48.8	91	5	ABB78150 Amino aci
16	231	48.4	91	5	ABB78158 Amino aci
17	231	48.4	91	5	ABB78157 Amino aci
18	230	48.2	87	5	ABB78156 Amino aci
19	230	48.2	93	7	ABB78151 Amino aci
20	228	47.8	93	7	ADP05158 Bacterial
21	228	47.8	88	5	ABB78160 Amino aci
22	228	47.8	91	5	ABB78161 Amino aci
23	228	47.8	91	5	ABB78159 Amino aci
24	228	47.8	91	5	ABB78162 Amino aci

25	227	47.6	87	5	ABB78175 Amino aci
26	223	46.8	90	5	ABB78155 Amino aci
27	223	46.8	107	7	ABO65445 Klebsiell
28	222.5	46.6	86	5	ABB78149 Amino aci
29	222	46.5	87	5	ABB78153 Amino aci
30	221	46.3	91	5	ABB78174 Amino aci
31	221	46.3	87	5	ABB78163 Amino aci
32	220	46.1	88	5	ABB78178 Amino aci
33	211	44.2	78	5	ABB78164 Amino aci
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37	207	43.4	88	5	ABB78173 Amino aci
38	207	43.4	88	5	ABB78172 Amino aci
39	182.5	38.3	90	5	ABB78167 Amino aci
40	175	36.7	76	5	ABB78166 Amino aci
41	175	36.7	68	1	ADN73327 Thale cre
42	73	15.3	158	3	AAQ10836 Arabidops
43	73	15.3	487	8	ADN74065 Thale cre
44	73	15.3	500	5	AAE27877 Arabidops
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55	70	14.7	185	8	ADP64627 Human onc
56	70	14.7	381	7	ADB65159 Human pro
57	70	14.7	400	3	AAE24352 Human pro
58	70	14.7	400	6	ABR47475 Human pro
59	70	14.7	400	7	ADB75332 Breast ca
60	70	14.7	400	9	ADY72549 Human gp7
61	70	14.7	401	3	AAV91526 Human sec
62	70	14.7	401	3	AAV93368 Human PRO
63	70	14.7	401	4	AAE66117 Protein o
64	70	14.7	401	4	AAU12414 Human PRO
65	70	14.7	401	4	AAE48770 Amyloid-b
66	70	14.7	401	4	AAE93295 Human pro
67	70	14.7	401	4	AAE88480 Human mem
68	70	14.7	401	5	ABP65020 Human pro
69	70	14.7	401	6	ABO17858 Novel hum
70	70	14.7	401	6	ABU91112 Human PRO
71	70	14.7	401	6	ABU66812 Human PRO
72	70	14.7	401	6	ABU59893 Novel sec
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ALIGNMENTS

RESULT 1
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XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
OS
XX
XX
XX US2002072118-A1.
XX

PD 13-JUN-2002.
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more Yggx protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.

Query Match	100.0%;	Score 477;	DB 5;	Length 87;
Best Local Similarity	100.0%;	Pred. No. 1.9e-52;		
Matches	87;	Conservative 0;	Mismatches 0;	Indels 0;
Gap				Gaps 0;
Db	1 MSRTVMCRKTHEELPGADRPYPYGAAGSDIYNNVSRKADDEMOKQTMLINERLNNMNA 60			
	1 MSRTVMCRKTHEELPGADRPYPYGAAGSDIYNNVSRKADDEMOKQTMLINERLNNMNA 60			
Qy	61 EDRKFLQOEMDKFLSGEDYAKADGYYP 87			
	61 EDRKFLQOEMDKFLSGEDYAKADGYYP 87			
Db	61 EDRKFLQOEMDKFLSGEDYAKADGYYP 87			
RESULT 2				
ABO74609				
ID	ABO74609	standard;	protein; 122 AA.	
XX	ABO74609;			
AC	ABO74609;			
XX				
DT	29-JUL-2004	(first entry)		
XX				
DE	Pseudomonas aeruginosa polypeptide #6784.			
XX				
KX	Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.			
XX				
OS	Pseudomonas aeruginosa.			
XX				
PN	US6551795-B1.			
XX				
PD	22-APR-2003.			
XX				
PF	18-FEB-1999;	99US-00252991.		
XX				
PR	18-FEB-1998;	98US-0074788P.		
XX	27-JUL-1998;	98US-0094190P.		
PA	(GENO-) GENOME THERAPEUTICS CORP.			
XX				
PI	Rubenfield MD, Nolling J, Deloughery C, Bush D;			
XX				
DR	WPI: 2003-615309/58.			

DR N-PSDB; ABD08180.

XX

XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

XX

XX

PS Disclosure; SEQ ID NO 23355; 455bp; English.

XX

XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biochip technology. Sequences AB067826-AB084336 represent *P. aeruginosa* polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPRO at seqdata.uspto.gov/sequence.html

XX

XX Sequence 122 AA;

Query Match	100.0%;	Score 477;	DB 7;	Length 122;
Best Local Similarity	100.0%;	Pred. No. 3e-52;		
Matches 87;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	MSRTVMCRKXHEELPGIDRPYPYGAKEGDIYNNVSRKAWDEWQKHQTMLINERRLNMANNA	60	
Db	33	MSRTVMCRKXHEELPGIDRPYPYGAKEGDIYNNVSRKAWDEWQKHQTMLINERRLNMANNA	92	
QY	61	EDRKFTLQEMDKFLSGEDYAKADGYYP	87	
Db	93	EDRKFTLQEMDKFLSGEDYAKADGYYP	119	
RESULT 3				
ID	ABB78168	standard; protein; 90 AA.		
AC	ABB78168;			
DT	05-NOV-2002	(first entry)		
DE		Amino acid sequence of a YggX homologue.		
KM		Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;		
OS		hydroxyl radical; DNA damage; YggX homologue.		
PN		Pseudomonas syringae.		
PD	US2002072118-A1.			
PF	13-JUN-2002.			
PR	18-SEP-2001; 2001US-00955502.			
PI	22-SEP-2000; 2000US-0234588P.			
PA	(DOWN/) DOWNS D.			
PI	(GRAL/) GRALNICK J A.			
PI	Downs D, Gralnick JA;			
PI	WPI, 2002-589476/63.			
PI		Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant		
PI		cell, comprises engineering the cell to produce more YggX protein, a		
PI		protein identified from Salmonella enterica serovar Typhimurium.		

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.41601 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502a-40

Perfect score: 477
Sequence: 1 MSRTVMCRKXHELPGLDRP.....QEMDKPLSGEDYAKADGVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR.80.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	477	100.0	90 2 H83003	conserved hypothe
2	236	49.5	90 2 G64013	hypothetical prote
3	231	48.4	91 2 A85954	hypothetical prote
4	231	48.4	91 2 A65082	hypothetical prote
5	231	48.4	91 2 F91108	hypothetical prote
6	228	47.8	91 2 AH0879	conserved hypothe
7	223	46.8	90 2 C82320	conserved hypothe
8	210	44.0	90 2 A10116	conserved hypothe
9	207	43.4	88 2 H81014	conserved hypothe
10	192	40.3	105 2 C82624	conserved hypothe
11	175	36.7	93 2 A84994	hypothetical prote
12	80.5	16.9	314 2 JC5534	hypothetical prote
13	73	15.3	500 2 E96739	hypothetical prote
14	72	15.1	435 2 D82905	hypothetical prote
15	71.5	15.0	314 2 S31402	hypothetical prote
16	71.5	15.0	2748 2 D87730	hypothetical prote
17	69	14.5	926 2 S57976	nuclear migration
18	68.5	14.4	506 2 H64618	hypothetical prote
19	68	14.3	1083 1 S53048	sigma-54 interacti
20	68	14.3	1148 2 D85360	alpha-mannosidase
21	67	14.0	282 2 D97138	hypothetical prote
22	66.5	13.9	532 2 H72730	DNA replication pr
23	66	13.8	1638 2 D87739	probable acyl-CoA
24	65.5	13.7	2488 2 T42739	protein unc-73b [i
25	65.5	13.7	314 2 JB0127	guanine nucleotide
26	65.5	13.7	342 2 T19021	catechol 2,3-dioxy
27	65.5	13.7	2485 1 H71621	probable inositol
28	65	13.6	468 2 T33857	serine/threonine-s
29	64.5	13.5	523 2 S23384	hypothetical prote
				protein kinase (EC

30	64.5	13.5	766	2 T48463	hypothetical prote
31	64	13.4	283	2 H86839	hypothetical prote
32	64	13.4	642	2 D96777	hypothetical prote
33	64	13.4	670	2 T29898	kinasin protein OS
34	64	13.4	1553	2 S67483	adenosinetriphosph
35	63.5	13.3	613	2 AH2358	hypothetical prote
36	63	13.2	506	2 G84646	hypothetical prote
37	63	13.2	506	2 F71895	hypothetical prote
38	63	13.2	900	2 T33734	hypothetical prote
39	63	13.2	1645	2 A37792	spectrin beta-H ch
40	62.5	13.1	316	2 T50027	annexin-like prote
41	62.5	13.1	433	2 G70345	hypothetical prote
42	62.5	13.1	637	2 S66236	acetylcholinestera
43	62.5	13.1	985	2 T10339	DNA-directed DNA p
44	62	13.0	244	2 C90580	DNA processing pro
45	62	13.0	830	2 B81418	adenylosuccinate l
46	62	13.0	830	2 S56940	factor arrest prot
47	62	13.0	921	2 A83968	isooleucyl-tRNA sym
48	62	13.0	1290	2 DVBY86	matng pheromone a
49	62	13.0	4063	2 T42993	probable spectrin
50	62	13.0	4101	2 T23630	hypothetical prote
51	61.5	12.9	218	2 C70536	hypothetical prote
52	61.5	12.9	455	2 D75043	seryl-tRNA synthet
53	61.5	12.9	509	2 T21512	hypothetical prote
54	61.5	12.9	767	2 T31558	hypothetical prote
55	61.5	12.9	1090	2 AG1749	glycosidase homolo
56	61.5	12.9	1091	2 AP1380	glycosidase homolo
57	61.5	12.9	1111	2 A86922	probable arabinosy
58	61.5	12.9	1120	2 H88449	protein F54D8.1 [i
59	61	12.8	284	2 G72662	hypothetical prote
60	61	12.8	367	2 B81379	probable membrane
61	61	12.8	378	2 H5045	mannitol-1-phospha
62	61	12.8	389	2 T14751	hypothetical prote
63	61	12.8	552	2 C83965	transposase (12) B
64	61	12.8	583	2 A70380	arginine-tRNA liga
65	61	12.8	964	2 T01860	reverse transcript
66	61	12.8	1203	2 A39607	DNA-directed RNA p
67	61	12.8	1232	2 D64413	cofaham biosynth
68	61	12.8	1822	2 S44849	K12H4.8 protein -
69	60.5	12.7	71	2 H97137	hypothetical prote
70	60.5	12.7	299	2 T29546	protein SPE-11 - C
71	60.5	12.7	303	2 A64423	modification methy
72	60.5	12.7	460	2 G71117	serine-tRNA ligase
73	60.5	12.7	1067	2 D96545	probable DNA polym
74	60.5	12.7	1142	2 B96519	probable reverse t
75	60	12.6	150	2 F90212	hypothetical prote

ALIGNMENTS

RESULT 1
H83003
conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A:Reference number: AB2950, PMID:20437337, PMID:10984043
A:Accession: H83003
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STD>
A:Cross-references: UNIPARC:UPI00000CSP26; GB:AB004927; GB:AB004091; NID:99951437; PIDN:
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5148
C:Superfamily: Fe(II) trafficking protein YggX

Query Match 100.0%; Score 477; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRTVMCRKTHBELPGIDRPPYPAKGEDYNNVSRKAMDEMOKHQTMLINERRLNMMNA 60
Db 1 MSRTVMCRKTHBELPGIDRPPYPAKGEDYNNVSRKAMDEMOKHQTMLINERRLNMMNA 60

Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87

RESULT 2
C64013
hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <TIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:915
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 49.5%; Score 236; DB 2; Length 90;
Best Local Similarity 54.5%; Pred. No. 1.3e-17;
Matches 48; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

Qy 1 MSRTVMCRKTHBELPGIDRPPYPAKGEDYNNVSRKAMDEMOKHQTMLINERRLNMMNA 60
Db 1 MARTVFCGYLLKKEABGLDPOLYPGELGKRIPDSVKOMGEWIKQQTMLVNEKLLNMMNA 60

Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EHRKFLQOEMVNFLEFGKDVHIEGYTP 87

RESULT 3
A85954
hypothetical protein Y9gx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Hiller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dinalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F
C/Genetics:
A/Experimental source: strain O157:H7, substrain EDL933
A/Gene: Y9gx
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 48.4%; Score 231; DB 2; Length 91;
Best Local Similarity 51.7%; Pred. No. 4.2e-17;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MSRTVMCRKTHBELPGIDRPPYPAKGEDYNNVSRKAMDEMOKHQTMLINERRLNMMNA 60
Db 1 MSRTVMCRKTHBELPGIDRPPYPAKGEDYNNVSRKAMDEMOKHQTMLINERRLNMMNA 60

Db 1 MSRTVICTFLQREABEGDLPOLYPGELGKRIYNISKEAWAQWQHQTMLINEKLLNMMNA 60

Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EHRKFLQOEMVNFLEFGKDVHIEGYTP 87

RESULT 4
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R/Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coi
A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:9742617; PMID:9278503
A/Accession: A65082
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:91
A/Experimental source: strain K-12, substrain MGL55
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 48.4%; Score 231; DB 2; Length 91;
Best Local Similarity 51.7%; Pred. No. 4.2e-17;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MSRTVMCRKTHBELPGIDRPPYPAKGEDYNNVSRKAMDEMOKHQTMLINERRLNMMNA 60
Db 1 MSRTVICTFLQREABEGDLPOLYPGELGKRIYNISKEAWAQWQHQTMLINEKLLNMMNA 60

Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EHRKFLQOEMVNFLEFGKDVHIEGYTP 87

RESULT 5
F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yaeunaga, T.; Kunihara, S.; Shida, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A9629; MUID:21156231; PMID:11258796
A/Accession: F91108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <HAW>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA837261.1;
A/Experimental source: strain O157:H7, substrain R1MD 0509952
C/Genetics:
A/Gene: ECs3838
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 48.4%; Score 231; DB 2; Length 91;
Best Local Similarity 51.7%; Pred. No. 4.2e-17;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MSRTVMCRKTHBELPGIDRPPYPAKGEDYNNVSRKAMDEMOKHQTMLINERRLNMMNA 60
Db 1 MSRTVICTFLQREABEGDLPOLYPGELGKRIYNISKEAWAQWQHQTMLINEKLLNMMNA 60

Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EHRKFLQOEMVNFLEFGKDVHIEGYTP 87

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.2638 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502a-40

Perfect score: 477
Sequence: 1 MSRTWCKRYHEBLGLDRP.....QEMDKFLSGBDYAKADGYP 87

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database: UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	100.0	90	1	FETP_PSEAE
2	420	88.1	90	2	Q4J228_AZOVI
3	408	85.5	90	1	FETP_PSRSM
4	408	85.5	90	2	Q4ZLJ3_PSRKY
5	401	84.1	90	2	Q4KJ22_PSEFS
6	400	83.9	90	1	FETP_PSRBP
7	383	80.3	90	2	Q6T7F6_PSRFL
8	258.5	54.2	90	1	FETP_ACIAD
9	250	52.4	96	2	Q4FVJ7_9GAWM
10	245	51.4	90	1	FETP_IDILO
11	244	51.2	91	1	FETP_MANSM
12	241	50.5	89	1	FETP_LKQPA
13	241	50.5	89	1	FETP_LKQPA
14	240	50.3	89	1	FETP_LKQPA
15	240	50.3	90	1	FETP_LKQPA
16	240	50.3	90	1	FETP_LKQPA
17	240	50.3	90	1	FETP_LKQPA
18	236	49.5	90	2	FETP_HASIN
19	236	49.5	90	2	Q4QMD9_HAKI8
20	235	49.3	90	1	FETP_METCA
21	235	49.3	92	1	FETP_SHRON
22	233	48.8	90	1	FETP_VIBFI
23	230	48.2	90	1	FETP_PASMU
24	229	48.0	90	1	FETP_PASMU
25	229	48.0	90	1	FETP_PASMU
26	228	47.8	90	1	FETP_PASMU
27	228	47.8	90	1	FETP_PASMU
28	227	47.6	90	1	FETP_PASMU
29	227	47.6	90	1	FETP_PASMU
30	227	47.6	90	1	FETP_PASMU
31	227	47.6	91	1	FETP_PASMU

32	227	47.6	91	1	FETP_BURPS	Q63J4 burkholderi
33	226	47.4	90	1	FETP_ECO57	Pa8B4 escherichia
34	226	47.4	90	1	FETP_ECOLI	Pa8B3 escherichia
35	226	47.4	90	1	FETP_SHIFL	Pa8B5 shigella fl
36	224	47.0	91	2	Q4L519_9BURK	Q4L519 burkholderi
37	223	46.8	90	1	FETP_SALCH	Q57K04 salmonella
38	223	46.8	90	1	FETP_SALPI	Q5PMU1 salmonella
39	223	46.8	90	1	FETP_SALPI	Q5PMU1 salmonella
40	223	46.8	90	1	FETP_SALTY	Q57K04 salmonella
41	223	46.8	90	1	FETP_VIRCH	Q9KJ4 vibrio chol
42	222	46.5	90	1	FETP_ECOL6	Q87E19 escherichia
43	222	46.5	90	1	FETP_VIRPA	Q87E19 escherichia
44	222	46.5	94	1	FETP_HARDU	Q7VK06 haemophilus
45	220	46.1	90	1	FETP_COXBU	Q83D06 coxiella bu
46	218	45.7	90	1	FETP_YERPS	Q66K03 yersinia ps
47	215	45.1	78	1	FETP_WIGRS	Q8D3C5 wigglesworth
48	210	44.0	90	1	FETP_CHRVO	Q7N814 chromobacte
49	210	44.0	90	1	FETP_YERPS	Q8ZHE7 yersinia pe
50	208	43.6	92	1	FETP_XANOR	Q5YV22 xanthomonas
51	207	43.4	88	1	FETP_NEIMA	Q5F553 neisseria g
52	207	43.4	88	1	FETP_NEIMA	Q5F553 neisseria m
53	207	43.4	88	1	FETP_NEIMA	Q5F553 neisseria m
54	204	42.8	91	1	FETP_XANAC	Q8P317 xanthomonas
55	202	42.3	87	1	FETP_FRATT	Q5N118 francisella
56	197	41.3	92	2	FETP_XANCP	Q8P317 xanthomonas
57	197	41.3	92	2	Q4UW14_XANCP	Q8P317 xanthomonas
58	195	40.9	78	1	FETP_BUCAP	Q8K925 buchiera ap
59	193	40.5	90	1	FETP_XYLFT	Q87D06 xyliella fas
60	192	40.3	90	1	FETP_XYLFA	Q9PC73 xyliella fas
61	190	39.8	79	1	FETP_CANBF	Q9PC73 xyliella fas
62	175	36.7	77	1	FETP_BUCAI	Q57618 buchiera ap
63	174	36.5	87	1	FETP_BUCBP	Q57618 buchiera ap
64	171	35.8	92	2	Q4NMQ4_9DELT	Q4NMQ4 anaeromyxob
65	81.5	17.1	326	2	Q55GT4_DICDI	Q55GT4 dictyospora
66	80.5	16.9	314	2	Q7MOR6_BURCE	Q7MOR6 burkholderi
67	79	16.6	703	2	Q4WPT2_ASFPU	Q4WPT2 aspergillus
68	78.5	16.5	1097	2	KIFPD_RAT	Q35787 rattus norv
69	78	16.4	410	2	Q8SRF4_ENCCU	Q8SRF4 encephalito
70	76.5	16.0	314	2	Q9RB85_9BURK	Q9RB85 burkholderi
71	75.5	15.8	280	2	Q81BK9_BACCR	Q81BK9 bacillus ce
72	75	15.7	681	2	Q9LV16_ARATH	Q9LV16 arabidopsis
73	74	15.5	525	2	Q6BNV8_DEBHA	Q6BNV8 debaromyces
74	73.5	15.4	307	2	Q6BPD3_PARTE	Q6BPD3 paramecium
75	73.5	15.4	549	2	Q6BKE2_DEBHA	Q6BKE2 debaromyces

ALIGNMENTS

RESULT 1	ID	FETP_PSEAE	STANDARD;	PRT;	90 AA.
AC	Q9H036;				
DT	10-OCT-2003 (Rel. 42, Created)				
DT	10-OCT-2003 (Rel. 42, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	Probable Fe(2+) trafficking protein.				
GN	OrderedLocName=PA5148;				
OS	Pseudomonas aeruginosa.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;				
OC	Pseudomonadaceae; Pseudomonas.				
OX	NCBI_TaxID=287;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC	STRAIN=ATCC 15692 / PAO1;				
RX	MDL=20437337; PubMed=10984043; DOI=10.1038/35023079;				
RA	Stover C.K., Pham X.-O.T., Erwin A.L., Mitoquchi S.D., Warren P.,				
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,				
RA	Garber R.L., Coulter S.N., Folger K.R., Kas A., Lapidis K., Yuan Y.,				
RA	Brody L.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,				
RA	Smith K.A., Saiter M.H. Jr., Hancock R.R.W., Lory S., Olson M.V.,				
RA	Ratner J., Saiter M.H. Jr., Hancock R.R.W., Lory S., Olson M.V.,				
RT	"Complete genome sequence of Pseudomonas aeruginosa PAO1, an				

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RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: AB004927; AAC08533.1; -; Genomic_DNA.
DR PDB: 1T07; X-ray; A=1-90.
DR SMR; Q9HJ36; 1-79.
DR HAVAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF455; 1.
DR 3D-structure; Complete proteome; Iron.
DR KW SEQUENCE 90 AA; 10625 MW; 02BB6CEBF7AEF39 CRC64;
SQ
Query Match 100.0%; Score 477; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 6,6e-42;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTVMCRKRYHELPGLDRPPYPGAKGEDIYNNVSRKAMDEWQKHQTMLINERRLNMMNA 60
DB 1 MSRTVMCRKRYHELPGLDRPPYPGAKGEDIYNNVSRKAMDEWQKHQTMLINERRLNMMNA 60
QY 61 EDRKFLQAEWEMKFLSGEDYAKADGYV 87
DB 61 EDRKFLQAEWEMKFLSGEDYAKADGYV 87

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RESULT 2

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ID Q4J228_AZOVI PRELIMINARY; PRT; 90 AA.
AC Q4J228;
DT 13-SEP-2005 (TRENBLREL. 31; Created)
DT 13-SEP-2005 (TRENBLREL. 31; Last sequence update)
DT 13-SEP-2005 (TRENBLREL. 31; Last annotation update)
DE Hypothetical protein.
GN ORFNames-AvindhRAFT_6916;
OS Azotobacter vinelandii AVOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammond N., Istrani S., Plickus S., Richardson P.,
RA Copeland N., Istrani S., Plickus S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AVOP."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AVOP."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute;
RA InterPro; IPR007457; YggX.
RA PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammond N., Istrani S., Plickus S., Richardson P.,
RA Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAU03000001; EMB08363.1; -; Genomic_DNA.
DR KW SEQUENCE 90 AA; 10777 MW; F6FE766143D3E5E1 CRC64;
SQ
Query Match 88.1%; Score 420; DB 2; Length 90;
Best Local Similarity 88.4%; Pred. No. 5,7e-36;
Matches 76; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 MSRTVMCRKRYHELPGLDRPPYPGAKGEDIYNNVSRKAMDEWQKHQTMLINERRLNMMNA 60
DB 1 MSRTVMCRKRYHELPGLDRPPYPGAKGEDIYNNVSRKAMDEWQKHQTMLINERRLNMMNA 60
QY 61 EDRKFLQAEWEMKFLSGEDYAKADGYV 86
DB 61 EDRKFLQAEWEMKFLSGEDYAKADGYV 86

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RESULT 3

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ID Q87UF5; STANDARD; PRT; 90 AA.
AC Q87UF5;
DT 10-OCT-2003 (Rel. 42; Created)
DT 10-OCT-2003 (Rel. 42; Last sequence update)
DT 13-SEP-2005 (Rel. 48; Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=PSPT05343;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DC3000;
RG MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Bueli C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidov N.B., Tran B., Russell D., Berry K.J.,
RA Khouiri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Utecherback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: AB016853; AA058769.1; -; Genomic_DNA.
DR SMR; Q87UF5; 1-79.
DR TIGR; PSP05343; -; 1.
DR HAVAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.4589 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502a-40

Perfect score: 477

Sequence: 1 MSRTVMCKRYHEBLPGIDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Issued Patents, AA:
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2: /cgm2_6/ptodata/1/1aa/6 COMB pep: *
3: /cgm2_6/ptodata/1/1aa/H COMB pep: *
4: /cgm2_6/ptodata/1/1aa/PCUTS COMB pep: *
5: /cgm2_6/ptodata/1/1aa/RE COMB pep: *
6: /cgm2_6/ptodata/1/1aa/Backfiles pep: *

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	100.0	122	2	US-09-252-991A-23355
2	262.5	55.0	92	2	US-09-328-352-5456
3	235	49.3	110	2	US-09-540-236-2859
4	230	48.2	93	2	US-09-543-681A-5443
5	223	46.8	107	2	US-09-489-039A-11962
6	72	15.1	314	2	US-09-716-865-4
7	71.5	15.0	506	1	US-08-849-480A-5
8	70	14.7	148	2	US-09-673-395A-389
9	70	14.7	381	2	US-10-104-047-3113
10	70	14.7	401	2	US-09-489-847-202
11	70	14.7	401	2	US-10-012-231A-100
12	70	14.7	401	2	US-10-015-389A-100
13	70	14.7	401	2	US-10-006-768A-100
14	70	14.7	401	2	US-10-015-671A-100
15	70	14.7	401	2	US-10-015-393A-100
16	70	14.7	401	2	US-10-011-833A-100
17	70	14.7	401	2	US-10-006-041A-100
18	70	14.7	401	2	US-10-012-064A-100
19	70	14.7	401	2	US-10-030-269A-8
20	70	14.7	422	2	US-09-489-847-357
21	68	14.3	443	2	US-09-248-796A-15816
22	67.5	14.2	505	2	US-09-543-681A-7151
23	67	14.0	563	2	US-09-902-540-14552
24	66	13.8	361	2	US-09-134-001C-3862
25	65.5	13.7	375	2	US-09-583-110-4950
26	65.5	13.7	382	2	US-09-107-433-3837
27	65	13.6	163	2	US-09-270-767-33714

28	65	13.6	420	2	US-09-248-796A-15323	Sequence 15323, A
29	65	13.6	1042	2	US-09-792-024-106	Sequence 106, App
30	64.5	13.5	327	2	US-09-902-540-10864	Sequence 10864, A
31	64.5	13.5	343	2	US-09-270-767-41701	Sequence 41701, A
32	64.5	13.5	839	2	US-09-758-282B-232	Sequence 232, App
33	64.5	13.5	839	2	US-09-577-304A-232	Sequence 232, App
34	64	13.4	1103	2	US-09-162-373-1	Sequence 1, Appl1
35	64	13.4	1103	2	US-09-467-946-1	Sequence 1, Appl1
36	64	13.4	1123	2	US-09-949-016-9935	Sequence 9935, App
37	63.5	13.3	403	2	US-09-543-681A-6083	Sequence 6083, App
38	63.5	13.3	1967	2	US-09-849-602-16	Sequence 16, Appl1
39	63	13.2	254	2	US-09-586-106D-111	Sequence 111, App
40	63	13.2	254	2	US-10-799-870-111	Sequence 111, App
41	62.5	13.1	3542	2	US-10-087-013-2	Sequence 2, Appl1
42	62	13.0	595	2	US-09-902-540-16334	Sequence 16334, A
43	61	12.8	193	2	US-09-252-991A-17828	Sequence 17828, A
44	61	12.8	378	2	US-09-583-110-3941	Sequence 3941, App
45	61	12.8	378	2	US-09-107-433-5197	Sequence 5197, App
46	61	12.8	381	2	US-09-949-016-9788	Sequence 9788, App
47	61	12.8	381	2	US-09-964-899-13	Sequence 13, Appl1
48	60.5	12.7	302	2	US-09-902-540-13084	Sequence 13084, A
49	60.5	12.7	315	2	US-10-164-595-12	Sequence 12, Appl1
50	60	12.6	243	2	US-09-248-796A-20306	Sequence 20306, A
51	60	12.6	286	2	US-09-248-796A-20057	Sequence 20057, A
52	60	12.6	331	2	US-08-961-083-212	Sequence 212, App
53	60	12.6	331	2	US-09-536-784-212	Sequence 212, App
54	60	12.6	331	2	US-09-765-271-212	Sequence 212, App
55	60	12.6	338	2	US-09-765-272A-212	Sequence 212, App
56	60	12.6	338	2	US-09-328-352-7427	Sequence 7427, App
57	60	12.6	341	2	US-09-252-991A-32797	Sequence 32797, App
58	60	12.6	344	2	US-08-961-083-192	Sequence 192, App
59	60	12.6	344	2	US-09-536-784-192	Sequence 192, App
60	60	12.6	344	2	US-09-765-271-192	Sequence 192, App
61	60	12.6	344	2	US-09-765-272A-192	Sequence 192, App
62	60	12.6	370	2	US-09-583-110-5251	Sequence 5251, App
63	60	12.6	370	2	US-09-769-787-160	Sequence 160, App
64	60	12.6	375	2	US-09-107-433-4121	Sequence 4121, App
65	60	12.6	454	2	US-09-771-161A-95	Sequence 95, Appl1
66	60	12.6	504	2	US-09-538-092-1170	Sequence 1170, App
67	60	12.6	505	2	US-09-949-016-6117	Sequence 6117, App
68	60	12.6	505	2	US-09-771-161A-186	Sequence 186, App
69	60	12.6	513	2	US-09-949-016-11517	Sequence 11517, App
70	60	12.6	531	2	US-09-540-236-2072	Sequence 2072, App
71	60	12.6	1122	2	US-10-146-704-2	Sequence 2, Appl1
72	59.5	12.5	488	1	US-08-911-824-95	Sequence 95, Appl1
73	59.5	12.5	491	2	US-08-912-129A-56	Sequence 56, Appl1
74	59.5	12.5	491	2	US-08-911-824-56	Sequence 56, Appl1
75	59.5	12.5	599	2	US-08-911-824-108	Sequence 108, App

ALIGNMENTS

RESULT 1
US-09-252-991A-23355
Sequence 23355, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074.788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094.190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23355
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-391A-23355

Query Match 100.0%; Score 477; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.6e-55;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTVMCKRYHEBELPGIDRPPYPGAKGEDYNNVSRKAMDQKHQOTMLINERLNNMNA 60
DB 33 MSRTVMCKRYHEBELPGIDRPPYPGAKGEDYNNVSRKAMDQKHQOTMLINERLNNMNA 92

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
DB 93 EDRKFLQOEMDKFLSGEDYAKADGYVP 119

RESULT 2
US-09-328-352-5456
Sequence 5456, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 5456

LENGTH: 92

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-5456

Query Match 55.0%; Score 262.5; DB 2; Length 92;
Best Local Similarity 52.3%; Pred. No. 5.9e-27;
Matches 46; Conservative 19; Mismatches 22; Indels 1; Gaps 1;

QY 1 MSRTVMCKRYHEBELPGIDRPPYPGAKGEDYNNVSRKAMDQKHQOTMLINERLNNMNA 60
DB 4 MSRTVMCKRYHEBELPGIDRPPYPGAKGEDYNNVSRKAMDQKHQOTMLINERLNNMNA 63

QY 61 EDRKFLQOEMDKFLSG-EDYAKADGYVP 87
DB 64 EAKKFLBQREKFFFNDSVEKAEQMKP 91

RESULT 3

US-09-540-236-2859

Sequence 2859, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

FILE REFERENCE: 2709.2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

PRIOR FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2859

LENGTH: 110

TYPE: PRT

ORGANISM: Moraxella catarrhalis

US-09-540-236-2859

Query Match 49.3%; Score 235; DB 2; Length 110;
Best Local Similarity 48.2%; Pred. No. 3.3e-23;
Matches 40; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 5 VMCRKYHEBELPGIDRPPYPGAKGEDYNNVSRKAMDQKHQOTMLINERLNNMNA 64
DB 25 VFCRYQOQLPFLPPFPFNAGQOIOTISAKANNAMLEIOTMLINERLNNMNA 84

QY 65 FLOQEMDKFLSGEDYAKADGYVP 87

DB 85 YLNGREKFLDNGDYKEXKPYKP 107

RESULT 4
US-09-543-681A-5443
Sequence 5443, Application US/09543681A
Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

PRIOR FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5443

LENGTH: 93

TYPE: PRT

ORGANISM: Proteus mirabilis

US-09-543-681A-5443

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Matches 45; Conservative 14; Mismatches 27; Indels 2; Gaps 2;

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DB 4 MSRTVMCKRYHEBELPGIDRPPYPGAKGEDYNNVSRKAMDQKHQOTMLINERLNNMNA 63

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
DB 64 DDKFLBQREKFFFNDSVEKAEQMKP 90

RESULT 5

US-09-489-039A-11962

Sequence 11962, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

PRIOR FILING DATE: 2000-01-27

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 11962

LENGTH: 107

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11962

Query Match 46.8%; Score 223; DB 2; Length 107;
Best Local Similarity 51.1%; Pred. No. 1.2e-21;
Matches 45; Conservative 13; Mismatches 28; Indels 2; Gaps 2;

QY 1 MSRTVMCKRYHEBELPGIDRPPYPGAKGEDYNNVSRKAMDQKHQOTMLINERLNNMNA 60
DB 17 MSRTVMCKRYHEBELPGIDRPPYPGAKGEDYNNVSRKAMDQKHQOTMLINERLNNMNA 76

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
DB 77 EDRKFLQOEMDKFLSGEDYAKADGYVP 103

RESULT 6
US-09-716-865-4
Sequence 4, Application US/09716865

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 54.4363 Seconds
(without alignments)
667.774 Million cell updates/sec

Title: US-09-955-502A-40

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	87	3	US-09-955-502-25
2	408	85.5	90	3	US-09-955-502-23
3	400	83.9	87	3	US-09-955-502-24
4	242	50.7	87	3	US-09-955-502-31
5	240	50.3	87	3	US-09-955-502-2
6	240	50.3	87	3	US-09-955-502-3
7	236	49.5	87	3	US-09-955-502-7
8	235	49.3	87	3	US-09-955-502-32
9	235	49.3	88	3	US-09-955-502-9
10	233	48.8	91	3	US-09-955-502-5
11	231	48.4	91	3	US-09-955-502-11
12	231	48.4	91	3	US-09-955-502-12
13	231	48.4	91	3	US-09-955-502-13
14	230	48.2	87	3	US-09-955-502-6
15	228	47.8	88	3	US-09-955-502-15
16	228	47.8	91	3	US-09-955-502-14
17	228	47.8	91	3	US-09-955-502-16
18	228	47.8	91	3	US-09-955-502-17
19	227	47.6	87	3	US-09-955-502-29
20	227	47.6	87	3	US-09-955-502-30
21	223	46.8	90	3	US-09-955-502-10
22	222.5	46.6	86	3	US-09-955-502-4
23	222	46.5	87	3	US-09-955-502-8
24	221	46.3	88	3	US-09-955-502-18
25	220	46.1	88	3	US-09-955-502-33
26	211	44.2	78	3	US-09-955-502-19
27	210	44.0	90	3	US-09-955-502-20

28	207	43.4	88	3	US-09-955-502-26	Sequence 26, Appl
29	207	43.4	88	3	US-09-955-502-27	Sequence 27, Appl
30	207	43.4	88	3	US-09-955-502-28	Sequence 28, Appl
31	192	40.3	89	3	US-09-955-502-22	Sequence 22, Appl
32	175	36.7	76	3	US-09-955-502-21	Sequence 21, Appl
33	175	36.7	76	3	US-09-955-502-21	Sequence 21, Appl
34	72.5	15.2	333	6	US-11-097-143-16017	Sequence 16017, A
35	72	15.1	732	4	US-10-425-114-55228	Sequence 55228, A
36	72	15.1	1043	4	US-10-310-154-449	Sequence 449, App
37	71	14.9	372	5	US-10-733-923-535	Sequence 535, App
38	70.5	14.8	381	4	US-10-424-599-239645	Sequence 239645, A
39	70	14.7	381	4	US-10-287-122A-52890	Sequence 52890, A
40	70	14.7	400	4	US-10-104-047-3313	Sequence 3313, App
41	70	14.7	400	4	US-10-205-823-156	Sequence 156, App
42	70	14.7	400	5	US-10-177-223-184	Sequence 184, App
43	70	14.7	400	5	US-10-759-803-2	Sequence 2, Appl
44	70	14.7	400	5	US-11-051-454-156	Sequence 156, App
45	70	14.7	401	3	US-09-946-374-100	Sequence 100, App
46	70	14.7	401	4	US-10-028-072-486	Sequence 486, App
47	70	14.7	401	4	US-10-140-808-486	Sequence 486, App
48	70	14.7	401	4	US-10-121-049-486	Sequence 486, App
49	70	14.7	401	4	US-10-123-904-486	Sequence 486, App
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51	70	14.7	401	4	US-10-175-746-486	Sequence 486, App
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53	70	14.7	401	4	US-10-176-921-486	Sequence 486, App
54	70	14.7	401	4	US-10-137-865-486	Sequence 486, App
55	70	14.7	401	4	US-10-140-474-486	Sequence 486, App
56	70	14.7	401	4	US-10-142-431-486	Sequence 486, App
57	70	14.7	401	4	US-10-143-114-486	Sequence 486, App
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65	70	14.7	401	4	US-10-143-032-486	Sequence 486, App
66	70	14.7	401	4	US-10-006-485A-100	Sequence 100, App
67	70	14.7	401	4	US-10-013-907A-100	Sequence 100, App
68	70	14.7	401	4	US-10-015-499A-100	Sequence 100, App
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71	70	14.7	401	4	US-10-123-261-486	Sequence 486, App
72	70	14.7	401	4	US-10-140-921-486	Sequence 486, App
73	70	14.7	401	4	US-10-140-928-486	Sequence 486, App
74	70	14.7	401	4	US-10-015-393A-100	Sequence 100, App
75	70	14.7	401	4	US-10-015-869A-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-955-502-25
Sequence 25, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
PTE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 25
LENGTH: 87
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-955-502-25

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Best Local Similarity 100.0%; Pred. No. 8,1e-49;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSTRVMCRKYHEELPGIDRPPYPGAKGEDIYNNVSRKAMDEMOHQOTMLINERRLNMNNA 60

Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87

RESULT 2

US-09-955-502-23
Sequence 23, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 23

LENGTH: 90

TYPE: PRT

ORGANISM: Pseudomonas syringae

US-09-955-502-23

Query Match 85.5%; Score 408; DB 3; Length 90;
Best Local Similarity 83.9%; Pred. No. 1.4e-40;
Matches 73; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSRTVMCRKYHEELPGIDRPPYPGAKGEDIYNNVSRKAMDEMOHQOTMLINERRLNMNNA 60
Db 1 MTRVTMCRKYHEELPGIDRPPYPGAKGEDIYNNVSRKAMDEMOHQOTMLINERRLNMNNA 60

Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87

RESULT 3

US-09-955-502-24
Sequence 24, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 24

LENGTH: 87

TYPE: PRT

ORGANISM: Pseudomonas putida

US-09-955-502-24

Query Match 83.9%; Score 400; DB 3; Length 87;

Best Local Similarity 79.3%; Pred. No. 1.2e-39;
Matches 69; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

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Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87

RESULT 4

US-09-955-502-31
Sequence 31, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 31

LENGTH: 87

TYPE: PRT

ORGANISM: Thiobacillus ferrooxidans

US-09-955-502-31

Query Match 50.7%; Score 242; DB 3; Length 87;
Best Local Similarity 51.7%; Pred. No. 8e-21;
Matches 45; Conservative 13; Mismatches 29; Indels 0; Gaps 0;

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Db 1 MSRTVMCRKYHEELPGIDRPPYPGAKGEDIYNNVSRKAMDEMOHQOTMLINERRLNMNNA 60

Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 KSRFTLEKQMEAYRFGDQASPGGYVP 87

RESULT 5

US-09-955-502-2
Sequence 2, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 87

TYPE: PRT

ORGANISM: Bordetella pertussis

US-09-955-502-2

Query Match 50.3%; Score 240; DB 3; Length 87;
Best Local Similarity 50.6%; Pred. No. 1.4e-20;
Matches 44; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.60992 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-40

Perfect score: 477

Sequence: 1 MSRTVMCKKXHEPLGLDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA New:*

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	207	43.4	88	6	US-10-467-657-968
2	70	14.7	381	7	US-11-072-512-3313
3	70	14.7	401	6	US-10-131-826A-486
4	65	13.6	353	7	US-11-098-686-10774
5	64.5	13.5	1560	7	US-11-059-982-1
6	60	12.6	370	6	US-10-873-528-160
7	58.5	12.3	310	7	US-11-198-746-88
8	58.5	12.3	310	7	US-11-198-794-88
9	58.5	12.3	315	7	US-11-198-746-91
10	58.5	12.3	315	7	US-11-198-794-91
11	58.5	12.3	322	7	US-11-198-746-89
12	58.5	12.3	322	7	US-11-198-794-89
13	58.5	12.3	528	7	US-11-198-746-90
14	58.5	12.3	528	7	US-11-198-794-90
15	58.5	12.3	548	7	US-11-198-746-86
16	58.5	12.3	548	7	US-11-198-794-86
17	58.5	12.3	695	7	US-11-198-746-87
18	58.5	12.3	695	7	US-11-198-794-87
19	58.5	12.3	832	7	US-11-065-943-100
20	58.5	12.3	832	7	US-11-007-797A-11
21	58.5	12.3	832	7	US-11-007-642B-11
22	58.5	12.3	832	7	US-11-198-746-4
23	58.5	12.3	832	7	US-11-198-794-4
24	58.5	12.3	832	7	US-11-242-730-1
25	58.5	12.3	833	7	US-11-198-746-85

ALIGNMENTS

RESULT 1

US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

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Sequence 3892, Ap
Sequence 2426, Ap
Sequence 110, App
Sequence 81, Appl
Sequence 8, Appl
Sequence 3845, Ap
Sequence 32, Appl
Sequence 8, Appl
Sequence 6, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 9, Appl
Sequence 264, App
Sequence 178, App
Sequence 1036, Ap
Sequence 722, App
Sequence 1635, Ap
Sequence 250, App
Sequence 33, Appl
Sequence 27, Appl
Sequence 124, App
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Sequence 176, App
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Sequence 326, App
Sequence 25, Appl
Sequence 5, Appl
Sequence 169, App
Sequence 80, Appl
Sequence 67, Appl
Sequence 3988, Ap
Sequence 20, Appl
Sequence 958, App
Sequence 1444, Ap
Sequence 3140, Ap
Sequence 546, App
Sequence 25, Appl
Sequence 37, Appl
Sequence 39, Appl

7 US-11-138-794-85
7 US-11-072-512-2914
6 US-10-467-657-72
6 US-10-467-657-3892
6 US-10-793-626-2426
7 US-11-054-281-110
6 US-10-858-730-81
6 US-11-069-642-8
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6 US-10-510-386-32
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7 US-11-091-643-6
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6 US-11-029-003-3
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6 US-10-763-712A-5
7 US-11-072-175-169
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GenCore version 5.1.7
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Run on: February 28, 2006, 19:26:45 ; Search time 70.7181 Seconds
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540.539 Million cell updates/sec

Title: US-09-955-502a-41

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Total number of hits satisfying chosen parameters: 2443163

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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	400	84.7	87	5	ABB78170 Amino aci
4	400	84.7	122	7	ABO74609 Pseudomon
5	265.5	56.2	92	6	ADA34169 Acinetoba
6	239	50.6	87	5	ABB78177 Amino aci
7	237	50.2	87	5	ABB78176 Amino aci
8	237	50.2	88	5	ABB78154 Amino aci
9	232	49.2	89	9	ABE41576
10	232	49.2	95	9	ABE38294 L. pneumo
11	229	48.5	87	5	ABB78175 Amino aci
12	229	48.5	87	5	ABB78152 Amino aci
13	228	48.3	90	5	ABB78155 Amino aci
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21	222	47.0	87	5	ABB78148 Amino aci
22	222	47.0	87	5	ABB78147 Amino aci
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24	219	46.4	88	5	ABB78171 Amino aci

25	219	46.4	88	5	ABB78172 Amino aci
26	219	46.4	88	5	ABB78173 Amino aci
27	219	46.4	88	6	ABP77219 N. gonorr
28	218	46.2	88	5	ABB78160 Amino aci
29	218	46.2	91	5	ABB78161 Amino aci
30	218	46.2	91	5	ABB78159 Amino aci
31	218	46.2	91	5	ABB78162 Amino aci
32	213	45.1	107	7	ABO65445 Amino aci
33	211	44.7	91	7	ABB78163 Amino aci
34	209	44.3	93	7	ADFO5158 Bacterial
35	204.5	43.3	86	5	ABB78149 Amino aci
36	204	43.2	88	5	ABB78178 Amino aci
37	197.5	41.8	78	5	ABB78164 Amino aci
38	188.5	39.9	90	5	ABB78167 Amino aci
39	188	39.8	90	5	ABB78165 Amino aci
40	159	33.7	76	5	ABB78166 Amino aci
41	153	15.5	451	7	ADFO7116 Bacterial
42	72	15.3	259	7	AGA43535 Arabidops
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44	72	15.3	795	4	ABG07025 Novel hum
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47	72	15.3	847	8	ADO54839 Human pro
48	72	15.3	901	8	ADT49817 Rat prick
49	70	14.8	670	8	ADN23314 Bacterial
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51	69	14.6	247	6	ABU33468 Protein e
52	69	14.6	251	4	AAM93928 Human pol
53	69	14.6	251	8	ADL32064 Human pro
54	67.5	14.3	689	5	ABB45714 Listeria
55	67.5	14.3	689	6	ABU33095 Protein e
56	67	14.2	559	8	ADN21954 Bacterial
57	67	14.2	567	8	ADN24711 Bacterial
58	66	14.0	140	5	ABBA7391 Listeria
59	66	14.0	250	8	ADN47605 Thermococ
60	66	14.0	967	8	ADE52670 Human pro
61	66	14.0	1490	6	ABP98817 Human str
62	66	14.0	1651	4	ABG14648 Novel hum
63	66	14.0	2142	6	ABP98818 Human str
64	66	14.0	2202	5	ABG97482 Human NOV
65	65.5	13.9	484	9	ABB37045 Amino aci
66	65.5	13.9	926	8	ADN24302 Bacterial
67	65.5	13.9	926	8	ADN24302 Bacterial
68	65	13.8	36946	9	ADV97835 Murine pr
69	64.5	13.7	309	4	ABG15321 Novel hum
70	64.5	13.7	323	2	AAV05836 Banana ri
71	64.5	13.7	350	4	ABE64322 Drosophi
72	64.5	13.7	1518	6	ABJ18375 Breast ep
73	64.5	13.7	1641	2	AAV05846 Banana ri
74	64	13.6	317	7	ADC95026 E. faeciu
75	64	13.6	1042	4	AAU15096 Protein e

ALIGNMENTS

RESULT 1
ABB78169 standard; protein; 87 AA.
ID ABB78169;
AC ABB78169;
XX 05-NOV-2002 (first entry)
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
KM Pseudomonas putida.
XX OS
XX US2002072118-A1.
XX PN

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX
SQ Sequence 87 AA;

Query Match 100.0%; Score 472; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.8e-51;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRTWCKRYOEELPGLEPPYPGAKGODIFEHISOKAMADWQKHOTMLINERKLNMMNA 60
Db 1 MTRTWCKRYOEELPGLEPPYPGAKGODIFEHISOKAMADWQKHOTMLINERKLNMMNA 60

QY 61 EDRKFLQEMDKFPAGEBYAQAEGYVP 87
Db 61 EDRKFLQEMDKFPAGEBYAQAEGYVP 87

RESULT 2
ABB78168

ID ABB78168 standard; protein; 90 AA.

XX
XX ABB78168;

XX
XX 05-NOV-2002 (first entry)

XX
XX Amino acid sequence of a YgX homologue.

XX
XX Superoxide damage; cell; YgX; *Salmonella enterica* serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.

XX
XX Pseudomonas syringae.

XX
XX US2002072118-A1.

XX
XX PD 13-JUN-2002.

XX
XX 18-SEP-2001; 2001US-00955502.

XX
XX 22-SEP-2000; 2000US-0234588P.

XX
XX (DOWN/) DOWNS D.

XX
XX (GRAL/) GRALNICK J A.

XX
XX Downs D, Gralnick JA;

DR WPI; 2002-589476/63.
XX
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX
SQ Sequence 90 AA;

Query Match 91.5%; Score 432; DB 5; Length 90;
Best Local Similarity 88.5%; Pred. No. 2.2e-46;
Matches 77; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRTWCKRYOEELPGLEPPYPGAKGODIFEHISOKAMADWQKHOTMLINERKLNMMNA 60
Db 1 MTRTWCKRYOEELPGLEPPYPGAKGODIFEHISOKAMADWQKHOTMLINERKLNMMNA 60

QY 61 EDRKFLQEMDKFPAGEBYAQAEGYVP 87
Db 61 EDRKFLQEMDKFPAGEBYAQAEGYVP 87

RESULT 3
ABB78170

ID ABB78170 standard; protein; 87 AA.

XX
XX ABB78170;

XX
XX 05-NOV-2002 (first entry)

XX
XX Amino acid sequence of a YgX homologue.

XX
XX Superoxide damage; cell; YgX; *Salmonella enterica* serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.

XX
XX Unidentified.

XX
XX US2002072118-A1.

XX
XX PD 13-JUN-2002.

XX
XX 18-SEP-2001; 2001US-00955502.

XX
XX 22-SEP-2000; 2000US-0234588P.

XX
XX (DOWN/) DOWNS D.

XX
XX (GRAL/) GRALNICK J A.

XX
XX Downs D, Gralnick JA;

XX
XX WPI; 2002-589476/63.

XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.

XX
XX Example; Fig 1A; 16pp; English.

XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YgX protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.41601 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-41

Perfect score: 472
Sequence: 1 MTRVWCRKQKQELPGLERP.....AEWDKFPAGBEVAGGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	400	84.7	90	2	H83003	conserved hypotet
2	229	48.5	90	2	C64013	hypothetical prote
3	228	48.3	90	2	C82320	conserved hypotet
4	225	47.7	91	2	A85954	hypothetical prote
5	225	47.7	91	2	A65082	hypothetical prote
6	225	47.7	91	2	P91108	hypothetical prote
7	219	46.4	88	2	H81014	conserved hypotet
8	218	46.2	91	2	AH0879	conserved hypotet
9	198	41.9	105	2	C82624	conserved hypotet
10	188	39.8	90	2	A10116	conserved hypotet
11	159	33.7	93	2	E84994	hypothetical prote
12	70	14.8	670	2	T29898	kinasin protein OS
13	69.5	14.7	1091	2	AF1380	glycosylase homolo
14	69	14.6	105	2	C75419	hypothetical prote
15	68.5	14.5	1090	2	AG1749	glycosylase homolo
16	68	14.4	388	1	QOYV	transforming prote
17	67.5	14.3	689	2	AC1408	transcription anti
18	66.5	14.1	1124	2	T30340	derRNA adenosine de
19	66	14.0	140	2	AB1428	transcription regu
20	66	14.0	1553	2	S67483	adenosinetriphosph
21	65.5	13.9	926	2	T24923	hypothetical prote
22	65.5	13.9	959	2	H69344	hypothetical prote
23	65	13.8	528	2	T24730	hypothetical prote
24	64.5	13.7	767	2	T31558	hypothetical prote
25	64	13.6	140	2	A11801	transcription regu
26	64	13.6	732	2	S23001	transcription regu
27	63.5	13.5	288	2	T45715	hypothetical prote
28	63.5	13.5	397	2	C87470	hypothetical prote
29	63.5	13.5	689	2	AC1784	transcription anti

30	63	13.3	150	2	P90212	hypothetical prote
31	63	13.3	555	2	C87515	ABC transporter, A
32	63	13.3	559	2	T12680	peroxisomal target
33	63	13.3	561	2	T06628	hypothetical prote
34	63	13.3	568	2	G84455	hypothetical prote
35	62.5	13.2	352	2	P84799	hypothetical prote
36	62.5	13.2	677	2	G69895	formate dehydrogen
37	62.5	13.2	985	2	S15965	hypothetical prote
38	62	13.1	242	2	S67270	CCAAT-binding fact
39	62	13.1	1175	2	D35815	myosin heavy chain
40	62	13.1	1175	2	C35815	myosin heavy chain
41	62	13.1	1201	2	A35815	myosin heavy chain
42	62	13.1	1201	2	B35815	myosin heavy chain
43	62	13.1	2385	2	A32491	myosin heavy chain
44	62	13.1	2411	2	B32491	myosin heavy chain
45	61.5	13.0	284	2	D82486	probable lipase ac
46	61.5	13.0	339	2	AG2041	guanine tRNA-ribos
47	61.5	13.0	430	2	I48755	msAplA - mouse
48	61.5	13.0	470	2	D84614	hypothetical prote
49	61.5	13.0	709	2	D86907	elongation factor
50	61.5	13.0	863	2	JC7537	beta-N-acetylgluco
51	61	12.9	213	2	B27898	beta-crystallin B3
52	61	12.9	245	2	S49045	luxp protein - Vib
53	61	12.9	310	2	A25027	arabinose operon r
54	61	12.9	389	2	T14751	hypothetical prote
55	61	12.9	410	1	O4BS6M	cytochrome P450 10
56	61	12.9	474	2	S16250	phytoene dehydroge
57	61	12.9	604	2	S36493	B1 protein - human
58	61	12.9	1212	2	B82809	exodeoxyribonuclea
59	60.5	12.8	88	2	A13122	IS3 family transpo
60	60.5	12.8	142	2	P81296	insertion element
61	60.5	12.8	323	2	B83215	conserved hypotet
62	60.5	12.8	335	2	T33483	hypothetical prote
63	60.5	12.8	458	2	P84275	hypothetical prote
64	60.5	12.8	508	2	S74848	neopullulanase - S
65	60.5	12.8	843	2	A47132	major vault protei
66	60.5	12.8	1083	1	S53048	alpha-nannosidase
67	60.5	12.7	177	2	D70862	hypothetical prote
68	60	12.7	282	2	D97138	DNA replication pr
69	60	12.7	290	2	UN0904	H+/K+-exchanging A
70	60	12.7	310	2	AB0275	arabinose operon r
71	60	12.7	326	2	G96812	protein R3P9.6 [lm
72	60	12.7	352	2	P89884	Phe-tRNA synthetas
73	60	12.7	373	2	A95927	probable N6-adenin
74	60	12.7	426	2	D87153	serine hydroxymeth

ALIGNMENTS

RESULT 1
H83003
conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C/Accession: H83003
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidis, K.; Lam,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: H83003
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <STO>
A/Cross-references: UNIPARC:UPI00000C5F26; GB:AB004927; GB:AB004091; NID:g9951437; PIDN:
C/Genetics:
A/Experimental source: strain PA01
A/Genes: PA5148
C/Superfamily: fe(II) trafficking protein YggX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.2638 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-41
Perfect score: 472
Sequence: 1 MTRVWCRKQEBLPGHERP.....AEMDKPFAEYQAEGYVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472	100.0	90	1	FETP_PSEBK
2	439	93.0	90	2	Q4KJ22_PSEFS
3	432	91.5	90	1	FETP_PSEBM
4	432	91.5	90	2	Q4ZLJ3_PSESY
5	411	87.1	90	2	Q6T7F6_PSEFL
6	400	84.7	90	1	FETP_PSEBAE
7	393	83.3	90	2	Q4J2Z8_AZQVI
8	261.5	55.4	90	1	FETP_ACTIAD
9	250	53.0	90	1	FETP_IDIIO
10	244	51.7	96	2	Q4FVJ7_SGAMM
11	239	50.6	90	1	FETP_METCA
12	237	50.2	92	1	FETP_SHEON
13	234	49.6	91	1	FETP_MANSM
14	233	49.4	91	1	FETP_RALSO
15	232	49.2	88	1	FETP_LEGRA
16	232	49.2	89	1	FETP_LEGRA
17	232	49.2	89	1	FETP_LEGRA
18	231	48.9	89	1	FETP_NITBU
19	229	48.5	90	1	FETP_HAEIN
20	229	48.5	90	1	FETP_PHOBR
21	229	48.5	90	2	Q4QWQ9_HAEI8
22	229	48.5	91	1	FETP_BURMA
23	229	48.5	91	1	FETP_BURMS
24	228	48.3	90	1	FETP_VIBCH
25	226	47.9	90	1	FETP_VIBVU
26	226	47.9	90	1	FETP_VIBVY
27	225	47.7	90	1	FETP_PASMU
28	225	47.7	90	1	FETP_VIBRA
29	223	47.2	91	2	Q4LS19_9BURK
30	222	47.0	90	1	FETP_BORBA
31	222	47.0	90	1	FETP_BORBA

32	222	47.0	90	1	FETP_BORBE	Q7WVC4 bordecella
33	220	46.6	90	1	FETP_ECO57	P0a8p3 escherichia
34	220	46.6	90	1	FETP_ECOLI	P0a8p3 escherichia
35	220	46.6	90	1	FETP_PHOHL	Q7n711 photorhabdu
36	220	46.6	90	1	FETP_SHIFL	P0a8p5 shigella fl
37	219	46.4	88	1	FETP_NEIMA	Q51553 neisseria g
38	219	46.4	88	1	FETP_NEIMA	P67615 neisseria m
39	219	46.4	88	1	FETP_NEIMB	P67616 neisseria m
40	219	46.4	90	1	FETP_ERWCT	Q6d8j9 erwina car
41	219	46.4	90	1	FETP_VIBRI	Q5e7t0 vibrio fusc
42	219	46.4	94	1	FETP_HAEU1	Q7VXB6 haemophilus
43	216	45.8	90	1	FETP_ECOL6	Q81e19 escherichia
44	213	45.1	90	1	FETP_SALCH	Q57K04 salmonella
45	213	45.1	90	1	FETP_SALPA	Q56mm1 salmonella
46	213	45.1	90	1	FETP_SALTI	P67618 salmonella
47	213	45.1	90	1	FETP_SALTY	P67617 salmonella
48	207	43.9	90	1	FETP_CHRYO	Q7mra4 chromobacte
49	206	43.6	91	1	FETP_XANAC	Q8p1h7 xanthomonas
50	206	43.6	92	1	FETP_XANOR	Q5gy22 xanthomonas
51	204	43.2	90	1	FETP_COXBU	Q83d06 coxiella bu
52	199	42.2	92	1	FETP_XANCP	Q8p829 xanthomonas
53	199	42.2	92	2	Q4UM14_XANCP	Q4um14 xanthomonas
54	198	41.9	90	1	FETP_XYLPA	Q9pc73 xyella fas
55	196	41.5	90	1	FETP_XYLPB	Q666m3 yersinia ps
56	194	41.1	90	1	FETP_XYLET	Q87d06 xyella fas
57	193	40.9	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
58	188	39.8	90	1	FETP_YERPE	Q8he77 yersinia pe
59	185	39.2	87	1	FETP_FRATY	Q5uhj8 francisella
60	180	38.1	79	1	FETP_CANBF	Q7rv93 candidatus
61	177	37.5	92	1	FETP_BUCAP	Q8k925 buchera ap
62	172	36.4	92	2	Q4NMQ4_9DELT	Q4nmq4 anaeromyxob
63	159	33.7	77	1	FETP_BUCAI	P57618 buchera ap
64	157	33.3	87	1	FETP_BUCBP	Q8p344 buchera ap
65	84	17.8	703	2	Q4WPT2_ASPTU	Q4wpt2 aspergillus
66	79.5	16.8	280	2	Q81BK9_BACCR	Q81bk9 bacillus ce
67	78.5	16.6	603	2	Q6PWF5_ORYSA	Q6pwf5 oryza sativ
68	74	15.7	220	2	Q5WAP4_BACSK	Q5wap4 bacillus cl
69	74	15.7	1141	2	Q5B3I8_EMENT	Q5b3i8 aspergillus
70	72	15.3	307	2	Q9R3J6_ARATH	Q9r3j6 arabidopsis
71	72	15.3	844	1	PRIC2_HUMAN	Q72396 homo sapien
72	72	15.3	845	1	PRIC2_MOUSE	Q80y24 mus musculu
73	71	15.0	437	2	Q60EHO_ORYSA	Q60eho oryza sativ
74	70.5	14.9	259	2	Q52J13_BRARE	Q52j13 brachydanto
75	70.5	14.9	353	2	Q6NN67_DROME	Q6nn67 drosophila

ALIGNMENTS

RESULT 1
FETP_PSEBK STANDARD; PRT; 90 AA.
ID FETP_PSEBK
AC Q8BR49;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Probable Pe(2+) trafficking protein.
GN OrderedLocustNames=PP0285;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160486;
RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22423060; PubMed=12534463;
DOI=10.1046/j.1462-2920.2002.00366.x;
RA Neilson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Matlins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Hance I., Neilson W.C., White O., Peterson J.D., Khouri H.M.,
RA Mauck T., Chris Lee P., Holtzapfle B.K., Scanlan D., Ryan K.,
RA Moazzaz A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hohnesiel J., Straetz M., Heim S.,

```

RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tremmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC
CC EMBL; AB016775; AAN65916.1; -; Genomic_DNA.
DR SNR; O88R49; 1-79.
DR TIGR; PP0285; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10596 MW; 0C802FD7163B75A2 CRC64;

Query Match 100.0%; Score 472; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 9.6e-44;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRTVMCRKYOEBLPGLERPYPGAKGQDIFEHISQKAMADWQKHQTLINERKLNMMNA 60
Db 1 MTRTVMCRKYOEBLPGLERPYPGAKGQDIFEHISQKAMADWQKHQTLINERKLNMMNA 60
61 EDRKFLQAEWDKFPAGEBYAQAEGYVP 87
61 EDRKFLQAEWDKFPAGEBYAQAEGYVP 87

RESULT 2
Q4KJ22.PSEF5
ID Q4KJ22.PSEF5 PRELIMINARY; PRT; 90 AA.
AC Q4KJ22;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PFL_0357;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=220664;
RX NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;
RX PubMed=15980661; DOI=10.1038/nbt1110.
RA Paulsen I.T., Press C., Kavel J., Kobayashi D., Myers G.S.,
RA Mayroldi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosevitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L., III, Thomasow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY95766.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 90 AA; 10483 MW; 816D3C774C2B7C12 CRC64;

Query Match 93.0%; Score 439; DB 2; Length 90;
Best Local Similarity 88.5%; Pred. No. 3.9e-40;
Matches 77; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

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RESULT 3
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AC 087UP5;
DT 10-OCT-2003 (Ref. 42, Created)
DT 10-OCT-2003 (Ref. 42, Last sequence update)
DT 13-SEP-2005 (Ref. 48, Last annotation update)
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OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
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RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindberg M., Sengenut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beaman M.J., Haft D.H.,
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Ureterback T.R., Van Aken S.B., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC EMBL; AB016853; AAO58769.1; -; Genomic_DNA.
DR SNR; O87UP5; 1-79.
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DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
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DR ProDom; PD029191; DUF495; 1.
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SQ SEQUENCE 90 AA; 10621 MW; 1086288D6532973 CRC64;

Query Match 91.5%; Score 432; DB 1; Length 90;
Best Local Similarity 88.5%; Pred. No. 2.3e-39;
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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:25:19 ; Search time 17.4589 Seconds
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Title: US-09-955-502a-41

Perfect score: 472
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	209	44.3	93	2	US-09-543-681A-5443
6	73	15.5	451	2	US-09-543-681A-7401
7	69	14.6	443	2	US-09-248-796A-16816
8	64.5	13.7	163	2	US-09-270-767-33714
9	64	13.6	317	2	US-09-107-532A-4653
10	64	13.6	420	2	US-09-248-796A-15323
11	64	13.6	1042	2	US-09-792-024-106
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23	61	12.9	381	2	US-09-949-016-9788
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25	60.5	12.8	205	2	US-09-918-039-238
26	60	12.7	352	1	US-08-785-052-2
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RESULT 1
US-09-252-991A-23355
Sequence 23355, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NEURIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23355
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 54.4363 Seconds
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667.774 Million cell updates/sec

Title: US-09-955-502a-41

Perfect score: 472

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30 197.5 41.8 78 3 US-09-955-502-19 Sequence 19, Appl
31 188 39.8 90 3 US-09-955-502-20 Sequence 20, Appl
32 159 33.7 76 3 US-09-955-502-21 Sequence 21, Appl
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Sequence 24, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 87
TYPE: PRT
ORGANISM: Pseudomonas putida

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.60992 Seconds

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280.957 Million cell updates/sec

US-09-955-502a-41

Title: 472
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Sequence:Scoring table: BLOSUM62
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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11	57	12.1	426	6	US-10-858-730-80
12	57	12.1	1386	7	US-11-091-643-6
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30	54.5	11.5	548	7	US-11-198-746-86	Sequence 86, Appl
31	54.5	11.5	548	7	US-11-198-794-86	Sequence 86, Appl
32	54.5	11.5	577	7	US-11-072-175-187	Sequence 187, Appl
33	54.5	11.5	648	6	US-10-467-657-2802	Sequence 2802, Ap
34	54.5	11.5	665	7	US-11-113-837-19	Sequence 19, Appl
35	54.5	11.5	695	7	US-11-198-746-87	Sequence 87, Appl
36	54.5	11.5	695	7	US-11-198-794-87	Sequence 87, Appl
37	54.5	11.5	832	7	US-11-065-943-100	Sequence 100, App
38	54.5	11.5	832	7	US-11-007-797A-11	Sequence 11, Appl
39	54.5	11.5	832	7	US-11-007-642B-11	Sequence 11, Appl
40	54.5	11.5	832	7	US-11-198-746-4	Sequence 4, Appl
41	54.5	11.5	832	7	US-11-198-794-4	Sequence 4, Appl
42	54.5	11.5	832	7	US-11-242-730-1	Sequence 1, Appl
43	54.5	11.5	833	7	US-11-198-746-85	Sequence 85, Appl
44	54.5	11.5	833	7	US-11-198-794-85	Sequence 85, Appl
45	54	11.4	313	6	US-10-986-501-124	Sequence 124, App
46	54	11.4	313	6	US-11-156-084-335	Sequence 335, App
47	54	11.4	362	6	US-10-517-939-88	Sequence 88, Appl
48	53.5	11.3	293	7	US-11-072-512-2088	Sequence 2088, App
49	53.5	11.3	293	7	US-11-072-512-2088	Sequence 2088, App
50	53.5	11.3	432	6	US-10-454-437-140	Sequence 140, App
51	53.5	11.3	432	7	US-11-055-822-184	Sequence 184, App
52	53.5	11.3	453	7	US-11-072-512-3394	Sequence 3394, Ap
53	53.5	11.3	691	7	US-11-098-686-11189	Sequence 11189, A
54	53.5	11.3	746	7	US-11-072-175-159	Sequence 169, App
55	53.5	11.3	919	6	US-10-821-234-1144	Sequence 1144, Ap
56	53.5	11.3	2335	6	US-10-821-234-1610	Sequence 1610, App
57	53	11.2	289	7	US-11-093-118-39	Sequence 39, Appl
58	53	11.2	327	7	US-11-093-118-37	Sequence 37, Appl
59	53	11.2	876	7	US-11-242-730-5	Sequence 5, Appl
60	53	11.2	1596	7	US-11-060-005-4	Sequence 4, Appl
61	52.5	11.1	215	6	US-10-131-826A-488	Sequence 488, App
62	52.5	11.1	215	7	US-11-080-991-112	Sequence 112, App
63	52.5	11.1	736	6	US-10-467-657-4780	Sequence 4780, Ap
64	52.5	11.1	926	6	US-11-232-405A-34	Sequence 34, Appl
65	52	11.0	236	6	US-10-927-641-72	Sequence 72, Appl
66	52	11.0	370	6	US-10-873-528-160	Sequence 160, App
67	52	11.0	381	7	US-11-072-512-3313	Sequence 3313, Ap
68	52	11.0	401	6	US-10-131-826A-486	Sequence 486, App
69	52	11.0	505	6	US-10-514-878A-3	Sequence 3, Appl
70	52	11.0	505	6	US-10-514-878A-5	Sequence 5, Appl
71	52	11.0	505	6	US-10-514-878A-7	Sequence 7, Appl
72	52	11.0	505	6	US-10-514-878A-13	Sequence 13, Appl
73	52	11.0	505	7	US-11-179-478-2	Sequence 2, Appl
74	52	11.0	593	7	US-11-194-246-317	Sequence 317, Appl
75	52	11.0	924	6	US-10-467-657-4290	Sequence 4290, Ap

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACT Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

```
; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968
```

```
Query Match          46.4%; Score 219; DB 6; Length 88;
Best Local Similarity 44.8%; Pred. No. 1,2e-18;
Matches 39; Conservative 19; Mismatches 29; Indels 0; Gaps 0;
```

```
QY 1 MTRTWCKRYQELPGLERPPYPGAKGODIFEHISOKANAWQKQTMLINEKRLMNA 60
DB 1 MARWFCVYLNKEAEKMPPLPNEIGKRIFFENVSQSAWAAWTRHQTMLINENRLSLADP 60
QY 61 EDRKFLQAEMLKFPAGEBYAQAEQYVP 87
DB 61 RAREYLAQMEQYFFGDDGADVAQGYVP 87
```

RESULT 2

```
US-10-453-372-852
; Sequence 852, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
```

```
; FILE REFERENCE: 21402-589 A
```

```
; CURRENT FILING DATE: 2003-06-03
```

```
; PRIOR APPLICATION NUMBER: 09/789390
```

```
; PRIOR FILING DATE: 2001-02-23
```

```
; PRIOR APPLICATION NUMBER: 60/185967
```

```
; PRIOR FILING DATE: 2000-03-01
```

```
; PRIOR APPLICATION NUMBER: 09/823187
```

```
; PRIOR FILING DATE: 2001-03-29
```

```
; PRIOR APPLICATION NUMBER: 60/195792
```

```
; PRIOR FILING DATE: 2000-03-10
```

```
; PRIOR APPLICATION NUMBER: 09/839446
```

```
; PRIOR FILING DATE: 2001-03-19
```

```
; PRIOR APPLICATION NUMBER: 60/199476
```

```
; PRIOR FILING DATE: 2000-03-25
```

```
; PRIOR APPLICATION NUMBER: 09/863776
```

```
; PRIOR FILING DATE: 2001-05-23
```

```
; PRIOR APPLICATION NUMBER: 60/208263
```

```
; PRIOR FILING DATE: 2000-05-31
```

```
; PRIOR APPLICATION NUMBER: 09/939398
```

```
; PRIOR FILING DATE: 2001-08-24
```

```
; PRIOR APPLICATION NUMBER: 60/227800
```

```
; PRIOR FILING DATE: 2000-08-25
```

```
; Remaining Prior Application data removed - See file wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 1609
```

```
; SOFTWARE: CuroSeqList version 0.1
```

```
; SEQ ID NO 852
```

```
; LENGTH: 844
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-10-453-372-852
```

```
Query Match          15.3%; Score 72; DB 6; Length 844;
Best Local Similarity 26.6%; Pred. No. 1.6;
Matches 29; Conservative 16; Mismatches 32; Indels 32; Gaps 6;
```

```
QY 4 TWMC-----KYQELPGLERPPY-----PGAKGODIFEHISQKA 38
DB 515 TQCCRRHPISLKYTEDMTPTQTPRGSMESLALSNATGLSADGAKRQ---EHLSPFS 571
QY 39 WADWQKHQTMLINEKRLM--MNAEDRKFLQAE-MDKFPAGEBYAQAE 84
DB 572 MPDLSDKSGMNVSEKLSNMGTLS-SMQFRSAESVRSLLSAQOYQEMEG 619
```

RESULT 3

```
US-10-453-372-856
```

```
; Sequence 856, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Alsobrook, et al.
```

```
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
```

```
; FILE REFERENCE: 21402-589 A
```

```
; CURRENT FILING DATE: 2003-06-03
```

```
; PRIOR APPLICATION NUMBER: 09/789390
```

```
; PRIOR FILING DATE: 2001-02-23
```

```
; PRIOR APPLICATION NUMBER: 60/185967
```

```
; PRIOR FILING DATE: 2000-03-01
```

```
; PRIOR APPLICATION NUMBER: 09/823187
```

```
; PRIOR FILING DATE: 2001-03-29
```

```
; PRIOR APPLICATION NUMBER: 60/195792
```

```
; PRIOR FILING DATE: 2000-03-10
```

```
; PRIOR APPLICATION NUMBER: 09/839446
```

```
; PRIOR FILING DATE: 2001-03-19
```

```
; PRIOR APPLICATION NUMBER: 60/199476
```

```
; PRIOR FILING DATE: 2000-03-25
```

```
; PRIOR APPLICATION NUMBER: 09/863776
```

```
; PRIOR FILING DATE: 2001-05-23
```

```
; PRIOR APPLICATION NUMBER: 60/208263
```

```
; PRIOR FILING DATE: 2000-05-31
```

```
; PRIOR APPLICATION NUMBER: 09/939398
```

```
; PRIOR FILING DATE: 2001-08-24
```

```
; PRIOR APPLICATION NUMBER: 60/227800
```

```
; PRIOR FILING DATE: 2000-08-25
```

```
; Remaining Prior Application data removed - See file wrapper or PALM.
```

```
; NUMBER OF SEQ ID NOS: 1609
```

```
; SOFTWARE: CuroSeqList version 0.1
```

```
; SEQ ID NO 856
```

```
; LENGTH: 844
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-10-453-372-856
```

```
Query Match          15.3%; Score 72; DB 6; Length 844;
Best Local Similarity 26.6%; Pred. No. 1.6;
Matches 29; Conservative 16; Mismatches 32; Indels 32; Gaps 6;
```

```
QY 4 TWMC-----KYQELPGLERPPY-----PGAKGODIFEHISQKA 38
DB 515 TQCCRRHPISLKYTEDMTPTQTPRGSMESLALSNATGLSADGAKRQ---EHLSPFS 571
QY 39 WADWQKHQTMLINEKRLM--MNAEDRKFLQAE-MDKFPAGEBYAQAE 84
DB 572 MPDLSDKSGMNVSEKLSNMGTLS-SMQFRSAESVRSLLSAQOYQEMEG 619
```

RESULT 4

```
US-11-059-982-1
```

```
; Sequence 1, Application US/11059982
```

```
; Publication No. US20050255507A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Jenkins, Robert B.
```

```
; APPLICANT: Yang, Ping
```

```
; APPLICANT: Thibodeau, Steve
```

```
; APPLICANT: Wang, Liang
```

```
; APPLICANT: Schaid, Daniel
```

```
; TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND
```

```
; TITLE OF INVENTION: PROGNOSIS OF PROLIFERATIVE DISORDERS
```

```
; FILE REFERENCE: 07039-505001
```

```
; CURRENT APPLICATION NUMBER: US/11/059,982
```

```
; CURRENT FILING DATE: 2005-02-17
```

```
; PRIOR APPLICATION NUMBER: US 60/545,573
```

```
; PRIOR FILING DATE: 2004-02-17
```

```
; NUMBER OF SEQ ID NOS: 50
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 1
```

```
; LENGTH: 1560
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:49:36 ; Search time 74.092 Seconds
(without alignments)
521.856 Million cell updates/sec

Title: US-09-955-502A-42
Perfect score: 467
Sequence: 1 MARWVFCVKLNKEAKMKP.....QMEQYFGDADAVQGVTPQ 88

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	5	ABB78171 Amino aci
2	467	100.0	88	5	ABB78172 Amino aci
3	467	100.0	88	5	ABB78173 Amino aci
4	467	100.0	88	6	ABP77219 N. gonorr
5	339	72.6	87	5	ABB78175 Amino aci
6	333	71.3	87	5	ABB78174 Amino aci
7	294	63.0	87	5	ABB78176 Amino aci
8	290	62.1	87	5	ABB78148 Amino aci
9	290	62.1	87	5	ABB78147 Amino aci
10	272.5	58.4	86	5	ABB78149 Amino aci
11	271	58.0	89	9	ABB41576 L. pneumo
12	271	58.0	95	9	ABB38294 L. pneumo
13	258	55.2	88	5	ABB78178 Amino aci
14	243	52.0	87	5	ABB78177 Amino aci
15	240	51.4	90	5	ABB78155 Amino aci
16	235	50.3	87	5	ABB78153 Amino aci
17	230	49.3	88	5	ABB78154 Amino aci
18	228	48.8	91	5	ABB78150 Amino aci
19	227	48.6	87	5	ABB78152 Amino aci
20	227	48.6	107	7	ABO65445 Klebsiell
21	225.5	48.3	107	6	ADA34169 Actinobac
22	221	47.3	93	7	ADF05158 Bacteroid
23	219	46.9	87	5	ABB78169 Amino aci
24	217	46.5	87	5	ABB78151 Amino aci

25	213	45.6	91	5	ABB78158 Amino aci
26	213	45.6	91	5	ABB78157 Amino aci
27	213	45.6	91	5	ABB78156 Amino aci
28	211	45.2	88	5	ABB78160 Amino aci
29	211	45.2	91	5	ABB78161 Amino aci
30	211	45.2	91	5	ABB78159 Amino aci
31	211	45.2	91	5	ABB78162 Amino aci
32	210	45.0	78	5	ABB78164 Amino aci
33	207	44.3	87	5	ABB78170 Amino aci
34	207	44.3	122	7	ABO74609 Pseudomon
35	202	43.3	91	5	ABB78163 Amino aci
36	198	42.4	90	5	ABB78165 Amino aci
37	198	42.4	90	5	ABB78168 Amino aci
38	193.5	41.4	90	5	ABB78167 Amino aci
39	182	39.0	110	8	ADL05173 M. catarr
40	158	33.8	76	5	ABB78166 Amino aci
41	74	15.8	1122	6	ABU22044 Protein e
42	70	15.0	1079	8	ABM90380 Rice abio
43	70	15.0	1079	8	ADN19463 Bacterial
44	69	14.8	774	4	ABG29304 Novel hum
45	68.5	14.7	361	7	ABO76259 Pseudomon
46	68	14.6	189	9	ADM18357 Pirus rad
47	67.5	14.5	466	7	ABO84015 Pseudomon
48	66.5	14.2	401	6	ABU19221 Protein e
49	66	14.1	418	7	ABO66638 Klebsiell
50	65.5	14.0	649	7	ADC94671 E. faeciu
51	65.5	14.0	1443	7	ADJ68530 Human hea
52	65.5	14.0	1935	7	ADJ70260 Human hea
53	65.5	14.0	3830	5	ABB81168 TRRAP pro
54	65.5	14.0	3830	8	ADJ78499 PAR/TRAP
55	65.5	14.0	3830	8	ADQ19749 Human sof
56	65.5	14.0	3830	8	ADQ89826 Antagonis
57	65.5	14.0	3859	7	ADJ68548 Human hea
58	65.5	14.0	3859	8	ADJ68548 Human hea
59	65	13.9	255	7	ADM27073 Hyperther
60	65	13.9	296	4	AAU35611 Haemophil
61	65	13.9	296	6	ABU30521 Protein e
62	65	13.9	442	2	AAV11015 H. pylori
63	65	13.9	442	2	AAW20830 H. pylori
64	65	13.9	465	2	AAW20303 H. pylori
65	64.5	13.8	207	9	ABM73508 Staphyloc
66	64.5	13.8	207	9	ADV16859 Staphyloc
67	64.5	13.8	207	9	ADW94758 Prolifera
68	64.5	13.8	362	7	ADP89476 Human ery
69	64.5	13.8	362	8	ADK48658 Human tra
70	64.5	13.8	362	8	ADP12457 Protein e
71	64	13.7	260	4	AAW38702 Human pol
72	64	13.7	378	4	AAW40488 Human tes
73	64	13.7	656	4	ABU53239 Human tes
74	64	13.7	656	8	ADJ28417 Human nuc
75	64	13.7	2426	2	ADH11285 Vertebrat

ALIGNMENTS

RESULT 1	ABB78171	standard; protein; 88 AA.
XX	ABB78171	
AC	ABB78171	
XX		
DT	29-AUG-2003	(revised)
DT	05-NOV-2002	(first entry)
XX		
XX		Amino acid sequence of a YggX homologue.
DE		
XX		
KW		Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX		hydroxyl radical; DNA damage; YggX homologue.
OS		Neisseria gonorrhoeae.
XX		
FN	US2002072118-A1.	

```
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnicks JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
XX Sequence 88 AA;
XX
XX Query Match 100.0%; Score 467; DB 5; Length 88;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-54;
XX Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MARWVFCVKLNKAEKGKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSIADP 60
XX DB 1 MARWVFCVKLNKAEKGKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSIADP 60
XX
XX QY 61 RAREYLAQOMEQYFFGADADAVOGYVPQ 88
XX DB 61 RAREYLAQOMEQYFFGADADAVOGYVPQ 88
XX
XX RESULT 2
XX ABB78172
XX ID ABB78172 standard; protein; 88 AA.
XX
XX AC ABB78172;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE Amino acid sequence of a YggX homologue.
XX
XX KM Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KM hydroxyl radical; DNA damage; YggX homologue.
XX
XX OS Neisseria meningitidis.
XX
XX PN US2002072118-A1.
XX
XX PD 13-JUN-2002.
XX
XX PF 18-SEP-2001; 2001US-00955502.
XX
XX PR 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
```

```
PI Downs D, Gralnicks JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
XX Sequence 88 AA;
XX
XX Query Match 100.0%; Score 467; DB 5; Length 88;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-54;
XX Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MARWVFCVKLNKAEKGKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSIADP 60
XX DB 1 MARWVFCVKLNKAEKGKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSIADP 60
XX
XX QY 61 RAREYLAQOMEQYFFGADADAVOGYVPQ 88
XX DB 61 RAREYLAQOMEQYFFGADADAVOGYVPQ 88
XX
XX RESULT 3
XX ABB78173
XX ID ABB78173 standard; protein; 88 AA.
XX
XX AC ABB78173;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE Amino acid sequence of a YggX homologue.
XX
XX KM Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KM hydroxyl radical; DNA damage; YggX homologue.
XX
XX OS Neisseria meningitidis.
XX
XX PN US2002072118-A1.
XX
XX PD 13-JUN-2002.
XX
XX PF 18-SEP-2001; 2001US-00955502.
XX
XX PR 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX PI Downs D, Gralnicks JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
```

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:27:00 ; Search time 10.8736 Seconds
(without alignments)
778.685 Million cell updates/sec

Title: US-09-955-502A-42
Perfect score: 467
Sequence: 1 NARMVFCVKNKAEAGMKFP.....QMEGYFPGDADAVGVYFQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	H81014	conserved hypothet
2	240	51.4	90	C82320	conserved hypothet
3	227	48.6	90	C64013	hypothetical prote
4	213	45.6	91	A85954	hypothetical prote
5	213	45.6	91	A65082	hypothetical prote
6	213	45.6	91	F91108	hypothetical prote
7	211	45.2	91	AH0879	conserved hypothet
8	207	44.3	90	H83003	conserved hypothet
9	201	43.0	105	C82624	conserved hypothet
10	198	42.4	90	A10116	conserved hypothet
11	158	33.8	93	B84994	hypothetical prote
12	72	15.4	1041	A81960	probable DNA helic
13	70	15.0	1079	T38913	translation initia
14	68.5	14.7	338	A83389	probable permease
15	68.5	14.7	549	A11457	ABC transporter ol
16	68	14.6	195	S74714	hypothetical prote
17	67.5	14.5	899	A83019	conserved hypothet
18	66.5	14.2	401	C70159	translation elonga
19	66	14.1	598	RGRCNX	nitrate/nitrite se
20	66	14.1	598	F85702	nitrate/nitrite se
21	66	14.1	598	G90844	cell division inh
22	65	13.9	296	A64110	nitrate/nitrite se
23	65	13.9	465	C71870	hypothetical prote
24	65	13.9	590	B85057	probable transpo
25	64.5	13.8	207	B89952	conserved hypothet
26	64.5	13.8	362	T45072	erythroid Kruppel-
27	64.5	13.8	400	A39254	inositol-1,4-bisph
28	64.5	13.8	1553	S67483	adenosinetriphosph
29	64	13.7	676	A45984	sperm-binding gly

30	64	13.7	677	2	S33664	flagella-associate
31	63.5	13.6	288	2	H95018	transcription regu
32	63.5	13.6	301	2	F82446	transcription regu
33	63	13.5	282	2	D97138	DNA replication pr
34	63	13.5	388	1	UC5461	cellulase (EC 3.2.
35	63	13.5	388	1	S43920	cellulase (EC 3.2.
36	62	13.3	120	2	G97833	hypothetical prote
37	62	13.3	200	2	B82203	transcription regu
38	62	13.3	259	2	S55033	transcription inh
39	62	13.3	570	2	D83177	probable phosphor
40	62	13.3	2314	2	T28698	hypothetical prote
41	61.5	13.2	211	2	T38645	hypothetical prote
42	61.5	13.2	288	2	B95122	transcription regu
43	61.5	13.2	374	2	A96502	probable acyl-acyl
44	61.5	13.2	412	2	G81581	tyrosyl-tRNA synth
45	61.5	13.2	422	2	G86535	tyrosyl-tRNA synth
46	61.5	13.2	422	2	D72088	lysine-tRNA liga
47	61.5	13.2	589	2	A83530	flagellar biosynth
48	61	13.1	425	2	T50184	mammalian swi/snf
49	61	13.1	563	2	F97028	arginyl-tRNA synth
50	61	13.1	969	2	T33156	hypothetical prote
51	61	13.1	1639	2	T50119	probable sensory t
52	60.5	13.0	186	1	WNR219	19k globulin precu
53	60.5	13.0	186	2	JC4784	alpha-globulin pre
54	60.5	13.0	261	2	S14875	diak-type molecula
55	60.5	13.0	357	2	F82892	heat-inducible tra
56	60.5	13.0	448	2	T45145	glutamate-ammonia
57	60.5	13.0	1888	2	T39009	hypothetical prote
58	60	12.8	292	2	A10422	conserved hypothet
59	60	12.8	306	2	A97249	Zn-binding lipopro
60	60	12.8	309	2	D95843	probable transcript
61	60	12.8	323	2	T35734	probable aminopept
62	60	12.8	335	2	D83142	hypothetical prote
63	60	12.8	397	2	A75503	hypothetical prote
64	60	12.8	410	2	T39115	formamide-like p
65	60	12.8	508	2	T02486	hypothetical prote
66	60	12.8	615	2	B81451	1-deoxyxylulose-5-
67	60	12.8	655	2	E75206	alpha-amylose (or
68	60	12.8	859	2	T39630	hypothetical prote
69	60	12.8	1006	2	A59384	oxycocinase/insuli
70	60	12.8	1021	2	AC2202	hypothetical prote
71	60	12.8	1025	2	A59383	oxycocinase/insuli
72	60	12.8	3788	2	T30851	lysosomal traffick
73	59.5	12.7	157	1	HHPM17	heat shock protein
74	59.5	12.7	237	2	A55218	sfp homolog gap -
75	59.5	12.7	295	2	T35330	probable RNA polym

ALIGNMENTS

RESULT 1

H81014 conserved hypothetical protein NMB2021 [Imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004

C:Accession: H81014, F81958
R:Retelien, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rt, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000

A:Author: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moron, E.R.; Rappuoli, R.; Ve

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: AB1000; MUID:2017555; PMID:10710307

A:Accession: H81014

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-88 <TET>

A:Cross-references: UNIPARC:UPI00000C4E7F; GB:AB002552; GB:AB002098; NID:g7227279; PIDN:

A:Experimental source: serogroup B, strain MC58

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jaseles, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:00:23 ; Search time 66.5057 Seconds
(without alignments)
933.551 Million cell updates/sec

Title: US-09-955-502A-42

Perfect score: 467
Sequence: 1 MARWFCVKLNKBAEMKFP.....QMEQYFGDADAVGVYVQ 88

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	100.0	88	1	FEPT_NEIG1
2	467	100.0	88	1	FEPT_NEIMA
3	467	100.0	88	1	FEPT_NEIMB
4	354	75.8	91	1	FEPT_NEISO
5	348	74.5	91	2	Q4LS19_PBUK
6	339	72.6	91	1	FEPT_BURPA
7	335	71.7	90	1	FEPT_BURPS
8	335	71.7	90	1	FEPT_CHRYO
9	319	68.3	90	1	FEPT_NITRU
10	290	62.1	90	1	FEPT_BORBR
11	290	62.1	90	1	FEPT_BORPA
12	290	62.1	90	1	FEPT_BORBP
13	275	58.9	89	1	FEPT_LEGPA
14	271	58.0	89	1	FEPT_LEGPA
15	271	58.0	89	1	FEPT_LEGPA
16	258	55.2	90	1	FEPT_COXRU
17	254	54.4	90	1	FEPT_VIBR1
18	252	54.0	92	2	Q4NMQ4_PDELT
19	243	52.0	90	1	FEPT_METCA
20	242	51.8	90	1	FEPT_IDILO
21	240	51.4	90	1	FEPT_VIBCH
22	239	51.2	90	1	FEPT_VIBRA
23	239	51.2	90	1	FEPT_VIBVU
24	239	51.2	90	1	FEPT_VIBVY
25	235	50.3	91	1	FEPT_XANXC
26	235	50.3	91	1	FEPT_XANXC
27	233	49.9	92	1	FEPT_XANOR
28	230	49.3	92	1	FEPT_XANOR
29	227	48.6	90	1	FEPT_XANOR
30	227	48.6	90	2	Q4QMD9_HAE18
31	225	48.2	92	1	FEPT_XANCP

32	225	48.2	92	2	Q4UW14_XANCP
33	224	48.0	91	1	FEPT_MANSM
34	220.5	47.2	90	1	FEPT_AC1AD
35	220	47.1	90	1	FEPT_PHOBR
36	219	46.9	90	1	FEPT_PSBPK
37	217	46.5	90	1	FEPT_PASMU
38	217	46.5	90	1	FEPT_PHOHL
39	211	45.2	90	2	Q6T7F6_PSEPL
40	209	44.8	90	1	FEPT_XYLFU
41	208	44.5	87	1	FEPT_FRAPT
42	208	44.5	90	1	FEPT_ECO57
43	208	44.5	90	1	FEPT_ECOLI
44	208	44.5	90	1	FEPT_ERWCT
45	208	44.5	90	1	FEPT_SHIFU
46	207	44.3	90	1	FEPT_PSBAR
47	207	44.3	90	2	Q4KJ22_PSEFS
48	206	44.1	90	1	FEPT_SALCH
49	206	44.1	90	1	FEPT_SALPA
50	206	44.1	90	1	FEPT_SALTI
51	206	44.1	90	1	FEPT_SALTY
52	206	44.1	90	1	FEPT_YERPS
53	206	44.1	96	2	Q4FVJ7_GGAMM
54	204	43.7	90	1	FEPT_ECOL6
55	201	43.0	90	1	FEPT_XYLFU
56	198	42.4	90	1	FEPT_PSESM
57	198	42.4	90	1	FEPT_YERPE
58	198	42.4	90	2	Q4ZLB3_PSESY
59	196	42.0	90	2	Q4J228_AZCVI
60	186	39.8	79	1	FEPT_CANBP
61	167	35.8	78	1	FEPT_BUCAP
62	167	35.8	78	1	FEPT_WIGBR
63	158	33.8	77	1	FEPT_BUCAI
64	127	27.2	87	1	FEPT_BUCBP
65	75	16.1	359	2	Q7WXA4_HAEUD
66	74	15.8	453	2	Q4BUL1_USTMA
67	74	15.8	1598	2	Q62CB0_BURPA
68	74	15.8	1599	2	Q63XS1_BURPS
69	73	15.6	820	2	Q52IA7_MAGGR
70	72.5	15.5	301	2	Q6LNU9_PHOPR
71	72	15.4	203	2	Q568W6_BRARE
72	72	15.4	1041	2	Q9UW05_NEIMA
73	71	15.2	346	2	Q8EFA2_SHEON
74	70.5	15.1	320	2	Q6PKY5_XENLA
75	70	15.0	1079	1	IRP2_SCHPO

ALIGNMENTS

RESULT 1	ID	FEPT_NEIG1	STANDARD;	PRT;	88 AA.
AC	Q5F553;				
DT	13-SEP-2005 (Rel. 48, Created)				
DT	13-SEP-2005 (Rel. 48, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	Probable Fe(2+) trafficking protein.				
GN	OrderedListNames=NGO2083;				
OS	Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
CC	Neisseriaceae; Neisseria.				
XX	NCBI_TaxId=242231;				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RA	Lewis L.A., Gillaspay A.F., McLaughlin R.E., Gipsen M., Ducey T.F.,				
RA	Owlsby T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,				
RA	Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,				
RA	Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.,				
RT	"The complete genome sequence of Neisseria gonorrhoeae."				
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.				
CC	-I- FUNCTION: Could be a mediator in iron transactions between iron				
CC	acquisition and iron-regulating processes, such as synthesis and/or				
CC	repair of Fe-S clusters in biosynthetic enzymes (By similarity).				

```

CC      -1- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      DR      EMBL: AB004969; AAW90684.1; -; Genomic_DNA.
CC      DR      HAMAP, MF: 00686; -; 1.
CC      DR      InterPro: IPR007457; YggX.
CC      DR      Pfam: PF04362; DUF495; 1.
CC      DR      PIRSF: PIRSF029827; Fe_trafftc_YggX; 1.
CC      DR      ProDom: PD029191; DUF495; 1.
CC      KW      Complete proteome; Iron.
CC      SQ      SEQUENCE 88 AA; 10180 MW; EBC6F2BF097F2F1 CRC64;
CC      -----
Oy      Query Match 100.0%; Score 467; DB 1; Length 88;
Db      Best Local Similarity 100.0%; Pred. No. 1e-45;
        Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 MAAWVFCYKLNKBAAGMKPEPLPNEIGRIENYSQBAWAAWTHQTLINENTSLADP 60
Db      1 MAAWVFCYKLNKBAAGMKPEPLPNEIGRIENYSQBAWAAWTHQTLINENTSLADP 60
Oy      61 RAREYLAQOMEQYFPFGDADAVQGVTPQ 88
Db      61 RAREYLAQOMEQYFPFGDADAVQGVTPQ 88
Oy      -----
RESULT 2
FETP_NEIMA STANDARD; PRT; 88 AA.
ID FETP_NEIMA
AC P67615; G9JQP5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=NMMA0419;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=656599;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Z2491 / Serogroup A / Serotype 4A.
RC MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RX Parthill J., Achman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagsels K., Leather S., Moulé S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds S., Skelton J.,
RA Whitehead S., Spratt B.G., Barrrell B.G.;
RA "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
CC      -1- FUNCTION: Could be a mediator in iron transactions between iron
CC      acquisition and iron-regulating processes, such as synthesis and/or
CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      DR      EMBL: AL162753; CAB83718.1; -; Genomic_DNA.
CC      DR      HAMAP, MF: 00686; -; 1.
CC      DR      InterPro: IPR007457; YggX.
CC      DR      Pfam: PF04362; DUF495; 1.
CC      DR      PIRSF: PIRSF029827; Fe_trafftc_YggX; 1.
CC      DR      ProDom: PD029191; DUF495; 1.

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[illegible]

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.81093 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502a-28

Perfect score: 467
Sequence: 1 MARWVCYKLNKAEKMKP.....QMEOYFGDADAVGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/2/pubpa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpa/PTCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpa/US05_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	US-10-467-657-968	Sequence 968, App
2	60	12.8	1092	US-10-821-234-999	Sequence 999, App
3	58	12.4	380	US-10-525-674-28	Sequence 28, Appl
4	58	12.4	614	US-11-165-576-2	Sequence 2, Appl
5	58	12.4	614	US-11-165-576-4	Sequence 4, Appl
6	57.5	12.3	200	US-10-793-626-1186	Sequence 1186, Ap
7	57.5	12.3	204	US-10-793-626-2390	Sequence 2390, Ap
8	57.5	12.3	204	US-11-098-686-10498	Sequence 10498, A
9	57.5	12.3	655	US-11-098-686-10464	Sequence 10464, A
10	57	12.2	384	US-11-219-282-19	Sequence 19, Appl
11	57	12.2	620	US-10-131-826A-324	Sequence 324, App
12	56.5	12.1	575	US-11-098-686-10635	Sequence 10635, A
13	56.5	12.1	688	US-11-165-226-124	Sequence 124, App
14	56	12.0	1124	US-11-090-617-688	Sequence 688, App
15	56	12.0	1376	US-10-995-561-809	Sequence 809, App
16	56	12.0	1376	US-11-100-640-32	Sequence 32, Appl
17	55.5	11.9	403	US-11-009-658-14	Sequence 14, Appl
18	55.5	11.9	408	US-10-821-234-1100	Sequence 1100, Appl
19	55.5	11.9	449	US-11-098-686-10535	Sequence 10535, A
20	55	11.8	258	US-11-090-439-38	Sequence 38, Appl
21	55	11.8	261	US-10-467-657-400	Sequence 400, App
22	55	11.8	611	US-10-454-437-54	Sequence 54, Appl
23	55	11.8	633	US-11-193-561-13	Sequence 13, Appl
24	55	11.8	633	US-11-193-771-13	Sequence 13, Appl
25	55	11.8	633	US-11-193-789-13	Sequence 13, Appl

26	55	11.8	633	7	US-11-193-806-13	Sequence 13, Appl
27	55	11.8	633	7	US-11-193-857-13	Sequence 13, Appl
28	55	11.8	925	6	US-10-454-437-50	Sequence 50, Appl
29	55	11.8	967	7	US-11-202-268-6	Sequence 6, Appl
30	55	11.8	1011	7	US-11-202-268-2	Sequence 2, Appl
31	54.5	11.7	719	7	US-11-087-227-14	Sequence 14, Appl
32	54	11.6	307	6	US-10-793-626-522	Sequence 522, App
33	54	11.6	685	7	US-11-098-686-10574	Sequence 10574, A
34	54	11.6	738	7	US-11-140-625-11	Sequence 11, Appl
35	53.5	11.5	291	6	US-10-883-512-103	Sequence 103, App
36	53.5	11.5	310	7	US-11-055-163-7	Sequence 7, Appl
37	53.5	11.5	344	7	US-11-055-163-6	Sequence 6, Appl
38	53.5	11.5	432	6	US-10-933-115-8	Sequence 8, Appl
39	53.5	11.5	432	7	US-11-056-354-4	Sequence 4, Appl
40	53.5	11.5	440	6	US-10-933-115-2	Sequence 2, Appl
41	53.5	11.5	473	6	US-10-131-826A-382	Sequence 382, App
42	53	11.3	288	6	US-10-467-657-3426	Sequence 3426, App
43	53	11.3	291	7	US-11-120-308-24	Sequence 24, Appl
44	53	11.3	710	7	US-11-124-367A-354	Sequence 354, App
45	53	11.3	710	7	US-11-124-367A-359	Sequence 359, App
46	53	11.3	713	7	US-11-124-367A-355	Sequence 355, App
47	53	11.3	713	7	US-11-124-367A-356	Sequence 356, App
48	53	11.3	713	7	US-11-124-367A-358	Sequence 358, App
49	53	11.3	734	6	US-10-821-234-1056	Sequence 1056, Ap
50	53	11.3	3507	7	US-11-075-185-7	Sequence 7, Appl
51	52.5	11.2	197	6	US-10-986-501-296	Sequence 296, App
52	52.5	11.2	229	6	US-10-793-626-2818	Sequence 2818, Ap
53	52.5	11.2	335	7	US-11-072-175-245	Sequence 245, App
54	52.5	11.2	754	7	US-11-140-625-10	Sequence 10, Appl
55	52.5	11.2	1476	6	US-10-647-956A-4	Sequence 4, Appl
56	52.5	11.2	4128	6	US-10-770-726-77	Sequence 77, Appl
57	52	11.1	223	7	US-11-018-868-140	Sequence 140, App
58	52	11.1	381	7	US-11-024-959-418	Sequence 418, App
59	52	11.1	390	7	US-11-019-711-65	Sequence 65, Appl
60	52	11.1	390	7	US-11-219-282-12	Sequence 12, Appl
61	52	11.1	1022	7	US-11-156-084-118	Sequence 118, App
62	51.5	11.0	209	5	US-09-995-493-94	Sequence 94, Appl
63	51.5	11.0	396	7	US-11-202-731-2	Sequence 2, Appl
64	51.5	11.0	403	7	US-11-074-176-354	Sequence 354, App
65	51.5	11.0	408	7	US-11-074-176-186	Sequence 186, App
66	51.5	11.0	447	7	US-11-024-959-286	Sequence 286, App
67	51.5	11.0	479	6	US-10-821-234-871	Sequence 871, App
68	51.5	11.0	1034	7	US-11-072-512-2343	Sequence 2343, Ap
69	51.5	11.0	1159	6	US-10-613-744-12	Sequence 12, Appl
70	51.5	11.0	1159	6	US-10-957-116-9	Sequence 9, Appl
71	51	10.9	326	7	US-11-098-686-10173	Sequence 10173, A
72	51	10.9	387	7	US-11-219-282-20	Sequence 20, Appl
73	50.5	10.8	124	7	US-11-065-642-10	Sequence 10, Appl
74	50.5	10.8	347	6	US-10-853-807A-45	Sequence 45, Appl
75	50.5	10.8	352	6	US-10-878-556A-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
Sequence 968, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASTRANI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMan99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 100.0%; Score 467; DB 6; Length 88;
Best Local Similarity 100.0%; Pred. No. 1,76-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARWVCYKLNKAEAGMKPPLNENLGRIFENVSQEAAMATRHQTLINENRSLADP 60
DB 1 MARWVCYKLNKAEAGMKPPLNENLGRIFENVSQEAAMATRHQTLINENRSLADP 60

QY 61 RAREYLAQOMEQYFFGGDADAVQGYVPQ 88
DB 61 RAREYLAQOMEQYFFGGDADAVQGYVPQ 88

RESULT 2

US-10-821-234-999
Sequence 999, Application US/10821234
Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821,234

PRIOR FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pc_seq_genes Version 1.0

SEQ ID NO 999

LENGTH: 1092

TYPE: PRT

ORGANISM: Homo sapiens

US-10-821-234-999

Query Match 12.8%; Score 60; DB 6; Length 1092;
Best Local Similarity 30.6%; Pred. No. 28;
Matches 15; Conservative 12; Mismatches 20; Indels 2; Gaps 2;

QY 31 FENVSQEAAMAT-RHQTLINENRSLADP-RAREYLAQOMEQYFFGD 77
DB 492 FENVSQEAAMAT-RHQTLINENRSLADP-RAREYLAQOMEQYFFGD 77

RESULT 3

US-10-525-674-28
Sequence 28, Application US/10525674
Publication No. US20060003425A1

GENERAL INFORMATION:

APPLICANT: Kroger, Burkhard

APPLICANT: Zelder, Oskar

APPLICANT: Kolpproge, Corinna

APPLICANT: Schroder, Hartwig

APPLICANT: Hafner, Stefan

TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing

FILE REFERENCE: 13111-00002-US

CURRENT APPLICATION NUMBER: US/10/525,674

PRIOR FILING DATE: 2005-02-24

PRIOR APPLICATION NUMBER: PCT/EP 2003/009452

PRIOR FILING DATE: 2003-08-26

PRIOR APPLICATION NUMBER: DE 102 39 073.8

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PatentIn version 3.3

SEQ ID NO 28

LENGTH: 380
TYPE: PRT
ORGANISM: Thermus thermophilus
US-10-525-674-28

Query Match 12.4%; Score 58; DB 6; Length 380;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 15; Conservative 14; Mismatches 22; Indels 6; Gaps 2;

QY 34 VSQEAAMATRHQTLINENR-LSLADP-RAREYLAQOMEQYFFGGDADAVQGYVPQ 88
DB 1 MSRIALEAMGBEALLLKPPRSPPLIPPKRPTAVLPERRRGFYTE---LGGTYPE 53

RESULT 4

US-11-165-576-2
Sequence 2, Application US/11165576
Publication No. US20060009388A1

GENERAL INFORMATION:

APPLICANT: M1, Sha

APPLICANT: Pepinsky, R. Blake

TITLE OF INVENTION: Treatment of Conditions Involving Demyelination

FILE REFERENCE: 2159,0460004

CURRENT APPLICATION NUMBER: US/11/165,576

PRIOR FILING DATE: 2005-06-24

PRIOR APPLICATION NUMBER: 60/680,475

PRIOR FILING DATE: 2005-05-13

PRIOR APPLICATION NUMBER: 60/628,435

PRIOR FILING DATE: 2004-11-15

PRIOR APPLICATION NUMBER: 60/617,297

PRIOR FILING DATE: 2004-10-07

PRIOR APPLICATION NUMBER: 60/582,966

NUMBER OF SEQ ID NOS: 79

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 614

TYPE: PRT

ORGANISM: Homo sapiens

US-11-165-576-2

Query Match 12.4%; Score 58; DB 7; Length 614;
Best Local Similarity 27.4%; Pred. No. 24;
Matches 17; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

QY 3 RMVFCVKNKEA-EGMKPPLNENLGRIFENVSQEAAMATRHQTLINENRSLADP 60
DB 47 RAVLCHRRKFAVAPGIPTEFTLIDLGKRRITKINODEFASFPILEBELNENIVSAVEP 106

QY 61 RA 62
DB 107 GA 108

RESULT 5

US-11-165-576-4
Sequence 4, Application US/11165576
Publication No. US20060009388A1

GENERAL INFORMATION:

APPLICANT: M1, Sha

APPLICANT: Pepinsky, R. Blake

TITLE OF INVENTION: Treatment of Conditions Involving Demyelination

FILE REFERENCE: 2159,0460004

CURRENT APPLICATION NUMBER: US/11/165,576

PRIOR FILING DATE: 2005-06-24

PRIOR APPLICATION NUMBER: 60/680,475

PRIOR FILING DATE: 2005-05-13

PRIOR APPLICATION NUMBER: 60/628,435

PRIOR FILING DATE: 2004-11-15

PRIOR APPLICATION NUMBER: 60/617,297

PRIOR FILING DATE: 2004-10-07

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 / Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502a-29

Perfect score: 465
Sequence: 1 MARHICAKLGRKAEGLDFP.....KQTEKYFPGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21.*
1: geneeqp19808:*
2: geneeqp19908:*
3: geneeqp20008:*
4: geneeqp20018:*
5: geneeqp20028:*
6: geneeqp20038a:*
7: geneeqp20038b:*
8: geneeqp20048:*
9: geneeqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	100.0	87	5	ABb78175 Amino aci
2	459	98.7	87	5	ABb78174 Amino aci
3	339	72.9	88	5	ABb78171 Amino aci
4	339	72.9	88	5	ABb78172 Amino aci
5	339	72.9	88	5	ABb78173 Amino aci
6	339	72.9	88	6	ABb77219 N. gonorr
7	310	66.7	87	5	ABb78176 Amino aci
8	300	64.5	87	5	ABb78148 Amino aci
9	300	64.5	87	5	ABb78147 Amino aci
10	282.5	60.8	86	5	ABb78149 Amino aci
11	278	59.8	89	9	ABb41576 L. pneumo
12	278	59.8	95	9	ABb38294 L. pneumo
13	276	59.4	87	5	ABb78177 Amino aci
14	263	56.6	88	5	ABb78178 Amino aci
15	255	54.8	87	5	ABb78153 Amino aci
16	245.5	52.8	92	6	ADa34169 Acinetoba
17	242	52.0	91	5	ABb78150 Amino aci
18	241	51.8	87	5	ABb78152 Amino aci
19	238	51.2	87	5	ABb78151 Amino aci
20	229	49.2	87	5	ABb78169 Amino aci
21	227	48.8	87	5	ABb78170 Amino aci
22	227	48.8	122	7	ABb74609 Pseudomon
23	226	48.6	88	5	ABb78154 Amino aci
24	226	48.6	90	5	ABb78155 Amino aci

25	218	46.9	93	7	ADb05158 Bacterial
26	211	45.4	107	7	ABb05445 Klebsiell
27	208	44.7	90	5	ABb78168 Amino aci
28	206	44.3	88	5	ABb78160 Amino aci
29	206	44.3	91	5	ABb78161 Amino aci
30	206	44.3	91	5	ABb78158 Amino aci
31	206	44.3	91	5	ABb78159 Amino aci
32	206	44.3	91	5	ABb78162 Amino aci
33	206	44.3	91	5	ABb78157 Amino aci
34	206	44.3	91	5	ABb78156 Amino aci
35	199	42.8	90	5	ABb78165 Amino aci
36	199	42.8	91	5	ABb78163 Amino aci
37	197.5	42.5	78	5	ABb78164 Amino aci
38	189.5	40.8	90	5	ABb78167 Amino aci
39	181	38.9	76	5	ABb78166 Amino aci
40	181	38.9	110	8	ADb05173 M. catarr
41	71.5	15.4	206	7	ADb92530 B. lichen
42	71.5	15.4	5458	6	ABb66970 Photorhab
43	71	15.3	511	9	ABb96738 M. xanthu
44	70	15.1	355	8	ADb57590 Plant pol
45	70	15.1	376	8	ADb09636 Plant ful
46	69.5	14.9	1104	7	ADb64352 Human pro
47	68.5	14.7	532	8	ADb73216 Plant ful
48	68.5	14.7	860	8	ADb93806 Plant ful
49	67	14.4	186	7	ADb08482 Novel pro
50	67	14.4	197	7	ABb067819 Klebsiell
51	67	14.4	265	6	ABb18123 Protein e
52	66.5	14.3	869	4	ABb60212 Drosophil
53	66	14.2	354	7	ADb54604 Mouse dec
54	66	14.2	446	2	ADb08889 Tobacco G
55	66	14.2	722	5	ABb54118 Lactococc
56	65.5	14.1	409	4	ADb90502 C glutam
57	65.5	14.1	678	5	ABb47819 Listeria
58	65.5	14.1	5024	4	ABb62835 S. epider
59	65	14.0	222	9	ABb92850 M. xanthu
60	65	14.0	285	3	ABb28710 Arabidops
61	65	14.0	510	5	ABb90889 Herbicida
62	65	14.0	510	8	ADb74505 Thale cre
63	65	14.0	2188	4	ABb65784 Drosophil
64	64.5	13.9	153	3	ADb24680 Arabidops
65	64.5	13.9	195	3	ADb24679 Arabidops
66	64.5	13.9	256	3	ADb24678 Arabidops
67	64.5	13.9	256	7	ADb31835 Plant (A.
68	64.5	13.9	256	7	ADb46663 Thalecres
69	64.5	13.9	256	7	ADb30524 Plant yle
70	64.5	13.9	256	8	ADb43971 Plant tra
71	64	13.8	396	7	ADb62298 Rat Prote
72	64	13.8	446	2	ADb08888 Potato Gn
73	64	13.8	508	3	ADb48146 Arabidops
74	64	13.8	508	5	ADb91938 Herbicida
75	64	13.8	533	3	ADb48145 Arabidops

ALIGNMENTS

RESULT 1
ID ABb78175 standard; protein; 87 AA.
AC ABb78175;
XX 05-NOV-2002 (first entry)
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
OS US2002072118-A1.
PN XX

PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 87 AA;

Query Match 100.0%; Score 465; DB 5; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.3e-50;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMTHCAKLGKAEGLDPPPLPGELGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60
 DB 1 MARMTHCAKLGKAEGLDPPPLPGELGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60
 QY 61 RARQYLMKQTEKYFPGEGADQASGYVP 87
 DB 61 RARQYLMKQTEKYFPGEGADQASGYVP 87

RESULT 2
 ABB78174
 ID ABB78174 standard; protein; 87 AA.
 XX
 AC ABB78174;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 XX

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.

XX Unidentified.

XX US2002072118-A1.

XX 13-JUN-2002.

XX 18-SEP-2001; 2001US-00955502.

XX 22-SEP-2000; 2000US-0234588P.

XX (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.

XX Downs D, Gralnick JA;
 XX
 CC

DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 87 AA;

Query Match 98.7%; Score 459; DB 5; Length 87;
 Best Local Similarity 98.9%; Pred. No. 7.6e-50;
 Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARMTHCAKLGKAEGLDPPPLPGELGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60
 DB 1 MARMTHCAKLGKAEGLDPPPLPGELGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60
 QY 61 RARQYLMKQTEKYFPGEGADQASGYVP 87
 DB 61 RARQYLMKQTEKYFPGEGADQASGYVP 87

RESULT 3
 ABB78171
 ID ABB78171 standard; protein; 88 AA.
 XX
 AC ABB78171;
 XX
 DT 29-AUG-2003 (revised)
 DT 05-NOV-2002 (first entry)
 XX
 XX

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.

XX *Neisseria gonorrhoeae*.

XX US2002072118-A1.

XX 13-JUN-2002.

XX 18-SEP-2001; 2001US-00955502.

XX 22-SEP-2000; 2000US-0234588P.

XX (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.

XX Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.

XX 18-SEP-2001; 2001US-00955502.

XX 22-SEP-2000; 2000US-0234588P.

XX (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.

XX Downs D, Gralnick JA;
 XX
 CC

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-29
Perfect score: 465
Sequence: 1 MARMHCNKLCKEAGLDLP.....KQTEKYFEGAGDQASGVVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	72.9	88	2	H81014
2	241	51.8	90	2	C64013
3	227	48.8	90	2	H83003
4	226	48.6	90	2	C82320
5	206	44.3	91	2	AH0879
6	206	44.3	91	2	A85954
7	206	44.3	91	2	A65082
8	206	44.3	91	2	P91108
9	199	42.8	90	2	A10116
10	197	42.4	105	2	C82624
11	181	38.9	93	2	B84994
12	74.5	16.0	203	2	A32009
13	71	15.3	269	2	A69997
14	70	15.1	916	2	S22864
15	68	14.6	677	2	S33664
16	67.5	14.5	1215	2	A86595
17	67.5	14.5	1215	2	B72029
18	66	14.2	354	2	A55454
19	66	14.2	722	2	B86725
20	65.5	14.1	192	2	A83798
21	65.5	14.1	678	2	AB1130
22	65	14.0	260	2	F81726
23	65	14.0	443	2	S21909
24	65	14.0	512	2	H86206
25	65	14.0	853	2	T08162
26	65	14.0	2186	2	T13169
27	64.5	13.9	256	2	T5817
28	64	13.8	396	2	I58168
29	64	13.8	508	2	T02486

30	64	13.8	823	2	A90761	hypothetical prote
31	64	13.8	823	2	B85822	hypothetical prote
32	64	13.8	823	2	F85624	hypothetical prote
33	63.5	13.7	252	2	B82181	oxidoreductase, sh
34	63.5	13.7	271	2	A84643	probable WRKY-type
35	63.5	13.7	1124	2	UJ0293	zinc finger protei
36	63.5	13.7	1154	2	A56242	E-box-binding repr
37	63.5	13.7	1509	2	B89985	hypothetical prote
38	63	13.5	164	2	H95176	acetyltransferase,
39	63	13.5	164	2	B98043	conserved hypot
40	63	13.5	434	2	F75425	cRNA nucleotidylt
41	63	13.5	610	2	F86453	granule-bound stea
42	62.5	13.4	134	2	H82969	hypothetical prote
43	62.5	13.4	236	1	T46967	dileme cyochrome
44	62.5	13.4	258	2	D95910	probable membrane-
45	62.5	13.4	399	2	F83633	hypothetical prote
46	62.5	13.4	488	2	AH2792	L-serine dehydrata
47	62.5	13.4	488	2	G97571	hypothetical prote
48	62.5	13.4	712	2	T48961	probable protein p
49	62	13.3	242	2	T18588	hypothetical prote
50	62	13.3	260	2	AH1639	transcription acti
51	62	13.3	295	2	AG1291	decorin precursor
52	62	13.3	354	2	S29145	hypothetical prote
53	62	13.3	413	2	T01043	hypothetical prote
54	62	13.3	489	2	D72762	hypothetical prote
55	62	13.3	611	2	A72393	hypothetical prote
56	61.5	13.2	295	2	T50798	hypothetical prote
57	61.5	13.2	373	2	B47911	P81 protein - yea
58	61.5	13.2	726	2	S52141	ATPase - Brwinia a
59	61	13.1	82	2	C71676	hypothetical prote
60	61	13.1	306	2	A97249	zn-binding lipopro
61	61	13.1	441	2	A41591	endothelin recepto
62	61	13.1	823	2	T02959	kaurene synthase A
63	60.5	13.0	326	2	H82455	1S5 transposase VC
64	60.5	13.0	335	2	S75668	DNA primase (EC 2.
65	60.5	13.0	1553	2	S67483	adenosinetriphosph
66	60.5	13.0	1827	1	UUHU	sucrose alpha-gluc
67	60.5	13.0	1867	2	S22775	MOT1 protein - yea
68	60	12.9	136	2	T17621	hypothetical prote
69	60	12.9	138	2	T15806	hypothetical prote
70	60	12.9	260	2	AH1276	hypothetical prote
71	60	12.9	282	2	D97138	DNA replication pr
72	60	12.9	333	1	S39699	monooxygenase homo
73	60	12.9	383	2	T17722	hypothetical prote
74	60	12.9	603	2	T02677	hypothetical prote
75	59.5	12.8	203	2	A30836	chlorophyll a/b-bi

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [Imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: H81014, F81958
R:Retelin, H.; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Piazza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:2015755; PMID:10710307
A:Accession: H81014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <TERT>
A:Cross-references: UNIPARC:UP100000C4E7F; GB:AE002552; GB:AE002098; NID:G7227279; PIDN:
A:Experimental source: serogroup B, strain MC58
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgen, K.; Leather, S.; Moute, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: F81958
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <PAR>
A:Cross-references: UNIPARC:UPI00000C4E7; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A:Experimental source: serogroup A, strain Z2491
C:Gene: NMB2021; NMA0419
C:Superfamily: fe(ii) trafficking protein Y93X

Query Match 72.9%; Score 339; DB 2; Length 88;
Best Local Similarity 67.8%; Pred. No. 2.2e-30;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

DB 1 MARMHCALKGKAEGLDPPELPGLGRLYESYSKQAMQDWLKKQOTMLINENRLNMDP 60
1 MARMVCVCLKNAEAGKFPPLPNELGKRIENVSQEMAAWTRHQTLINENRLSLADP 60

QY 61 RARQYLMKQTEKYPFGGADQASGYVP 87
61 RAREYLAQWQWQGYFPGGADAVQGYVP 87

RESULT 2
C64013
hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C:Accession: C64013
R:Flerschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gockyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64013
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-90 <TIGR>
A:Cross-references: UNIPROT:P44048; UNIPARC:UPI00013B0M4; GB:U32760; GB:IL42023; NID:915
C:Superfamily: fe(ii) trafficking protein Y93X

Query Match 51.8%; Score 241; DB 2; Length 90;
Best Local Similarity 54.5%; Pred. No. 1.5e-19;
Matches 48; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

QY 1 MARMHCALKGKAEGLDPPELPGLGRLYESYSKQAMQDWLKKQOTMLINENRLNMDP 60
1 MARTVPCBYLKKGEAGLDFQLYPGELGKRIFDSVSKQAMGEWIKKQOTMLVNEKKLNNMNA 60

DB 61 RARQYLMKQTEKYPFGGADQASGYVP 87
61 EHRKLEQEMVNFLE-EGKDVHIGGYVP 87

QY 61 RARQYLMKQTEKYPFGGADQASGYVP 87
61 EHRKLEQEMVNFLE-EGKDVHIGGYVP 87

RESULT 3
H83003
conserved hypothetical protein PA5148 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: H83003
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437373; PMID:10984043
A:Accession: H83003
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-90 <STO>
A:Cross-references: UNIPARC:UPI000000C5F26; GB:AE004927; GB:AE004091; NID:g9951437; PIDN:/z
A:Experimental source: strain PAOI
C:Genetics:
A:Gene: PA5148
C:Superfamily: fe(II) trafficking protein YggX

Query Match 48.8%; Score 227; DB 2; Length 90;
Best Local Similarity 47.1%; Pred. No. 5.3e-18;
Matches 41; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

Db
1 MARMHCAKLGKEARGLDPPLPGELGKRLYESVSQAKODWIKQOTMLINENRLNNMADP 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
1 MSRTVMCKRTHBELPGLDRPPYFGAKGEDITYNNVSKANDEMWKQTMTLINERKLNNMNA 60

Oy
61 RAROYLMOQTEKYKPFEGAGDAQSGYYP 87
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
61 EDRKFLQGEMOKFLSGEDYAKADGYYP 87

RESULT 4
CB2320
conserved hypotheoretical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogroup C)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: CB2320
R:Characterization: J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
charidson, D.; Emolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragoi, I.; Sellers, P.
l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:2040683; PMID:10952501
A:Accession: CB2320
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <HEI>
A:Cross-references: UNIPARC:UPI000000CCCF; GB:AE004113; GB:AE003852; NID:g9954871; PIDN:/z
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0451
A:Map position: 1
C:Superfamily: fe(II) trafficking protein YggX

Query Match 48.6%; Score 226; DB 2; Length 90;
Best Local Similarity 48.9%; Pred. No. 6.8e-18;
Matches 43; Conservative 16; Mismatches 27; Indels 2; Gaps 2;

Oy
1 MARMHCAKLGKEARGLDPPLPGELGKRLYESVSQAKODWIKQOTMLINENRLNNMADP 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
1 MARVTCTLOKRADLDLQLYPGLGSKRIFDNICREAWOMOTQTMILINERKLNNMDP 60

Db
61 RAROYLMOQTEKYKPFEGAGDAQSGYYP 87
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
61 EHRKLEGMWNFLF-EGRKVHIEGYTP 87

RESULT 5
AH0879
conserved hypotheoretical protein STY326 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typh
A>Note: This species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C:Accession: AH0879
R:Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
Th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0879
A>Status: preliminary
A:Molecule type: DNA

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-29

Perfect score: 465
Sequence: 1 MARWICAKLGKRAKGLDPP.....KQTEKYFPGAGDQNSGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	100.0	91	1	FETP_BURMA
2	465	100.0	91	1	FETP_BURMA
3	442	95.1	91	2	Q41S19_9BURK
4	409	88.0	91	1	FETP_RALSO
5	355	76.3	90	1	FETP_CHRYO
6	339	72.9	88	1	FETP_NEIG1
7	339	72.9	88	1	FETP_NEIMA
8	339	72.9	88	1	FETP_NEIMA
9	330	71.0	90	1	FETP_NITEU
10	300	64.5	90	1	FETP_BORER
11	300	64.5	90	1	FETP_BORER
12	300	64.5	90	1	FETP_BORER
13	282	60.6	89	1	FETP_LEGPI
14	278	59.8	89	1	FETP_LEGPI
15	278	59.8	89	1	FETP_LEGPI
16	276	59.4	90	1	FETP_MERCA
17	263	56.6	90	1	FETP_MERCA
18	255	54.8	94	1	FETP_HABOU
19	243	52.3	90	1	FETP_IDILO
20	241	51.8	90	1	FETP_HABIN
21	241	51.8	90	2	Q4QMD9_HABIS
22	240	51.6	92	2	Q4NM04_9DELT
23	238	51.2	90	1	FETP_PASBU
24	238	51.2	90	1	FETP_PASBU
25	237.5	51.0	90	1	FETP_PASBU
26	237.5	51.0	90	2	Q4U228_AZOV1
27	236	50.8	92	1	FETP_XANOR
28	233	50.1	90	1	FETP_VIBRA
29	232	49.9	90	1	FETP_VIBRI
30	231	49.7	90	1	FETP_VIBVU
31	231	49.7	90	1	FETP_VIBVU

32	230	49.5	90	2	Q6T7F6_PSEFL	Q6T7F6_pseudomonas
33	229	49.2	90	1	FETP_PSEPK	Q88449_pseudomonas
34	228	49.0	92	1	FETP_XANCP	Q88829_xanthomonas
35	228	49.0	90	2	Q4UW14_XANCP	Q4UW14_xanthomonas
36	227	48.8	90	1	FETP_PSEAB	Q9N36_pseudomonas
37	226	48.6	90	1	FETP_VIBCH	Q9K44_vibrio chol
38	226	48.6	92	1	FETP_SHEON	Q88X6_shewanella
39	223	48.0	91	1	FETP_MANGM	Q65VCT_mangrovia
40	222	47.7	90	1	FETP_PHOLL	Q7N711_photobacter
41	219	47.1	90	2	Q4K1T2_PSEFS	Q4K1T2_pseudomonas
42	216	46.5	96	2	Q4FVJ7_9GAMM	Q4FVJ7_psychrobact
43	212	45.6	90	1	FETP_PHOPR	Q61MK7_photobacter
44	208	44.7	90	1	FETP_PSEBM	Q87LMK_pseudomonas
45	208	44.7	90	2	Q4ZLF3_PSESY	Q4ZLF3_pseudomonas
46	207	44.5	90	1	FETP_YERPS	Q66M3_yersinia ps
47	204	43.9	90	1	FETP_XYLPT	Q87D06_xyliella fas
48	203.5	43.8	87	1	FETP_FRATY	Q5nhJ8_francisella
49	201	43.2	90	1	FETP_ECO57	Q08B34_escherichia
50	201	43.2	90	1	FETP_ECOLI	Q08B34_escherichia
51	201	43.2	90	1	FETP_ERWCT	Q68B39_erwinia car
52	201	43.2	90	1	FETP_SALCH	Q57K04_salmonella
53	201	43.2	90	1	FETP_SALPA	Q57K04_salmonella
54	201	43.2	90	1	FETP_SALTI	Q57K04_salmonella
55	201	43.2	90	1	FETP_SALTY	Q67617_salmonella
56	201	43.2	90	1	FETP_SHIFL	Q08B35_shigella fl
57	199	42.8	90	1	FETP_YERPE	Q82he7_yersinia pe
58	197	42.4	90	1	FETP_ECOL6	Q82he7_yersinia pe
59	197	42.4	90	1	FETP_XYLPA	Q82he7_yersinia pe
60	189	40.6	78	1	FETP_BUCAP	Q82he7_yersinia pe
61	183	39.4	77	1	FETP_CANBP	Q82he7_yersinia pe
62	181	38.9	77	1	FETP_BUCAI	Q82he7_yersinia pe
63	169	36.3	78	1	FETP_WIGBR	Q82he7_yersinia pe
64	150	32.3	64	1	FETP_BUCRP	Q82he7_yersinia pe
65	75.5	16.2	661	2	Q63P78_BURPS	Q82he7_yersinia pe
66	75	16.1	1222	2	Q7NG45_GLOVI	Q82he7_yersinia pe
67	74.5	16.0	461	2	Q82XAT_NITEU	Q82he7_yersinia pe
68	73	15.7	187	2	Q72JET_THRT2	Q82he7_yersinia pe
69	73	15.7	187	2	Q72JET_THRT2	Q82he7_yersinia pe
70	72.5	15.6	1328	2	Q5CR96_CRYPV	Q82he7_yersinia pe
71	72	15.5	917	1	ATG9_MAGGR	Q82he7_yersinia pe
72	71.5	15.4	192	2	Q4NQ77_9DELT	Q82he7_yersinia pe
73	71.5	15.4	206	2	Q65LS8_BACDL	Q82he7_yersinia pe
74	71.5	15.4	5457	2	Q7N2F7_PHOLL	Q82he7_yersinia pe
75	71	15.3	269	2	Q34935_BACSU	Q82he7_yersinia pe

ALIGNMENTS

RESULT 1
ID FETP_BURMA STANDARD, PRT; 91 AA.
AC Q621U9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocNames=BMA1752;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., Deshaizer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouli H.M., Kolonay J.F.,
RA Madupu N., Mohamoud Y., Nelson W.C., Rodehorst C.M.,
RA Sarría S., Selengut J., Shambin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.,

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CC "Structural flexibility in the Burkholderia mallei genome.";
CC Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: CP000010; AAU48201.1; -; Genomic_DNA.
CC TIGR: BM1752; -.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;
CC -----
Query Match 100.0%; Score 465; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 1 MARMHCAGKAGKAEAGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMDP 60
DB 1 MARMHCAGKAGKAEAGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMDP 60
QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
DB 61 RARQYLMKQTEKYFFEGADQASGYVP 87
CC -----
RESULT 2
PTEP_BURPS STANDARD; PRT; 91 AA.
ID PTEP_BURPS
AC Q63S34;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BPSL2326;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.040302101;
RA Holden M.T.G., Tittball R.W., Peacock S.J., Csereno-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahnia M., Thomson N.R., Bacon N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Chervach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., Deshazer D.,
RA Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagals K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songelivili S., Stevens K., Tumapa S., Vesaratchaveest M.,
RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis.
RT Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: BX571965; CAH36329.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;
CC -----
Query Match 100.0%; Score 465; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
QY 1 MARMHCAGKAGKAEAGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMDP 60
DB 1 MARMHCAGKAGKAEAGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMDP 60
QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
DB 61 RARQYLMKQTEKYFFEGADQASGYVP 87
CC -----
RESULT 3
Q4LS19_9BURK
ID Q4LS19_9BURK PRELIMINARY; PRT; 91 AA.
AC Q4LS19;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_3773;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Lattimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Lattimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL: AAH0100021; EAM18958.1; -; Genomic_DNA.
CC Hypothetical protein.
CC SEQUENCE 91 AA; 10327 MW; 0A540A880A76E284 CRC64;
CC -----
Query Match 95.1%; Score 442; DB 2; Length 91;
Best Local Similarity 94.3%; Pred. No. 2e-40;
Matches 82; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC -----
QY 1 MARMHCAGKAGKAEAGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMDP 60
DB 1 MARMHCAGKAGKAEAGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMDP 60
QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
DB 61 RARQYLMKQTEKYFFEGADQASGYVP 87

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-29
Perfect score: 465
Sequence: 1 MARMHCATKGEKAEGLDFP.....KQTEKYPFGAGDQASGVVP 87

Scoring table: BIOSIM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: Issued Patents AA.*
2: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245.5	52.8	92	US-09-328-352-5456	Sequence 5456, Ap
2	227	48.8	122	US-09-252-991A-23355	Sequence 23355, A
3	218	46.9	93	US-09-543-681A-5443	Sequence 5443, Ap
4	211	45.4	107	US-09-489-039A-11962	Sequence 11962, A
5	181	38.9	110	US-09-540-236-2859	Sequence 2859, Ap
6	71	15.3	511	US-09-902-540-15937	Sequence 15937, A
7	69.5	14.9	1104	US-10-104-047-2506	Sequence 2506, Ap
8	67.5	14.5	1218	US-09-438-185A-837	Sequence 837, App
9	67	14.4	197	US-09-489-039A-14336	Sequence 14336, A
10	66	14.2	446	US-09-591-466C-4	Sequence 4, Appli
11	65.5	14.1	342	US-09-605-703B-1526	Sequence 1526, Ap
12	65.5	14.1	342	US-09-605-703B-1528	Sequence 1528, Ap
13	65.5	14.1	5024	US-09-710-279-2964	Sequence 1049, A
14	65	14.0	222	US-09-902-540-12049	Sequence 12049, A
15	64	13.8	446	US-09-591-466C-2	Sequence 2, Appli
16	64	13.8	1479	US-08-840-062-4	Sequence 4, Appli
17	63.5	13.7	398	US-09-710-279-1498	Sequence 44, Appli
18	63.5	13.7	398	US-09-710-279-1498	Sequence 1498, Ap
19	63.5	13.7	417	US-09-134-001C-3810	Sequence 3810, Ap
20	63.5	13.7	1125	US-09-949-016-10194	Sequence 10194, Ap
21	63.5	13.7	1509	US-09-676-519-27	Sequence 27, Appli
22	62.5	13.4	10182	US-09-134-001C-3159	Sequence 3159, Ap
23	62.5	13.4	179	US-09-252-991A-17099	Sequence 17099, A
24	62.5	13.4	401	US-09-252-991A-17272	Sequence 17272, A
25	62	13.3	498	US-09-058-260-16	Sequence 16, Appli
26	62	13.3	503	US-08-781-802-2	Sequence 2, Appli
27	62	13.3	503	US-08-781-802-10	Sequence 10, Appli

ALIGNMENTS

28	62	13.3	503	1	US-08-781-802-12	Sequence 12, Appli
29	62	13.3	503	2	US-08-694-078-2	Sequence 2, Appli
30	62	13.3	503	2	US-09-058-260-2	Sequence 2, Appli
31	62	13.3	503	2	US-09-058-260-10	Sequence 10, Appli
32	62	13.3	503	2	US-09-058-260-12	Sequence 12, Appli
33	62	13.3	503	2	US-09-058-260-28	Sequence 28, Appli
34	62	13.3	503	2	US-09-058-260-30	Sequence 30, Appli
35	62	13.3	636	2	US-10-138-075-4	Sequence 4, Appli
36	62	13.3	1564	2	US-09-976-594-309	Sequence 309, App
37	62	13.3	1215	2	US-09-607-787A-50	Sequence 50, Appli
38	61.5	13.2	266	2	US-09-640-211A-762	Sequence 762, App
39	61.5	13.2	555	2	US-09-328-352-5873	Sequence 5873, Ap
40	61.5	13.2	1277	2	US-09-602-787A-54	Sequence 54, Appli
41	61	13.1	163	2	US-09-270-767-37714	Sequence 37714, A
42	61	13.1	823	1	US-08-261-465-1	Sequence 1, Appli
43	61	13.1	823	1	US-08-405-254-5	Sequence 5, Appli
44	60.5	13.0	266	2	US-09-252-991A-21786	Sequence 21786, A
45	60.5	13.0	266	2	US-09-270-767-33833	Sequence 33833, A
46	60.5	13.0	269	2	US-09-270-767-49050	Sequence 49050, A
47	60.5	13.0	277	2	US-09-902-540-14772	Sequence 14772, A
48	60.5	13.0	455	2	US-09-270-767-45790	Sequence 45790, A
49	60.5	13.0	1003	2	US-09-949-016-10627	Sequence 10627, A
50	60.5	13.0	1827	2	US-09-443-780C-14	Sequence 14, Appli
51	60.5	13.0	1827	2	US-09-079-723-179	Sequence 179, App
52	60.5	13.0	1867	2	US-09-824-574-5	Sequence 5, Appli
53	60	12.9	292	2	US-09-328-352-5836	Sequence 5836, Ap
54	60	12.9	414	2	US-09-902-540-12109	Sequence 12109, A
55	59.5	12.8	103	2	US-09-081-320-33	Sequence 33, Appli
56	59.5	12.8	103	2	US-09-574-141A-33	Sequence 33, Appli
57	59.5	12.8	103	2	US-09-707-780-33	Sequence 33, Appli
58	59.5	12.8	103	2	US-09-568-189A-33	Sequence 33, Appli
59	59.5	12.8	236	2	US-09-270-767-27158	Sequence 37158, A
60	59.5	12.8	236	2	US-09-270-767-22375	Sequence 52375, A
61	59.5	12.8	1017	2	US-09-762-724-12	Sequence 12, Appli
62	59.5	12.8	1017	2	US-09-762-724-14	Sequence 14, Appli
63	59.5	12.8	1792	1	US-08-962-284-4	Sequence 2, Appli
64	59.5	12.8	1838	2	US-09-120-663-2	Sequence 2, Appli
65	59.5	12.8	1838	2	US-09-431-614-8	Sequence 8, Appli
66	59.5	12.8	1838	2	US-09-536-784-2	Sequence 28, Appli
67	59.5	12.8	1838	2	US-09-412-100-28	Sequence 14490, A
68	59	12.7	510	2	US-09-248-796A-14490	Sequence 15299, A
69	59	12.7	925	2	US-09-902-540-15299	Sequence 11, Appli
70	58.5	12.6	259	2	US-09-081-320-11	Sequence 11, Appli
71	58.5	12.6	259	2	US-09-574-141A-11	Sequence 11, Appli
72	58.5	12.6	259	2	US-09-707-780-11	Sequence 11, Appli
73	58.5	12.6	259	2	US-09-568-189A-11	Sequence 11, Appli
74	58.5	12.6	421	2	US-09-710-279-1820	Sequence 1820, Ap
75	58.5	12.6	427	2	US-09-134-001C-5141	Sequence 5141, Ap

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US-09-328-352-5456
Sequence 5456, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-02PA
CURRENT APPLICATION NUMBER: US/09/328.352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5456
LENGTH: 92
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5456
Query Match 52.8%; Score 245.5; DB 2; Length 92;
Best Local Similarity 51.1%; Pred. No. 2.5e-24;

Matches 45; Conservative 17; Mismatches 25; Indels 1; Gaps 1;
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Db 4 MSRQVFCRKYOKMEGLDFAFPFGAKGQEFENVSQAWQEWLQHOTTLINERKLNVFEP 63
Qy 61 RARQYLMKQTEKYPFG-EGADQASGYVP 87
Db 64 EAKKFLBQREKFPNNDSEYKAEKGMKP 91
RESULT 2
US-09-252-991A-23355
; Sequence 23355; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355
Query Match 48.8%; Score 227; DB 2; Length 122;
Best Local Similarity 47.1%; Pred. No. 9.4e-22;
Matches 41; Conservative 17; Mismatches 29; Indels 0; Gaps 0;
Qy 1 MARMHCAGKAGKAEGLDPPPLPGLGKRLYESVSQAWMDLKKQOTMLINENRLNMDP 60
Db 33 MSRTWCKRYHELRGLRPPPGAKGSDIYNVSRKANDWQKQOTMLINERKLNMNNA 92
Qy 61 RARQYLMKQTEKYPFGEGADQASGYVP 87
Db 93 EDRKFLQEMKXFLSGEDVAKADGYVP 119
RESULT 3
US-09-543-681A-5443
; Sequence 5443; Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443
Query Match 46.9%; Score 218; DB 2; Length 93;
Best Local Similarity 48.9%; Pred. No. 9.8e-21;
Matches 43; Conservative 15; Mismatches 28; Indels 2; Gaps 2;
Qy 1 MARMHCAGKAGKAEGLDPPPLPGLGKRLYESVSQAWMDLKKQOTMLINENRLNMDP 60
Db 4 MSRTIFCTFLNKAGDGLDFQLYPGLGKRLIFNEISKEAWQAWMAKQOTMLINEKKLNTMNP 63

Qy 61 RARQYLMKQTEKYPFGEGAD-QASGYVP 87
Db 64 DDKRLLEGWVRFLP-EGHDVHIDGYTP 90
RESULT 4
US-09-489-039A-11962
; Sequence 11962; Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962
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Best Local Similarity 47.7%; Pred. No. 9.7e-20;
Matches 42; Conservative 15; Mismatches 29; Indels 2; Gaps 2;
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Db 17 MSRTIFCTFLQREADGDFQLYPGLGKRLYESVSKEAWQAWQKQOTMLINEKKLSMNP 76
Qy 61 RARQYLMKQTEKYPFGEGAD-QASGYVP 87
Db 77 EHRKLLBQEMVQFLP-BGKDVHIGGYTP 103
RESULT 5
US-09-540-236-2859
; Sequence 2859; Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859
Query Match 38.9%; Score 181; DB 2; Length 110;
Best Local Similarity 39.3%; Pred. No. 8.3e-16;
Matches 33; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
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Db 24 MVFCRKYQONLPLPPLPPNAKGOEIOPTISAKAMAWLEQOTMLINEKHSMDPOAK 83
Qy 64 QYLMKQTEKYPFGEGADQASGYVP 87
Db 84 KYLMEQREKFLDNGDYKPAGYTP 107
RESULT 6
US-09-902-540-15937
; Sequence 15937; Application US/09902540

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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 54.8952 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-29

Perfect score: 465

Sequence: 1 MARMHCNKLCKEAGLDLP.....KQTEKYPFGAGDQASGVVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_AA_Main:
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	339	72.9	88	3	US-09-955-502-26
4	339	72.9	88	3	US-09-955-502-27
5	339	72.9	88	3	US-09-955-502-28
6	310	66.7	87	3	US-09-955-502-31
7	300	64.5	87	3	US-09-955-502-2
8	300	64.5	87	3	US-09-955-502-3
9	282.5	60.8	86	3	US-09-955-502-4
10	276	59.4	87	3	US-09-955-502-32
11	263	56.6	88	3	US-09-955-502-33
12	255	54.8	87	3	US-09-955-502-8
13	242	52.0	91	3	US-09-955-502-5
14	241	51.8	87	3	US-09-955-502-7
15	238	51.2	87	3	US-09-955-502-6
16	229	49.2	87	3	US-09-955-502-24
17	227	48.8	87	3	US-09-955-502-25
18	226	48.6	88	3	US-09-955-502-9
19	226	48.6	90	3	US-09-955-502-10
20	208	44.7	90	3	US-09-955-502-23
21	206	44.3	88	3	US-09-955-502-15
22	206	44.3	91	3	US-09-955-502-11
23	206	44.3	91	3	US-09-955-502-12
24	206	44.3	91	3	US-09-955-502-13
25	206	44.3	91	3	US-09-955-502-14
26	206	44.3	91	3	US-09-955-502-16
27	206	44.3	91	3	US-09-955-502-17

28	199	42.8	90	3	US-09-955-502-20	Sequence 20, Appl
29	199	42.8	91	3	US-09-955-502-18	Sequence 19, Appl
30	197.5	42.5	78	3	US-09-955-502-19	Sequence 18, Appl
31	197	42.4	89	3	US-09-955-502-22	Sequence 22, Appl
32	181	38.9	76	3	US-09-955-502-21	Sequence 21, Appl
33	71.5	15.4	206	5	US-10-510-812-76	Sequence 76, Appl
34	70	15.1	355	5	US-10-739-930-7667	Sequence 76, Appl
35	70	15.1	376	5	US-10-425-114-55451	Sequence 65451, Ap
36	69.5	14.9	1104	4	US-10-104-047-2506	Sequence 2506, Ap
37	69	14.8	313	4	US-10-437-963-173240	Sequence 173240, A
38	68.5	14.7	532	4	US-10-425-114-42582	Sequence 42582, A
39	68.5	14.7	860	4	US-10-425-114-56470	Sequence 56470, A
40	68.5	14.7	942	4	US-10-425-115-349562	Sequence 349562, A
41	67.5	14.5	1027	4	US-10-437-963-156087	Sequence 156087, A
42	67.5	14.5	1215	5	US-10-732-923-8185	Sequence 8185, Ap
43	67.5	14.5	1215	5	US-10-732-923-8195	Sequence 8195, Ap
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45	67	14.4	439	4	US-10-437-963-166724	Sequence 166724, A
46	67	14.4	443	5	US-10-732-923-17533	Sequence 17533, A
47	66.5	14.3	869	6	US-11-097-143-17428	Sequence 7428, Ap
48	66	14.2	354	4	US-10-319-130-20	Sequence 20, Appl
49	66	14.2	362	4	US-10-424-599-248696	Sequence 248696, A
50	66	14.2	374	5	US-10-732-923-17415	Sequence 17415, A
51	66	14.2	446	4	US-10-615-144-4	Sequence 4, Appl1
52	66	14.2	526	4	US-10-437-963-156176	Sequence 156176, A
53	65.5	14.1	409	3	US-09-738-626-4256	Sequence 4256, Ap
54	65.5	14.1	546	5	US-10-732-923-10268	Sequence 10268, A
55	65.5	14.1	851	4	US-10-437-963-113913	Sequence 113913, A
56	65	14.0	2188	5	US-10-732-923-17535	Sequence 17535, A
57	65	14.0	2188	6	US-11-097-143-24144	Sequence 24144, A
58	64.5	13.9	142	4	US-10-437-963-172454	Sequence 172454, A
59	64.5	13.9	256	4	US-10-286-264-62	Sequence 62, Appl
60	64.5	13.9	256	4	US-10-295-403-68	Sequence 68, Appl
61	64.5	13.9	256	4	US-10-225-066A-556	Sequence 556, App
62	64.5	13.9	256	4	US-10-374-780A-2434	Sequence 2434, App
63	64.5	13.9	256	5	US-10-732-923-16237	Sequence 16237, A
64	64.5	13.9	256	5	US-10-732-923-16236	Sequence 16236, A
65	64.5	13.9	256	5	US-10-225-066A-556	Sequence 556, App
66	64	13.8	237	4	US-10-425-115-319141	Sequence 319141, A
67	64	13.8	446	4	US-10-615-144-2	Sequence 2, Appl1
68	64	13.8	485	4	US-10-424-599-164730	Sequence 164730, A
69	64	13.8	1011	4	US-10-437-963-173328	Sequence 17328, A
70	63.5	13.7	205	5	US-10-732-923-7779	Sequence 77306, A
71	63.5	13.7	252	4	US-10-282-122A-77306	Sequence 88, Appl
72	63.5	13.7	271	4	US-10-295-403-88	Sequence 942, App
73	63.5	13.7	271	4	US-10-225-066A-942	Sequence 2068, Ap
74	63.5	13.7	271	4	US-10-374-780A-2068	Sequence 652, App
75	63.5	13.7	271	4	US-10-412-699B-652	

ALIGNMENTS

RESULT 1
US-09-955-502-29
Sequence 29, Application US/09955502
Patent No. US2002072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia mallei

US-09-955-502-29

Query Match 100.0%; Score 465; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 4,7e-47;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARMHCAKLGKAEGLDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60

Qy 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 2
US-09-955-502-30

Sequence 30, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30

LENGTH: 87

TYPE: PRT

ORGANISM: Burkholderia pseudomallei

Query Match 100.0%; Score 465; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 4,7e-47;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARMHCAKLGKAEGLDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60
Db 1 MARMHCAKLGKAEGLDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60

Qy 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 3
US-09-955-502-26

Sequence 26, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 26

LENGTH: 88

TYPE: PRT

ORGANISM: Neisseria gonorrhoeae

Query Match 72.9%; Score 339; DB 3; Length 88;

Best Local Similarity 67.8%; Pred. No. 3,9e-32;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MARMHCAKLGKAEGLDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60
Db 1 MARMHCAKLGKAEGLDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60

Qy 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 4
US-09-955-502-27

Sequence 27, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 27

LENGTH: 88

TYPE: PRT

ORGANISM: Neisseria meningitidis B

Query Match 72.9%; Score 339; DB 3; Length 88;
Best Local Similarity 67.8%; Pred. No. 3,9e-32;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MARMHCAKLGKAEGLDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60
Db 1 MARMHCAKLGKAEGLDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNMDP 60

Qy 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 5
US-09-955-502-28

Sequence 28, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 28

LENGTH: 88

TYPE: PRT

ORGANISM: Neisseria meningitidis A

Query Match 72.9%; Score 339; DB 3; Length 88;
Best Local Similarity 67.8%; Pred. No. 3,9e-32;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.75626 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502A-29

Perfect score: 465
Sequence: 1 MARMHCATKCKEAGLDGP.....KQTEKYFEGAGDQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications_MA_New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	339	72.9	88	US-10-467-657-968	Sequence 968, App
2	69.5	14.9	1104	US-11-072-512-2506	Sequence 2506, App
3	67	14.4	446	US-11-119-351-8	Sequence 8, Appli
4	65.5	14.1	5024	US-10-793-626-2964	Sequence 2964, Ap
5	63.5	13.7	398	US-10-793-626-44	Sequence 44, Appl
6	63.5	13.7	398	US-10-793-626-1498	Sequence 1498, Ap
7	59.5	12.8	832	US-11-098-686-10182	Sequence 10182, A
8	59.5	12.8	1841	US-11-057-058-63	Sequence 63, Appl
9	58.5	12.6	421	US-10-793-626-1820	Sequence 1820, Ap
10	57.5	12.4	447	US-11-024-959-286	Sequence 286, App
11	57.5	12.4	787	US-10-467-657-2832	Sequence 2832, App
12	57	12.3	209	US-09-995-493-94	Sequence 94, Appl
13	56.5	12.2	575	US-11-098-686-10635	Sequence 10635, A
14	56.5	12.2	1077	US-11-054-281-110	Sequence 110, App
15	56	12.0	381	US-11-098-686-11284	Sequence 11284, A
16	56	12.0	867	US-11-072-512-3052	Sequence 3052, Ap
17	56	12.0	3803	US-10-995-561-773	Sequence 773, App
18	56	12.0	3960	US-10-995-561-777	Sequence 777, App
19	56	12.0	5335	US-10-995-561-774	Sequence 774, App
20	56	12.0	5406	US-10-995-561-779	Sequence 779, App
21	56	12.0	5415	US-10-995-561-775	Sequence 775, App
22	56	12.0	5464	US-10-995-561-775	Sequence 775, App
23	55.5	11.9	360	US-11-019-711-67	Sequence 360, Appl
24	55.5	11.9	563	US-11-072-512-3460	Sequence 3460, Ap
25	55.5	11.9	622	US-11-070-080-22	Sequence 22, Appl

26	54.5	11.7	107	US-09-995-493-34	Sequence 34, Appl
27	54.5	11.7	299	US-10-362-772-2	Sequence 2, Appli
28	54.5	11.7	355	US-10-878-556A-10	Sequence 10, Appl
29	54.5	11.7	505	US-11-072-512-3519	Sequence 3519, Ap
30	54.5	11.7	668	US-11-111-239-13	Sequence 13, Appl
31	54.5	11.7	805	US-11-108-539-2	Sequence 2, Appli
32	54.5	11.7	1134	US-11-043-889-34	Sequence 34, Appl
33	54.5	11.7	1187	US-11-043-889-46	Sequence 46, Appl
34	54.5	11.7	1476	US-10-647-956A-4	Sequence 4, Appli
35	54	11.6	437	US-10-454-477-84	Sequence 84, Appl
36	54	11.6	593	US-11-194-246-117	Sequence 317, App
37	54	11.6	629	US-10-821-234-1528	Sequence 1528, Ap
38	54	11.6	634	US-11-072-512-2300	Sequence 2300, Ap
39	54	11.6	8746	US-11-098-686-10232	Sequence 10232, A
40	53.5	11.5	389	US-11-012-762-12	Sequence 72, Appl
41	53.5	11.5	757	US-11-067-121-16	Sequence 16, Appl
42	53.5	11.5	757	US-11-186-284-41	Sequence 41, Appl
43	53	11.4	532	US-10-063-703-72	Sequence 72, Appl
44	53	11.4	532	US-11-102-240-72	Sequence 72, Appl
45	53	11.4	620	US-10-453-372-1130	Sequence 1130, Ap
46	53	11.4	624	US-10-453-372-1126	Sequence 1126, Ap
47	53	11.4	925	US-10-453-372-1124	Sequence 1124, Ap
48	53	11.4	931	US-11-230-145-2	Sequence 2, Appli
49	53	11.4	966	US-10-877-346-32	Sequence 32, Appl
50	53	11.4	972	US-10-453-372-1128	Sequence 1128, Ap
51	52.5	11.3	160	US-10-821-234-1359	Sequence 1359, Ap
52	52.5	11.3	384	US-11-219-282-19	Sequence 19, Appl
53	52.5	11.3	398	US-11-012-762-74	Sequence 74, Appl
54	52.5	11.3	407	US-10-995-561-1014	Sequence 1014, Ap
55	52.5	11.3	470	US-10-485-517-319	Sequence 319, App
56	52.5	11.3	481	US-10-467-657-420	Sequence 420, App
57	52.5	11.3	1261	US-11-234-786-538	Sequence 538, App
58	52.5	11.3	1325	US-10-328-258-10	Sequence 10, Appl
59	52.5	11.3	1325	US-11-124-367A-410	Sequence 410, App
60	52	11.2	190	US-10-467-657-1426	Sequence 1426, Ap
61	52	11.2	241	US-10-873-528-116	Sequence 116, App
62	52	11.2	271	US-11-098-686-10795	Sequence 10795, A
63	52	11.2	291	US-10-883-512-103	Sequence 103, App
64	52	11.2	383	US-11-072-512-3579	Sequence 3579, Ap
65	52	11.2	436	US-11-072-512-2338	Sequence 2338, Ap
66	52	11.2	457	US-10-131-826A-236	Sequence 236, App
67	52	11.2	465	US-10-467-657-5040	Sequence 5040, Ap
68	52	11.2	495	US-11-072-512-3469	Sequence 3469, Ap
69	52	11.2	617	US-10-982-545-2	Sequence 2, Appli
70	52	11.2	922	US-11-072-512-2694	Sequence 2694, Ap
71	51.5	11.1	117	US-10-771-257-60	Sequence 60, Appl
72	51.5	11.1	117	US-11-127-677-58	Sequence 58, Appl
73	51.5	11.1	662	US-11-072-175-184	Sequence 184, App
74	51.5	11.1	893	US-11-072-512-3504	Sequence 3504, Ap
75	51.5	11.1	1438	US-10-511-559-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 72.9%; Score 339; DB 6; Length 88;
Best Local Similarity 67.8%; Pred. No. 4.5e-33;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 MARMHCAKLGKAEAGLDPPLPGELGKRLYESVSKQAMODMLKQOTMLINENRLNADP 60
DB 1 MARVFCVKLNKEAGKMPPLPNEIGKRIEYNSQAMAMWTHQOTMLINENRLSLADP 60

QY 61 PAROYLMKQTEKYFFGSGADQASGYVP 87
DB 61 RAREYLAQOMEQYFFGSGADAVQGYVP 87

RESULT 2

US-11-072-512-2506
Sequence 2506, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTOKI
APPLICANT: MASUHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2506
LENGTH: 1104
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2506

Query Match 14.9%; Score 69.5; DB 7; Length 1104;
Best Local Similarity 26.1%; Pred. No. 3.9;
Matches 23; Conservative 12; Mismatches 36; Indels 17; Gaps 4;
QY 13 EAEGL---DPPP---LPGELGKRLYESVSKQAMODMLKQOTMLINENRLNADP 65
DB 52 DCEGPEDDLPLDQTVLPGRSSER--ESNAKSCWMDIKDCECEDANENQNDPVEEF 109
QY 66 LMKQTEKYFFGSGADQASGY 85
DB 110 LQODTAVITFPAAREDDQSGTPEASGH 137

RESULT 3
US-11-119-351-8

Sequence 8, Application US/1119351
Publication No. US20060010519A1
GENERAL INFORMATION:
APPLICANT: Kadowaki, Koichi
APPLICANT: Takahashi, Sakiko
APPLICANT: Kawamukai, Makoto
APPLICANT: Shimada, Hiroaki
TITLE OF INVENTION: Method for Producing Ubiquitinone-10 in Plant
FILE REFERENCE: 59150-8034
CURRENT APPLICATION NUMBER: US/11/119,351
CURRENT FILING DATE: 2005-04-29
PRIOR APPLICATION NUMBER: JP 2004-136906
PRIOR FILING DATE: 2004-04-30
PRIOR APPLICATION NUMBER: JP 2005-000984
PRIOR FILING DATE: 2005-01-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 446
TYPE: PRT
ORGANISM: Nicotiana tabacum
US-11-119-351-8

Query Match 14.4%; Score 67; DB 7; Length 446;
Best Local Similarity 31.2%; Pred. No. 2.6;
Matches 20; Conservative 8; Mismatches 20; Indels 16; Gaps 4;

QY 19 PPLPGELGKRLYESVSKQAMODMLKQOTMLINENRLNADP 60
DB 264 PPLGSMWLSKSTWDELSPKWPAYWDMRL-----LKNH-----RGRPFIREVERSY 312

QY 74 PFGE 77
DB 313 NFGE 316

RESULT 4

US-10-793-626-2964
Sequence 2964, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P13480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2964
LENGTH: 5024
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (5024)
OTHER INFORMATION: variable amino acid
US-10-793-626-2964

Query Match 14.1%; Score 65.5; DB 6; Length 5024;
Best Local Similarity 41.5%; Pred. No. 71;
Matches 17; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 32 ESVSKQAMODMLKQOTMLINENRLNADP 60
DB 3822 QNEAKQALQOLINATSLNGPERLHAPRALRYI-KSLK 3861

RESULT 5

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 / Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-30
Perfect score: 465
Sequence: 1 MARMHCARKIKEARGLDFP.....KQTEKYFGRGADQASGVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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- 2: geneseqp1930s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	100.0	87	5	ABB78175 Amino aci
2	459	98.7	87	5	ABB78174 Amino aci
3	339	72.9	88	5	ABB78171 Amino aci
4	339	72.9	88	5	ABB78172 Amino aci
5	339	72.9	88	5	ABB78173 Amino aci
6	339	72.9	88	6	ABP77219 N. gonorr
7	310	66.7	87	5	ABB78176 Amino aci
8	300	64.5	87	5	ABB78148 Amino aci
9	300	64.5	87	5	ABB78147 Amino aci
10	282.5	60.8	86	5	ABB78149 Amino aci
11	278	59.8	89	9	ABE341576 L. pneumo
12	278	59.8	95	9	ABE341576 L. pneumo
13	276	59.4	87	5	ABB78177 Amino aci
14	265	56.6	88	5	ABB78178 Amino aci
15	255	54.8	87	5	ABB78153 Amino aci
16	245.5	52.8	92	6	ADA34169 Actinobac
17	242	52.0	91	5	ABB78150 Amino aci
18	241	51.8	87	5	ABB78152 Amino aci
19	238	51.2	87	5	ABB78151 Amino aci
20	229	49.2	87	5	ABB78169 Amino aci
21	227	48.8	87	5	ABB78170 Amino aci
22	227	48.8	122	7	ABO74609 Pseudomon
23	226	48.6	88	5	ABB78154 Amino aci
24	226	48.6	90	5	ABB78155 Amino aci

25	218	46.9	93	7	ADP05158	Adf05158 Bacterial
26	211	45.4	107	5	ABO65445	ABO65445 Klebsiell
27	208	44.7	90	7	ABB78168	ABB78168 Amino aci
28	206	44.3	88	5	ABB78160	ABB78160 Amino aci
29	206	44.3	91	5	ABB78161	ABB78161 Amino aci
30	206	44.3	91	5	ABB78158	ABB78158 Amino aci
31	206	44.3	91	5	ABB78159	ABB78159 Amino aci
32	206	44.3	91	5	ABB78162	ABB78162 Amino aci
33	206	44.3	91	5	ABB78157	ABB78157 Amino aci
34	206	44.3	91	5	ABB78156	ABB78156 Amino aci
35	199	42.8	90	5	ABB78165	ABB78165 Amino aci
36	199	42.8	91	5	ABB78163	ABB78163 Amino aci
37	197.5	42.5	78	5	ABB78164	ABB78164 Amino aci
38	189.5	40.8	90	5	ABB78167	ABB78167 Amino aci
39	181	38.9	76	5	ABB78166	ABB78166 Amino aci
40	181	38.9	110	8	ADL05173	ADL05173 Amino aci
41	171.5	15.4	206	7	ADS92530	ADS92530 Amino aci
42	171.5	15.4	5458	6	ABM66970	ABM66970 Photornab
43	171.5	15.3	511	9	ABM96738	ABM96738 M. xanthu
44	170	15.1	355	8	ADT57590	ADT57590 Plant pol
45	170	15.1	376	8	ADY09636	ADY09636 Plant ful
46	69.5	14.9	1104	7	ADB64352	ADB64352 Human pro
47	68.5	14.7	532	8	ADX73216	ADX73216 Plant ful
48	68.5	14.7	860	8	ADX93806	ADX93806 Plant ful
49	67	14.4	186	7	ADBE08482	ADBE08482 Novel pro
50	67	14.4	197	7	ABO67819	ABO67819 Klebsiell
51	67	14.4	265	6	ABU18123	ABU18123 Protein e
52	66.5	14.3	869	4	ABB60212	ABB60212 Drosophil
53	66	14.2	354	7	ADH54604	ADH54604 Mouse dec
54	66	14.2	446	2	AAV08889	AAV08889 Tobacco G
55	66	14.2	722	5	ABBS4118	ABBS4118 Lactococc
56	65.5	14.1	409	4	AAAG90502	AAAG90502 C glucam
57	65.5	14.1	678	5	ABBA7819	ABBA7819 Listeria
58	65.5	14.1	5024	4	AAAG82935	AAAG82935 S. epider
59	65	14.0	222	9	ABM92850	ABM92850 M. xanthu
60	65	14.0	285	3	AAAG28710	AAAG28710 Arabidops
61	65	14.0	510	5	ABBS90889	ABBS90889 Herbicida
62	65	14.0	510	8	ADN74505	ADN74505 Thale cre
63	65	14.0	2188	4	ABBS5784	ABBS5784 Drosophil
64	64.5	13.9	153	3	AAAG24680	AAAG24680 Arabidops
65	64.5	13.9	195	3	AAAG24679	AAAG24679 Arabidops
66	64.5	13.9	256	3	AAAG24678	AAAG24678 Arabidops
67	64.5	13.9	256	7	ADCB31835	ADCB31835 Plant (A.
68	64.5	13.9	256	7	ADCC46663	ADCC46663 Thalecres
69	64.5	13.9	256	7	ADDD30524	ADDD30524 Plant yie
70	64.5	13.9	256	8	AD143971	AD143971 Plant tra
71	64	13.8	396	7	ADBE62298	ADBE62298 Rat Prote
72	64	13.8	446	2	AAV08888	AAV08888 Potato Gn
73	64	13.8	508	3	AAAG48146	AAAG48146 Arabidops
74	64	13.8	508	5	ABB91938	ABB91938 Herbicida
75	64	13.8	533	3	AAAG48145	AAAG48145 Arabidops

ALIGNMENTS

RESULT 1
ABB78175 standard; protein; 87 AA.
ID ABB78175;
AC ABB78175;
XX 05-NOV-2002 (first entry)
DT
XX Amino acid sequence of a YggX homologue.
DE
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
OS
XX US2002072118-A1.
PN

```
PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
PI
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 87 AA;

Query Match 100.0%; Score 465; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMHCAKLGKAEAGLDFPLPGELGKRLYESYSKQAMQDWLKKQOTMLINENRLNMDP 60
DB 1 MARMHCAKLGKAEAGLDFPLPGELGKRLYESYSKQAMQDWLKKQOTMLINENRLNMDP 60

QY 61 RARQYLMKQTEKTEKFFEGADQASGYVP 87
DB 61 RARQYLMKQTEKTEKFFEGADQASGYVP 87

RESULT 2
ABB78174
ID ABB78174 standard; protein; 87 AA.
XX
XX ABB78174;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar Typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
PI
XX
```

```
DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 87 AA;

Query Match 98.7%; Score 459; DB 5; Length 87;
Best Local Similarity 98.9%; Pred. No. 7.6e-50;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARMHCAKLGKAEAGLDFPLPGELGKRLYESYSKQAMQDWLKKQOTMLINENRLNMDP 60
DB 1 MARMHCAKLGKAEAGLDFPLPGELGKRLYESYSKQAMQDWLKKQOTMLINENRLNMDP 60

QY 61 RARQYLMKQTEKTEKFFEGADQASGYVP 87
DB 61 RARQYLMKQTEKTEKFFEGADQASGYVP 87

RESULT 3
ABB78171
ID ABB78171 standard; protein; 88 AA.
XX
XX ABB78171;
XX
XX 29-AUG-2003 (revised)
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar Typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Neisseria gonorrhoeae.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
PI
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
```

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-30

Perfect score: 465
Sequence: 1 MARMHCAKIKGKAEGLDFP.....KQTEKYPFGAGDQASGVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : PIR 80:*

1: p1r1:***
2: p1r2:***
3: p1r3:***
4: p1r4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	72.9	88	2	H81014
2	241	51.8	90	2	C64013
3	227	48.8	90	2	H83003
4	226	48.6	90	2	C82320
5	206	44.3	91	2	AH0879
6	206	44.3	91	2	A85954
7	206	44.3	91	2	A65082
8	206	44.3	91	2	F91108
9	199	42.4	90	2	A10116
10	197	42.4	105	2	C82624
11	181	38.9	93	2	B84994
12	74.5	16.0	203	2	A32009
13	71	15.3	269	2	A69997
14	70	15.1	916	2	S22864
15	68	14.6	917	2	S33664
16	67.5	14.5	1215	2	A86595
17	67.5	14.5	1215	2	B72029
18	66	14.2	354	2	A55454
19	66	14.2	722	2	B86725
20	65.5	14.1	192	2	A83798
21	65.5	14.1	678	2	A81130
22	65	14.0	260	2	F87276
23	65	14.0	443	2	S21909
24	65	14.0	512	2	H86206
25	65	14.0	853	2	T08152
26	65	14.0	2186	2	T13169
27	64.5	13.9	256	2	T45817
28	64	13.8	396	2	I58168
29	64	13.8	508	2	T02486

30	64	13.8	823	2	A90761	hypothetical prote
31	64	13.8	823	2	B85822	hypothetical prote
32	64	13.8	823	2	F85624	hypothetical prote
33	63.5	13.7	252	2	B82181	oxidoreductase, sh
34	63.5	13.7	271	2	A84643	probable WRKY-type
35	63.5	13.7	1124	2	JX0293	zinc finger protei
36	63.5	13.7	1154	2	A56242	E-box-binding repr
37	63.5	13.7	1509	2	B89985	hypothetical prote
38	63	13.5	164	2	A95176	acetyltransferase,
39	63	13.5	164	2	B98043	conserved hypotet
40	63	13.5	434	2	F75425	tRNA nucleotidyltr
41	63	13.5	610	2	F86453	granule-bound star
42	62.5	13.4	134	2	H82969	hypothetical prote
43	62.5	13.4	236	1	T46967	dieme cytochrome
44	62.5	13.4	258	2	D95910	probable membrane-
45	62.5	13.4	399	2	F83633	hypothetical prote
46	62.5	13.4	488	2	AH2792	L-serine dehydrata
47	62.5	13.4	488	2	G97571	1-serine dehydrata
48	62.5	13.4	712	2	T48961	hypothetical prote
49	62	13.3	242	2	T18588	probable protein p
50	62	13.3	260	2	AH1639	hypothetical prote
51	62	13.3	295	2	AG1291	transcription acti
52	62	13.3	354	2	S29145	decorin precursor
53	62	13.3	413	2	T01043	hypothetical prote
54	62	13.3	489	2	D72762	hypothetical prote
55	62	13.3	611	2	A72393	hypothetical prote
56	61.5	13.2	295	2	T50798	hypothetical prote
57	61.5	13.2	373	2	S47911	PSI protein - Yea
58	61.5	13.2	726	2	S52141	AtPase - Brwnia a
59	61	13.1	82	2	C71676	hypothetical prote
60	61	13.1	306	2	A97249	Zn-binding lipopro
61	61	13.1	441	2	A41591	endothelin recepto
62	61	13.1	823	2	T02959	kaurene synthase A
63	60.5	13.0	326	2	H82455	1S5 transposase VC
64	60.5	13.0	326	2	S75668	DNA primase (BC 2.
65	60.5	13.0	1553	2	S67483	adenosinetriphosph
66	60.5	13.0	1827	1	UUHU	sucrose alpha-gluc
67	60.5	13.0	1867	2	S22775	MOT1 protein - Yea
68	60	12.9	136	2	T17621	hypothetical prote
69	60	12.9	138	2	T15806	hypothetical prote
70	60	12.9	260	2	AH1276	hypothetical prote
71	60	12.9	282	2	D97138	DNA replication pr
72	60	12.9	333	1	S39699	monooxygenase homo
73	60	12.9	383	2	T17722	hypothetical prote
74	60	12.9	603	2	T02677	hypothetical prote
75	59.5	12.8	205	2	A30836	chlorophyll a/b-bi

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: H81014; F81958
R:Telletlin, H.; Saunders, N.J.; Haidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eise, J.A
Hickey, E.R.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizsa, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappelli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:2015755; PMID:10710307
A:Accession: H81014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <Ter>
A:Cross-references: UNIPARC:UP100000C4E7F; GB:A8002552; GB:A8002098; NID:G7227279; PIDN:
A:Experimental source: serogroup B, strain MC58
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-30
Perfect score: 465
Sequence: 1 MARMHCATKLGKABGLDFP.....KQTEKYFGAGDAQSGVYP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	100.0	91	1	FETP_BURMA
2	465	100.0	91	1	FETP_BURMA
3	442	95.1	91	2	Q41S19 BURK
4	409	88.0	90	1	FETP_RALSO
5	355	76.3	90	1	FETP_CHRYO
6	339	72.9	88	1	FETP_NEIGI
7	339	72.9	88	1	FETP_NEIMA
8	339	72.9	88	1	FETP_NEIMA
9	330	71.0	90	1	FETP_NITRU
10	300	64.5	90	1	FETP_BORER
11	300	64.5	90	1	FETP_BORER
12	300	64.5	90	1	FETP_BORER
13	282	59.6	89	1	FETP_LEGPL
14	278	58.8	89	1	FETP_LEGPL
15	278	59.8	89	1	FETP_LEGPL
16	276	59.4	90	1	FETP_METCA
17	263	56.6	90	1	FETP_COXU
18	255	54.8	94	1	FETP_HAEPU
19	243	52.3	90	1	FETP_IDILO
20	241	51.8	90	1	FETP_HAEIN
21	241	51.8	90	2	Q4OWD9 HAE18
22	240	51.6	92	2	Q4NM04_9DEL
23	238	51.2	90	1	FETP_PASNU
24	238	51.2	90	1	FETP_PASNU
25	237.5	51.0	90	1	FETP_PASNU
26	237.5	51.0	90	2	Q4J228 AZOVI
27	236	50.8	92	1	FETP_XANOR
28	233	50.1	90	1	FETP_VIBRA
29	232	49.9	90	1	FETP_VIBRI
30	231	49.7	90	1	FETP_VIBRI
31	231	49.7	90	1	FETP_VIBRI

32	230	49.5	90	2	Q6T7F6_PSEFL	Q6T7F6 pseudomonas
33	229	49.0	90	1	FETP_PSEBK	Q8B49 pseudomonas
34	228	49.0	92	1	FETP_XANCP	Q8B829 xanthomonas
35	228	49.0	92	2	Q4UM14_XANCP	Q4UM14 xanthomonas
36	227	48.8	90	1	FETP_PSEBK	Q9NU36 pseudomonas
37	226	48.6	90	1	FETP_VIBCH	Q9KUR4 vibrio chol
38	226	48.6	92	1	FETP_SHEON	Q8B8X6 shewanella
39	223	48.0	91	1	FETP_MANEM	Q6V727 manihella
40	222	47.7	90	1	FETP_PHOHL	Q7U712 photorhabdu
41	219	47.1	90	2	Q4KT2_PSEFS	Q4KT2 pseudomonas
42	216	46.5	96	2	Q4VU7_9GAMM	Q4VU7 psychrobact
43	212	45.6	90	1	FETP_PHOHR	Q6LIM7 photobacter
44	208	44.7	90	1	FETP_PSEBM	Q8U7F5 pseudomonas
45	208	44.7	90	2	Q4ZLP3_PSEBS	Q4ZLP3 pseudomonas
46	207	44.5	90	1	FETP_YERPS	Q66FM3 yersinia ps
47	204	43.9	90	1	FETP_XYLPT	Q87D06 xyella fas
48	203.5	43.8	87	1	FETP_FRAT	Q87D06 xyella fas
49	201	43.2	90	1	FETP_ECO57	Q87D06 xyella fas
50	201	43.2	90	1	FETP_ECOLI	Q87D06 xyella fas
51	201	43.2	90	1	FETP_ERMCT	Q87D06 xyella fas
52	201	43.2	90	1	FETP_SALCH	Q87D06 xyella fas
53	201	43.2	90	1	FETP_SALPA	Q87D06 xyella fas
54	201	43.2	90	1	FETP_SALTY	Q87D06 xyella fas
55	201	43.2	90	1	FETP_SALTY	Q87D06 xyella fas
56	201	43.2	90	1	FETP_SALTY	Q87D06 xyella fas
57	199	42.8	90	1	FETP_YERPE	Q87D06 xyella fas
58	197	42.4	90	1	FETP_ECOL6	Q87D06 xyella fas
59	197	42.4	90	1	FETP_XYLPA	Q87D06 xyella fas
60	189	40.6	78	1	FETP_BUCAP	Q87D06 xyella fas
61	183	39.4	79	1	FETP_CANBF	Q87D06 xyella fas
62	181	38.9	77	1	FETP_BUCAL	Q87D06 xyella fas
63	169	36.3	78	1	FETP_MIGBR	Q87D06 xyella fas
64	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
65	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
66	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
67	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
68	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
69	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
70	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
71	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
72	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
73	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
74	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas
75	150	32.3	87	1	FETP_BUCBP	Q87D06 xyella fas

ALIGNMENTS

RESULT 1	
ID FETP_BURMA	STANDARD; PRT; 91 AA.
AC Q621U9;	
DT 13-SEP-2005 (Rel. 48, Created)	
DT 13-SEP-2005 (Rel. 48, Last sequence update)	
DT 13-SEP-2005 (Rel. 48, Last annotation update)	
DE Probable Fe(2+) trafficking protein.	
GN OrderedLocustNames=BMA1752;	
OC Burkholderia mallei (Pseudomonas mallei).	
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;	
OC Burkholderiaceae; Burkholderia.	
OX NCBI_TaxID=13373;	
RN [1]	
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC STRAIN=ATCC 23344;	
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;	
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,	
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,	
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dainton G., Dodson R.J.,	
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouli H.M., Kolonay J.F.,	
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,	
RA Sarría S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,	
RA Zafar N., Zhou L., Fraser C.M.;	

```
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
CC -1- FUNCTION: Could be a mediator in iron transacctions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: CP000010; AAU48201.1; -, Genomic_DNA.
DR TIGR: BMA1752; -.
DR HAMAP: MF_00686; -, 1.
DR InterPro: IPR007457; YggX.
DR Pfam: PF04362; DUF495; 1.
DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom: PD029191; DUF495; 1.
DR Complete proteome: Iron.
KM SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;
SQ
Query Match 100.0%; Score 465; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMHCAKLGKEABGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMAP 60
DB 1 MARMHCAKLGKEABGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMAP 60

QY 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
DB 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 2
FETP_BURPS
ID FETP_BURPS STANDARD; PRT; 91 AA.
AC Q63J5J4;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BPSL2326;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
[1]
NM NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Tlhalali R.W., Peacock S.J., Cerdano-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bacon N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosslet B., Davis P., Deshazer D.,
RA Fellwell T., Frazer A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songajavala S., Stevens K., Tumapa S., Venarathavast M.,
RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.P., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
CC -1- FUNCTION: Could be a mediator in iron transacctions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
```

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL: BX571965; CAH36329.1; -, Genomic_DNA.
DR HAMAP: MF_00686; -, 1.
DR InterPro: IPR007457; YggX.
DR Pfam: PF04362; DUF495; 1.
DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom: PD029191; DUF495; 1.
DR Complete proteome: Iron.
KM SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;
SQ
Query Match 100.0%; Score 465; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMHCAKLGKEABGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMAP 60
DB 1 MARMHCAKLGKEABGLDPPPLPGLGKRLYESVSKQAWQDWLKKQQTMLINENRLNMAP 60

QY 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
DB 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 3
Q4LS19_9BURK
ID Q4LS19_9BURK PRELIMINARY; PRT; 91 AA.
AC Q4LS19;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFL_3773;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cecapcia complex.
OX NCBI_TaxID=331272;
[1]
NM NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Laitner F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT H12424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC hypothetical protein.
DR EMBL: AAHL0100021; EAM18958.1; -, Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 91 AA; 10327 MW; 0A540A880A768284 CRC64;

Query Match 95.1%; Score 442; DB 2; Length 91;
Best Local Similarity 94.3%; Pred. No. 2e-40;
Matches 82; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
DB 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-30
Perfect score: 465
Sequence: 1 MARWHCAKLGKAEGLDFP.....KQTEKFFEGADQASGVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	245.5	52.8	92	2	US-09-328-352-5456 Sequence 5456, Ap
2	227	48.8	122	2	US-09-252-991A-23355 Sequence 23355, A
3	218	46.9	93	2	US-09-543-681A-5443 Sequence 5443, Ap
4	211	45.4	107	2	US-09-489-039A-11962 Sequence 11962, A
5	181	38.9	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	71	15.3	511	2	US-09-902-540-15937 Sequence 15937, A
7	69.5	14.9	1104	2	US-10-104-047-2506 Sequence 2506, Ap
8	67.5	14.5	1218	2	US-09-438-185A-837 Sequence 837, App
9	67	14.4	197	2	US-09-489-039A-14336 Sequence 14336, A
10	66	14.2	446	2	US-09-591-466C-4 Sequence 4, Appl
11	65.5	14.1	342	2	US-09-605-703B-1526 Sequence 1526, Ap
12	65.5	14.1	342	2	US-09-605-703B-1528 Sequence 1528, Ap
13	65.5	14.1	5024	2	US-09-710-279-2964 Sequence 10194, A
14	65	14.0	222	2	US-09-902-540-12049 Sequence 12049, A
15	64	13.8	446	2	US-09-591-466C-2 Sequence 2, Appl
16	64	13.8	1479	2	US-08-840-062-4 Sequence 44, Appl
17	63.5	13.7	398	2	US-09-710-279-44 Sequence 1498, Ap
18	63.5	13.7	398	2	US-09-710-279-1498 Sequence 3810, Ap
19	63.5	13.7	417	2	US-09-134-001C-3810 Sequence 10194, A
20	63.5	13.7	1125	2	US-09-949-016-10194 Sequence 27, Appl
21	63.5	13.7	1509	2	US-09-676-519-27 Sequence 3159, Ap
22	63.5	13.7	10182	2	US-09-134-001C-3159 Sequence 117099, A
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30	62	13.3	503	2	US-09-058-260-2 Sequence 10, Appl
31	62	13.3	503	2	US-09-058-260-10 Sequence 12, Appl
32	62	13.3	503	2	US-09-058-260-12 Sequence 28, Appl
33	62	13.3	503	2	US-09-058-260-28 Sequence 30, Appl
34	62	13.3	503	2	US-09-058-260-30 Sequence 309, App
35	62	13.3	503	2	US-10-138-075-4 Sequence 50, Appl
36	62	13.3	1564	2	US-09-976-594-109 Sequence 762, App
37	62	13.3	2012	2	US-09-602-787A-50 Sequence 5873, Ap
38	61.5	13.2	125	2	US-09-640-211A-762 Sequence 54, Appl
39	61.5	13.2	555	2	US-09-328-352-5873 Sequence 33714, A
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41	61	13.1	163	2	US-09-270-767-33714 Sequence 5, Appl
42	61	13.1	823	1	US-08-261-465-1 Sequence 1, Appl
43	61	13.1	823	1	US-08-405-254-5 Sequence 21786, A
44	60.5	13.0	266	2	US-09-252-991A-21786 Sequence 33833, A
45	60.5	13.0	269	2	US-09-270-767-33833 Sequence 49050, A
46	60.5	13.0	269	2	US-09-270-767-49050 Sequence 14772, A
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51	60.5	13.0	1827	2	US-09-079-723-179 Sequence 5, Appl
52	60.5	13.0	1867	2	US-09-824-574-5 Sequence 5836, Ap
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56	59.5	12.8	103	2	US-09-574-141A-33 Sequence 33, Appl
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59	59.5	12.8	236	2	US-09-270-767-236 Sequence 52375, A
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62	59.5	12.8	1023	1	US-09-962-284-4 Sequence 2, Appl
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66	59.5	12.8	1838	2	US-09-412-100-28 Sequence 14490, A
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69	59	12.7	925	2	US-09-081-320-11 Sequence 11, Appl
70	58.5	12.6	259	2	US-09-574-141A-11 Sequence 11, Appl
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74	58.5	12.6	421	2	US-09-134-001C-5141
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ALIGNMENTS

RESULT 1
US-09-328-352-5456
Sequence 5456, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5456
LENGTH: 92
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5456
Query Match 52.8%; Score 245.5; DB 2; Length 92;
Best Local Similarity 51.1%; Pred. No. 2,5e-24;

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:24:18 ; Search time 54.8952 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-30

Perfect score: 465
Sequence: 1 MARMHCAKLGKAEGLDFP.....KQTEKYPFGAGDQASGVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Published Applications_MA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	339	72.9	88	US-09-955-502-27	Sequence 27, Appl
5	339	72.9	88	US-09-955-502-28	Sequence 28, Appl
6	310	66.7	87	US-09-955-502-31	Sequence 31, Appl
7	300	64.5	87	US-09-955-502-2	Sequence 2, Appl
8	300	64.5	87	US-09-955-502-3	Sequence 3, Appl
9	282.5	59.4	86	US-09-955-502-4	Sequence 4, Appl
10	276	56.6	88	US-09-955-502-32	Sequence 32, Appl
11	263	54.8	87	US-09-955-502-33	Sequence 33, Appl
12	255	54.8	87	US-09-955-502-8	Sequence 8, Appl
13	242	52.0	91	US-09-955-502-5	Sequence 5, Appl
14	241	51.8	87	US-09-955-502-7	Sequence 7, Appl
15	238	51.2	87	US-09-955-502-6	Sequence 6, Appl
16	229	49.2	87	US-09-955-502-24	Sequence 24, Appl
17	227	48.8	87	US-09-955-502-25	Sequence 25, Appl
18	226	48.6	88	US-09-955-502-9	Sequence 9, Appl
19	226	48.6	90	US-09-955-502-10	Sequence 10, Appl
20	208	44.7	90	US-09-955-502-23	Sequence 23, Appl
21	206	44.3	88	US-09-955-502-15	Sequence 15, Appl
22	206	44.3	91	US-09-955-502-11	Sequence 11, Appl
23	206	44.3	91	US-09-955-502-12	Sequence 12, Appl
24	206	44.3	91	US-09-955-502-13	Sequence 13, Appl
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27	206	44.3	91	US-09-955-502-17	Sequence 17, Appl

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32	181	38.9	76	US-09-955-502-21	Sequence 21, Appl
33	71.5	15.4	206	US-10-510-812-76	Sequence 76, Appl
34	70	15.1	355	US-10-739-920-7667	Sequence 76, Appl
35	70	15.1	376	US-10-425-114-55451	Sequence 65451, Ap
36	69.5	14.9	1104	US-10-104-047-2506	Sequence 2506, Ap
37	69	14.8	532	US-10-437-963-173240	Sequence 173240, Ap
38	68.5	14.7	532	US-10-425-114-42582	Sequence 42582, A
39	68.5	14.7	860	US-10-425-114-56470	Sequence 56470, A
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61	64.5	13.9	256	US-10-374-780A-2434	Sequence 2434, App
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67	64	13.8	485	US-10-424-599-164730	Sequence 164730, A
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71	63.5	13.7	271	US-10-295-403-68	Sequence 88, Appl
72	63.5	13.7	271	US-10-225-066A-942	Sequence 942, App
73	63.5	13.7	271	US-10-374-780A-2068	Sequence 2068, Ap
74	63.5	13.7	271	US-10-412-699B-652	Sequence 652, App
75	63.5	13.7	271	US-10-412-699B-652	Sequence 652, App

ALIGNMENTS

RESULT 1
US-09-955-502-29
Sequence 29, Application US/0955502
Patent No. US2002072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
PTE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 29
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia mallei

US-09-955-502-29

Query Match 100.0%; Score 465; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.7e-47;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARMHCAKIGKAEAGDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNADP 60

Qy 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 2

US-09-955-502-30
Sequence 30, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

Query Match 100.0%; Score 465; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.7e-47;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 3

US-09-955-502-26
Sequence 26, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-09-955-502-26

Query Match 72.9%; Score 339; DB 3; Length 88;

Best Local Similarity 67.8%; Pred. No. 3.9e-32;
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Qy 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 4

US-09-955-502-27
Sequence 27, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria meningitidis B
US-09-955-502-27

Query Match 72.9%; Score 339; DB 3; Length 88;
Best Local Similarity 67.8%; Pred. No. 3.9e-32;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MARMHCAKIGKAEAGDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNADP 60
Db 1 MARMHCAKIGKAEAGDPPPLPGLGKRLYESVSKQAMQDWLKOQTMLINENRLNADP 60

Qy 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 5

US-09-955-502-28
Sequence 28, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria meningitidis A
US-09-955-502-28

Query Match 72.9%; Score 339; DB 3; Length 88;
Best Local Similarity 67.8%; Pred. No. 3.9e-32;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.75626 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502a-30
Perfect score: 465
Sequence: 1 MARWHCAKLGKBAEGLDFP.....KQTEKYFFGAGDAGSYVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications NA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	339	72.9	88	6	US-10-467-657-968 Sequence 968, App
2	69.5	14.9	1104	7	US-11-072-512-2506 Sequence 2506, Ap
3	67	14.4	446	7	US-11-119-351-8 Sequence 8, Appli
4	65.5	14.1	5024	6	US-10-793-626-2964 Sequence 2964, Ap
5	63.5	13.7	398	6	US-10-793-626-44 Sequence 44, Appli
6	59.5	12.8	832	7	US-11-098-686-1498 Sequence 1498, Ap
7	59.5	12.8	832	7	US-11-098-686-10182 Sequence 10182, A
8	58.5	12.6	1841	7	US-11-057-058-63 Sequence 63, Appli
9	58.5	12.6	447	6	US-10-793-626-1820 Sequence 1820, Ap
10	57.5	12.4	447	6	US-11-024-959-286 Sequence 286, App
11	57.5	12.4	787	6	US-10-467-657-2832 Sequence 2832, Ap
12	57	12.3	209	5	US-09-995-493-94 Sequence 94, Appli
13	56.5	12.2	575	7	US-11-098-686-10635 Sequence 10635, A
14	56.5	12.2	1077	7	US-11-054-281-110 Sequence 110, App
15	56	12.0	381	7	US-11-098-686-11284 Sequence 11284, A
16	56	12.0	867	7	US-11-072-512-3052 Sequence 3052, Ap
17	56	12.0	3803	6	US-10-995-561-773 Sequence 773, App
18	56	12.0	3960	6	US-10-995-561-771 Sequence 771, App
19	56	12.0	5335	6	US-10-995-561-777 Sequence 777, App
20	56	12.0	5406	6	US-10-995-561-774 Sequence 774, App
21	56	12.0	5415	6	US-10-995-561-779 Sequence 779, App
22	56	12.0	5464	6	US-10-995-561-775 Sequence 775, App
23	55.5	11.9	360	7	US-11-019-711-67 Sequence 67, Appli
24	55.5	11.9	563	7	US-11-072-512-3460 Sequence 3460, Ap
25	55.5	11.9	622	7	US-11-070-080-22 Sequence 22, Appli

26	54.5	11.7	107	5	US-09-995-493-34 Sequence 34, Appli
27	54.5	11.7	299	6	US-10-362-772-2 Sequence 2, Appli
28	54.5	11.7	355	6	US-10-878-556A-10 Sequence 10, Appli
29	54.5	11.7	505	7	US-11-072-512-3519 Sequence 3519, Ap
30	54.5	11.7	668	7	US-11-111-239-13 Sequence 13, Appli
31	54.5	11.7	805	7	US-11-108-539-2 Sequence 2, Appli
32	54.5	11.7	1134	7	US-11-043-889-34 Sequence 34, Appli
33	54.5	11.7	1187	7	US-11-043-889-46 Sequence 46, Appli
34	54.5	11.7	1476	6	US-10-647-956A-4 Sequence 4, Appli
35	54	11.6	437	6	US-10-454-437-84 Sequence 84, Appli
36	54	11.6	593	7	US-11-194-246-117 Sequence 317, App
37	54	11.6	629	6	US-10-821-234-1528 Sequence 1528, Ap
38	54	11.6	634	7	US-11-072-512-2300 Sequence 12032, A
39	54	11.6	8746	7	US-11-098-686-10232 Sequence 72, Appli
40	53.5	11.5	389	7	US-11-012-762-12 Sequence 16, Appli
41	53.5	11.5	757	7	US-11-067-121-16 Sequence 41, Appli
42	53.5	11.5	757	7	US-11-186-284-41 Sequence 72, Appli
43	53	11.4	532	6	US-10-063-703-72 Sequence 72, Appli
44	53	11.4	532	7	US-11-102-240-72 Sequence 1130, Ap
45	53	11.4	620	6	US-10-453-372-1130 Sequence 1126, Ap
46	53	11.4	624	6	US-10-453-372-1126 Sequence 1124, Ap
47	53	11.4	925	6	US-10-453-372-1124 Sequence 2, Appli
48	53	11.4	931	7	US-11-230-145-2 Sequence 1014, Ap
49	53	11.4	966	6	US-10-877-346-32 Sequence 32, Appli
50	53	11.4	972	6	US-10-453-372-1128 Sequence 1359, Ap
51	52.5	11.3	160	6	US-10-821-234-1359 Sequence 19, Appli
52	52.5	11.3	384	7	US-11-219-282-19 Sequence 74, Appli
53	52.5	11.3	398	7	US-11-012-762-74 Sequence 1014, Ap
54	52.5	11.3	407	6	US-10-995-561-1014 Sequence 319, App
55	52.5	11.3	470	6	US-10-485-517-319 Sequence 420, App
56	52.5	11.3	481	6	US-10-467-657-420 Sequence 538, App
57	52.5	11.3	1261	7	US-11-234-786-538 Sequence 10, Appli
58	52.5	11.3	1325	6	US-10-329-258-10 Sequence 410, App
59	52.5	11.3	1325	7	US-11-124-367A-410 Sequence 1426, App
60	52	11.2	190	6	US-10-467-657-1426 Sequence 116, App
61	52	11.2	241	6	US-10-873-528-116 Sequence 10795, A
62	52	11.2	271	7	US-11-098-686-10795 Sequence 103, App
63	52	11.2	291	6	US-10-883-512-103 Sequence 2338, Ap
64	52	11.2	383	7	US-11-072-512-3579 Sequence 230, App
65	52	11.2	436	7	US-11-072-512-3338 Sequence 5040, App
66	52	11.2	456	6	US-10-131-826A-236 Sequence 3469, Ap
67	52	11.2	465	6	US-10-467-657-5040 Sequence 2, Appli
68	52	11.2	495	7	US-11-072-512-3469 Sequence 264, Ap
69	52	11.2	617	6	US-10-982-545-2 Sequence 60, Appli
70	52	11.2	922	7	US-11-072-512-2694 Sequence 58, Appli
71	51.5	11.1	117	6	US-10-771-257-50 Sequence 184, App
72	51.5	11.1	117	7	US-11-127-677-58 Sequence 3504, Ap
73	51.5	11.1	662	7	US-11-072-512-3504 Sequence 73, Appli
74	51.5	11.1	893	7	US-11-072-512-3504 Sequence 73, Appli
75	51.5	11.1	1438	6	US-10-511-559-73 Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; CURRENT APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: *Neisseria gonorrhoeae*
US-10-467-657-968

Query Match 72.9%; Score 339; DB 6; Length 88;
Best Local Similarity 67.8%; Pred. No. 4.5e-33;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 MARMHCAKLGKAEAGLDPPPLPSELGKRLYESVSKQAMQDWLKKQOTMLINENRLNADP 60
DB 1 MARWVFCVKNKEAGKMFPLPNELGKRIPEVNSQEMAAWTRHQTMLINENRLSLADP 60

QY 61 RARQYLMKQTEKYFPFGADADAGSYVP 87
DB 61 RAREYLAQWMEQYFPFGADADAVGYP 87

RESULT 2
US-11-072-512-2506

Sequence 2506, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: MAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUTOKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHITAKA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 08435-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2506
LENGTH: 1104
TYPE: PRT
ORGANISM: *Homo sapiens*
US-11-072-512-2506

Query Match 14.9%; Score 69.5; DB 7; Length 1104;
Best Local Similarity 26.1%; Pred. No. 3.9;
Matches 23; Conservative 12; Mismatches 36; Indels 17; Gaps 4;

QY 13 EABGL---DPPP---LPGELGKRLYESVSKQAMQDWLKKQOTMLINENRLNADP 65
DB 52 DCEGPEDDLPTDQTVLPGSSER--ESNAKSCWMDIKDCESDANEONHDPNVEEP 109

QY 66 LMKQTEKYFPGS-----GADQASGY 85
DB 110 LQQQDTAVIFPRAPEBDQRGTPRASH 137

RESULT 3
US-11-119-351-8

Sequence 8, Application US/1119351
Publication No. US20060010519A1
GENERAL INFORMATION:
APPLICANT: Kadowaki, Koichi
APPLICANT: Takahashi, Sakiko
APPLICANT: Kawamukai, Makoto
APPLICANT: Shimada, Hiroaki
TITLE OF INVENTION: Method for Producing Ubiquitinone-10 in Plant
FILE REFERENCE: 59150-8034
CURRENT APPLICATION NUMBER: US/11/119,351
CURRENT FILING DATE: 2005-04-29
PRIOR APPLICATION NUMBER: JP 2004-136906
PRIOR FILING DATE: 2004-04-30
PRIOR APPLICATION NUMBER: JP 2005-000984
PRIOR FILING DATE: 2005-01-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 8
LENGTH: 446
TYPE: PRT
ORGANISM: *Nicotiana tabacum*
US-11-119-351-8

Query Match 14.4%; Score 67; DB 7; Length 446;
Best Local Similarity 31.2%; Pred. No. 2.6;
Matches 20; Conservative 8; Mismatches 20; Indels 16; Gaps 4;

QY 19 PPPPLGRLGKRLYESVSKQAMQDWLKKQOTMLINENRLNADP 73
DB 264 FPGGLWMLSKSTWDELSPKPKAYWMDWL-----LKENH-----RGRQFIREVCRSY 312

QY 74 FPG 77
DB 313 NFGE 316

RESULT 4
US-10-793-626-2964

Sequence 2964, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2964
LENGTH: 5024
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
FEATURE:
NAME/KEY: MOD_RBS
LOCATION: (5024)
OTHER INFORMATION: variable amino acid
US-10-793-626-2964

Query Match 14.1%; Score 65.5; DB 6; Length 5024;
Best Local Similarity 41.5%; Pred. No. 71;
Matches 17; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 32 ESVSKQAMQDWLKKQOTMLINENRLNADP 72
DB 3822 QNEAKQHLQQLINAEISLNGFERLNHARPRALRYI-KSLRK 3861

RESULT 5

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: February 28, 2006, 19:03:38 ; Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-31

Perfect score: 471

Sequence: 1 MSRMVQCVRKLGHBAGLDRP.....KQMEAYFPDGAQSGEGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	471	100.0	87	5	ABB78176 Amino aci
2	310	65.8	87	5	ABB78175 Amino aci
3	304	64.5	87	5	ABB78174 Amino aci
4	294	62.4	88	5	ABB78171 Amino aci
5	294	62.4	88	5	ABB78172 Amino aci
6	294	62.4	88	5	ABB78173 Amino aci
7	294	62.4	88	5	ABP77219 N. gonorr
8	291	61.8	87	5	ABB78177 Amino aci
9	286	60.7	88	5	ABB78178 Amino aci
10	286	60.7	89	9	ABE41576 L. pneumo
11	286	60.7	95	9	ABE38294 L. pneumo
12	275	58.4	87	5	ABB78148 Amino aci
13	275	58.4	87	5	ABB78147 Amino aci
14	257.5	54.7	86	5	ABB78149 Amino aci
15	242	51.4	87	5	ABB78170 Amino aci
16	242	51.4	122	7	ABO74609 Pseudomon
17	237	50.3	92	6	ABD34169 Acinetoba
18	225.5	47.9	90	5	ABB78154 Amino aci
19	219	46.5	88	5	ABB78153 Amino aci
20	213	44.8	90	5	ABB78167 Amino aci
21	211	44.3	91	5	ABB78150 Amino aci
22	208.5	44.2	93	7	ADF05158 Bacterial
23	208	44.2			
24	208	44.2			

25	208	44.2	107	7	ABO65445	AbO65445 Klebsiell
26	204	43.3	90	5	ABB78155	AbB78155 Amino aci
27	202	42.9	87	5	ABB78152	AbB78152 Amino aci
28	200	42.5	87	5	ABB78151	AbB78151 Amino aci
29	200	42.5	91	5	ABB78158	AbB78158 Amino aci
30	200	42.5	91	5	ABB78157	AbB78157 Amino aci
31	200	42.5	91	5	ABB78156	AbB78156 Amino aci
32	197	41.8	88	5	ABB78160	AbB78160 Amino aci
33	197	41.8	91	5	ABB78161	AbB78161 Amino aci
34	197	41.8	91	5	ABB78159	AbB78159 Amino aci
35	197	41.8	91	5	ABB78162	AbB78162 Amino aci
36	196	41.6	78	5	ABB78164	AbB78164 Amino aci
37	190	40.3	91	5	ABB78163	AbB78163 Amino aci
38	186	39.5	90	5	ABO82328	AbO82328 Pseudomon
39	177	37.6	110	8	ADL05173	AdL05173 M. catarr
40	166	35.2	76	5	ABB78166	AbB78166 Amino aci
41	166	35.2	2285	4	ABE63057	AbE63057 Drosophi
42	166	35.2	387	7	AAU35394	AAU35394 Haemophil
43	166	35.2	523	4	AAU30183	AAU30183 Protein e
44	166	35.2	523	6	ADN22552	ADN22552 Bacterial
45	166	35.2	568	8	AAW22052	AAW22052 DNA poly
46	166	35.2	1263	2	AAW97098	AAW97098 Pfu DNA p
47	166	35.2	1263	3	AAV51659	AAV51659 Pyrococcu
48	166	35.2	1263	3	AAV52030	AAV52030 P. furios
49	166	35.2	249	8	ADS28293	AdS28293 Bacterial
50	166	35.2	536	6	ABU40906	ABU40906 Protein e
51	166	35.2	536	7	ADP06692	AdP06692 Bacterial
52	166	35.2	536	9	AEA50037	AEA50037 Rice glob
53	166	35.2	536	9	ADA56784	AdA56784 Human sec
54	166	35.2	319	6	ADA40633	AdA40633 Human sec
55	166	35.2	319	6	ABR47664	ABR47664 Human sec
56	166	35.2	319	6	ABR00028	ABR00028 Human gen
57	166	35.2	319	7	ADC74042	AdC74042 Human sec
58	166	35.2	319	7	AAV30730	AAV30730 Amino aci
59	166	35.2	561	6	ADA54803	AdA54803 Human pro
60	166	35.2	907	5	ABG91058	ABG91058 Neisseria
61	166	35.2	915	2	AAV51770	AAV51770 N. gonorr
62	166	35.2	915	2	AAV07476	AAV07476 N. gonorr
63	166	35.2	915	5	AAH80374	AAH80374 N. gonorr
64	166	35.2	915	5	AAE20190	AAE20190 Neisseria
65	166	35.2	915	5	AAU35678	AAU35678 Haemophil
66	166	35.2	950	4	ABU30652	ABU30652 Protein e
67	166	35.2	1798	8	ADN46771	AdN46771 Thermococ
68	166	35.2	204	9	AEA50033	AEA50033 Rice glo
69	166	35.2	972	4	ABB70158	AbB70158 Drosophi
70	166	35.2	186	7	ADF58994	AdF58994 Human pol
71	166	35.2	186	7	ADC07962	AdC07962 Rice prot
72	166	35.2	186	7	ADC07948	AdC07948 Rice prot
73	166	35.2	186	7	ABG23100	AbG23100 Novel hum
74	166	35.2				
75	166	35.2				

ALIGNMENTS

RESULT 1	ABB78176	standard; protein; 87 AA.
ID	ABB78176	
XX	ABB78176	
AC	29-AUG-2003 (revised)	
XX	05-NOV-2002 (first entry)	
DT	Amino acid sequence of a YggX homologue.	
XX	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
XX	hydroxyl radical; DNA damage; YggX homologue.	
XX	Acidithiobacillus ferrooxidans.	
OS	US2002072118-A1.	
PN		

```

XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from Salmonella
XX enterica serovar Typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB7817-78 represent YggX homologues. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
XX Sequence 87 AA;
XX
XX Query Match 100.0%; Score 471; DB 5; Length 87;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-51;
XX Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRMVQCVKLGHEAGLDPRPPGALGARITYQSVSKAMQGMWKHQTMLINERLSPIDP 60
Db 1 MSRMVQCVKLGHEAGLDPRPPGALGARITYQSVSKAMQGMWKHQTMLINERLSPIDP 60

Qy 61 KSRTFLKQMEAYFFGDGAQSPGTYVP 87
Db 61 KSRTFLKQMEAYFFGDGAQSPGTYVP 87

RESULT 2
ABB78175
ID ABB78175 standard; protein; 87 AA.
XX
XX ABB78175;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX

```

```

PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from Salmonella
XX enterica serovar Typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
XX Sequence 87 AA;
XX
XX Query Match 65.8%; Score 310; DB 5; Length 87;
XX Best Local Similarity 64.4%; Pred. No. 4.4e-31;
XX Matches 56; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MSRMVQCVKLGHEAGLDPRPPGALGARITYQSVSKAMQGMWKHQTMLINERLSPIDP 60
Db 1 MARIHICAKIGKBAEGDPPFLPQELGKRLYESVSKAQMDWKQTMLINERNLNADP 60

Qy 61 KSRTFLKQMEAYFFGDGAQSPGTYVP 87
Db 61 RARQYLMKQTEKXYFFGEGADQASGYVP 87

RESULT 3
ABB78174
ID ABB78174 standard; protein; 87 AA.
XX
XX ABB78174;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX

```

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-31
Perfect score: 471
Sequence: 1 MSRMVQCVKLGHEAGLDLP.....KOMEAYFGDGAQSPGEGVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : PIR_80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	# Query Match	Length	DB ID	Description
1	294	62.4	88	2 H81014	conserved hypotnet
2	242	51.4	90	2 H81003	conserved hypotnet
3	215	45.6	105	2 C82624	conserved hypotnet
4	204	43.3	90	2 C82320	conserved hypotnet
5	202	42.9	90	2 C64013	hypothetical prote
6	200	42.5	91	2 A85954	hypothetical prote
7	200	42.5	91	2 A65082	hypothetical prote
8	200	42.5	91	2 P91108	hypothetical prote
9	197	41.8	91	2 AH0879	conserved hypotnet
10	186	39.5	90	2 AL0116	conserved hypotnet
11	166	35.2	93	2 B84994	hypothetical prote
12	71.5	15.2	383	2 F83321	hypothetical prote
13	71	15.1	523	1 T64055	GMP synthase (glut
14	71	15.1	568	2 T25152	Frizzled-1 protein
15	70	14.9	1197	2 I39613	pyruvate (flavodox
16	70	14.9	1199	2 AD2156	pyruvate-flavodoxi
17	69.5	14.8	501	2 T35009	probable phosphol
18	69	14.6	1263	2 T43934	DNA-directed DNA p
19	68.5	14.5	249	2 A83963	hypothetical prote
20	67.5	14.3	564	2 T49322	related to RNA-bin
21	67	14.2	915	2 A43335	transferrin-bindin
22	66	14.0	950	2 B64135	oxoglutarate dehyd
23	65.5	13.9	186	1 WMR219	1K globulin precu
24	65.5	13.9	186	2 T31103	alpha-globulin pre
25	65.5	13.9	368	2 T31103	probable GMP synch
26	65	13.8	159	2 AD0348	probable membrane
27	65	13.8	159	2 G12322	hypothetical prote
28	65	13.8	159	2 G12322	hypothetical prote
29	64.5	13.7	914	2 T17233	hypothetical prote

30	64.5	13.7	4273	2 C69679	polyketide synthas
31	.64	13.6	205	2 AD0788	heme exporter prot
32	64	13.6	205	2 AC0960	heme exporter prot
33	64	13.6	306	2 A97249	Zn-binding lipopro
34	64	13.6	364	2 C48376	orf2 5' to pnbC -
35	64	13.6	598	2 A75531	hypothetical prote
36	63.5	13.5	376	2 C82310	sulfate ABC transp
37	63.5	13.5	609	2 S36481	E1 protein - human
38	63.5	13.5	1199	2 S77082	pyruvate (flavodox
39	63.5	13.5	1243	2 JC5615	membrane-associate
40	63	13.4	265	2 T46733	clkr protein (limpo
41	63	13.4	443	2 T48593	hypothetical prote
42	63	13.4	468	2 F87359	leucine aminopepti
43	63	13.4	705	2 S18733	glutelin high mole
44	63	13.4	1455	2 B51939	DNA-directed DNA p
45	62.5	13.3	243	2 J01437	hypothetical 27k p
46	62.5	13.3	289	2 T46370	hypothetical prote
47	62.5	13.3	393	2 T49257	protein kinase-11k
48	62.5	13.3	475	2 S54993	reverse transcript
49	62.5	13.3	475	2 S54994	reverse transcript
50	62.5	13.3	510	2 A96735	hypothetical prote
51	62.5	13.3	513	2 A1921	hypothetical prote
52	62.5	13.3	605	2 S36469	E1 protein - human
53	62	13.2	316	2 C91272	hypothetical prote
54	62	13.2	316	2 C86113	hypothetical prote
55	62	13.2	503	2 AF2029	hypothetical prote
56	62	13.2	512	1 FOMVGS	gag polyprotein -
57	62	13.2	520	1 FOLUHL	gag polyprotein -
58	62	13.2	662	2 T41215	probable acetate-C
59	62	13.2	662	2 T15187	hypothetical prote
60	61	13.0	316	2 B37318	delta(2)-isopenten
61	61	13.0	430	2 B96031	hypothetical prote
62	61	13.0	457	2 S73419	signal recognition
63	61	13.0	457	1 JC4993	biphenyl dioxygena
64	61	13.0	525	1 SYECGU	GMP synthase (glut
65	61	13.0	525	2 F85894	GMP synthase (gl
66	61	13.0	525	2 AD0820	GMP synthase (glut
67	61	13.0	525	2 A91050	GMP synthetase (lm
68	61	13.0	535	2 AP0103	probable sulfatase
69	61	13.0	915	2 F81196	transferrin-bindin
70	60.5	12.8	359	2 T26813	hypothetical prote
71	60.5	12.8	475	2 S54996	reverse transcript
72	60.5	12.8	475	2 S54998	reverse transcript
73	60	12.7	342	2 T19021	probable inositol
74	60	12.7	352	2 D69410	cell division cont
75	60	12.7	375	2 T39364	probable galactosy

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014, F81958
R/RefSeq: H. J. Saunders, N. J. Heidelberg, J. Jeffries, A. C. Nelson, K. E. Eisen, J. A
Hickey, E. K. Hatt, D. H. Salzberg, S. L. White, O. Fleischmann, R. D. Dougherty, B. A.
ri, H. Qiu, H. Vamathevan, J. Gill, J. Scarlato, V. Maignani, V. Piazza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H. O.; Fraser, C. M.; Moxon, B. R.; Rappunli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:2015755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TTR>
A/Cross-references: UNIPARC:UP100000C4B7F; GB:AE002552; GB:AE002098; MTD:q7227279; PIDN:
A/Experimental source: serogroup B, strain MC58
R/Parikh, J.; Achtmann, M.; James, K. D.; Bentley, S. D.; Churcher, C.; Klee, S. R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moutre, S.; Mungall, K.; Quail, M. A.; Rajandream,
Nature 404, 502-506, 2000

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-31
Perfect score: 471
Sequence: 1 MSRMVQCCKLGHAEAGLDRP.....KOMEAYFFGDAQSPGVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	331	70.3	91	2	Q4LS19_9BURK
2	319	67.7	90	1	FETP_CHRYO
3	313	66.5	90	1	FETP_NITREU
4	310	65.8	91	1	FETP_BURKA
5	310	65.8	91	1	FETP_BURPS
6	309	65.6	91	1	FETP_RALSO
7	294	62.4	88	1	FETP_NEIG1
8	294	62.4	88	1	FETP_NEIMA
9	294	62.4	88	1	FETP_NEIMA
10	291	61.8	90	1	FETP_METCA
11	286	60.7	89	1	FETP_LEGPA
12	286	60.7	89	1	FETP_LEGPA
13	286	60.7	90	1	FETP_COXBU
14	284	60.3	89	1	FETP_LBGLI
15	275	58.4	90	1	FETP_BOBR
16	275	58.4	90	1	FETP_BOBR
17	275	58.4	90	1	FETP_BOBR
18	261	55.4	91	1	FETP_XANOR
19	255	54.1	92	1	FETP_XANOR
20	252	53.5	92	1	FETP_XANOR
21	252	53.5	92	1	FETP_XANOR
22	249	52.9	92	2	Q4UMW4_XANCP
23	242	51.4	90	1	FETP_PSEAB
24	238	50.5	90	1	FETP_PSEAB
25	237	50.3	90	1	FETP_PSEBP
26	231	49.0	90	2	Q4JZ28_AZOV1
27	229	48.6	90	2	O6T7P6_PSEFL
28	224.5	47.7	90	1	FETP_ACIAD
29	222	47.1	90	1	FETP_XYLFT
30	222	47.1	90	2	Q4KJ72_PSEFS
31	220	46.7	90	1	FETP_VIBR1

32	219	46.5	90	1	FETP_PSESM	O87u15 pseudomonas
33	219	46.5	90	2	Q4LIP3_PSESY	Q4LIP3 pseudomonas
34	218	46.3	90	1	FETP_PHOIL	O7n711 photobacter
35	215	45.6	90	1	FETP_XYLFA	O9pc73 xyloella fas
36	213	45.2	92	1	FETP_SHRON	O8ebx6 shewanella
37	211	44.8	90	1	FETP_VIBVU	O8dcd5 vibrio vuln
38	211	44.8	90	1	FETP_VIBVU	O7mbh4 vibrio vuln
39	211	44.8	94	1	FETP_HAEPU	O7vxb6 haemophilus
40	208	44.2	90	1	FETP_VIBPA	O87l15 vibrio para
41	204	43.3	90	1	FETP_VIBCH	O9kura4 vibrio chol
42	203	43.1	87	1	FETP_FRATT	O5nhj8 francisella
43	202	42.9	90	1	FETP_HAEIN	P44048 haemophilus
44	202	42.9	90	2	Q4QMD9_HAEI8	Q4qmd9 haemophilus
45	200	42.5	90	1	FETP_PASVU	O9c1b9 pseudococcus
46	200	42.5	91	1	FETP_MANSW	O5v77 manheimia
47	197	41.8	90	1	FETP_ERRCT	O6d8j9 erwinia car
48	195	41.4	90	1	FETP_ECOS7	P0a8p4 escherichia
49	195	41.4	90	1	FETP_ECOLI	P0a8p3 escherichia
50	195	41.4	90	1	FETP_SHIFL	P0a8p5 shigella fl
51	194	41.2	90	1	FETP_YERPS	O66fm3 yersinia ps
52	192	40.8	90	1	FETP_PHOPR	O6lunk7 photobacter
53	192	40.8	90	1	FETP_SALCH	O57k04 salmonella
54	192	40.8	90	1	FETP_SALPA	O5ymml1 salmonella
55	192	40.8	90	1	FETP_SALTI	P67618 salmonella
56	192	40.8	90	1	FETP_SALTY	P67617 salmonella
57	191	40.6	90	1	FETP_ECOL6	O8fe19 escherichia
58	186	39.5	90	1	FETP_YERPE	O8zhe9 yersinia pe
59	179	38.0	78	1	FETP_BUCAP	O8k925 buchera ap
60	172	36.5	78	1	FETP_WIGBR	O8d3cs wigleswort
61	172	36.5	79	1	FETP_CANBP	O4fvj7 psychobact
62	167	35.2	96	2	Q4FVJ7_9GAMW	P57618 buchera ap
63	166	35.2	77	1	FETP_BUCAI	O89a44 buchera ap
64	142	30.1	87	1	FETP_BUCBP	O7eif4 alcaligenes
65	78.5	16.7	825	1	AOXB_ALCPA	O6wb60 alcaligenes
66	78.5	16.7	825	2	O6WB60_ALCPA	O6mq14 belliovibri
67	72.5	15.4	484	2	O6WQ14_BDEBA	O9vp17 desulfovibr
68	72.5	15.4	2308	2	O9VP17_BDOME	O8vnu2 desulfovibr
69	72	15.3	514	2	O8VNU2_DESDP	O910p0 pseudomonas
70	71.5	15.2	359	2	O4N608_THERPA	O910p0 pseudomonas
71	71.5	15.2	383	2	O910P0_PSEAB	Q4nu62 anaeromyxob
72	71.5	15.2	1200	2	Q4NU62_9DELT	O7sh99 oryza sativ
73	71.5	15.2	1322	2	O7SHA9_ORYSA	P44335 haemophilus
74	71	15.1	523	1	GUAA_HAEIN	Q4qmw4 haemophilus
75	71	15.1	523	2	Q4QMW4_HAEI8	

ALIGNMENTS

RESULT 1
ID Q4LS19_9BURK PRELIMINARY; PRT; 91 AA.
AC Q4LS19;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_3773;
OS Burkholderia cenocepacia H12424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331212;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hannon N., Israni S., Pitluck S., Richardson P.;
*Sequencing of the draft genome assembly of Burkholderia cenocepacia
H12424.*;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

```

RC STRAIN=H12424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
H12424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
    EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
    preliminary data.
CC EMBL; AAH01000021; EAM18958.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10327 MW; 0A540A880A76E284 CRC64;

Query Match 70.3%; Score 331; DB 2; Length 91;
Best Local Similarity 70.1%; Pred. No. 4.1e-29;
Matches 61; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSRMVQCVKLGHEAGLDPRPPYGGALGARLYQEVSKKAWGMLKHQMTLINETRLSPIDP 60
Db 1 MARMVQCCKKGEAGLDPPPLPGLGRIVESVSKKAWGMLKHQMTLINENKLNADP 60
QY 61 KSRTFLEKOMEAYFFGGAGSPGGYVP 87
Db 61 RARQYLMKQTEKYEFGDAGDAGSYVP 87

RESULT 2
FETP CHRVO STANDARD; PRT; 90 AA.
AC Q7NSR4;
DT 05-JUN-2004 (Rel. 44, Created)
DT 05-JUN-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
CX NCBI_TaxID=536;
OX

[1]
NM NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida P.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Andrade J.J., Bataus L.A.M.,
RA Ascoti-Filho S., Azevedo V., Baptista A.J., de Araujo M.F.F.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brito M.M., Brito C.A., Brocchi M., Burlty H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Cheltre L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantihiati F., Farias I.P., Felipe M.S.S., Furlan L.R.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.P.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manlio G.P., Maranhao A.O., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.V., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Senaez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Umenyi T.,
RA Vettore A., Wasseem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
    remarkable and exploitable bacterial adaptability."
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
    acquisition and iron-regulating processes, such as synthesis and/or

```

```

CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB016922; AA061020.1; ALT_INIT; Genomic DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe-traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10095 MW; 60492ED67A9ABE78 CRC64;

Query Match 67.7%; Score 319; DB 1; Length 90;
Best Local Similarity 65.5%; Pred. No. 8.8e-28;
Matches 57; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSRMVQCVKLGHEAGLDPRPPYGGALGARLYQEVSKKAWGMLKHQMTLINETRLSPIDP 60
Db 1 MARMVQCCKKGEAGLDPPPLPGLGRIVESVSKKAWGMLKHQMTLINENKLNADP 60
QY 61 KSRTFLEKOMEAYFFGGAGSPGGYVP 87
Db 61 RARQYLMKQTEKYEFGDAGDAGSYVP 87

RESULT 3
FETP NITEU STANDARD; PRT; 90 AA.
ID FETP_NITEU
AC Q82XF2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS Nitrosomonas europaea.
GN OrderedLocustNames=NB0322;
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
CX NCBI_TaxID=915;
OX

[1]
NM NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
DOI=10.1128/JB.185.9.2759-2773.2003;
RA Hausen P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Arctero D.M., Hommes N.G., Whitaker M.M., Aip D.J.,
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
    obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
    acquisition and iron-regulating processes, such as synthesis and/or
    repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BX31857; CAD84233.1; -; Genomic DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe-traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-31

Perfect score: 471
Sequence: 1 MSRVQCVKLGHEAGLDRP.....KQMEAYFFGDAQSGPEGVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

1: Issued Patents AA:*
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6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	225.5	47.9	92	2	US-09-328-352-5456
3	208	44.2	93	2	US-09-543-681A-5443
4	208	44.2	107	2	US-09-489-039A-11962
5	177	37.6	110	2	US-09-540-236-2859
6	71.5	15.2	387	2	US-09-252-991A-31074
7	69	14.6	1263	2	US-09-446-504-6
8	69	14.6	1263	2	US-09-712-266-6
9	69	14.6	1263	2	US-09-091-889A-4
10	68	14.4	569	2	US-09-543-681A-6977
11	67	14.2	320	2	US-09-716-129-77
12	67	14.2	353	2	US-09-716-129-169
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14	67	14.2	915	1	US-08-363-124A-2
15	67	14.2	915	1	US-08-478-435-96
16	67	14.2	915	1	US-08-337-483-96
17	67	14.2	915	1	US-08-478-373-96
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19	67	14.2	915	2	US-08-483-577A-96
20	67	14.2	915	2	US-08-613-009A-18
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23	67	14.2	915	2	US-08-649-518-96
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25	67	14.2	915	2	US-09-059-584-24
26	67	14.2	917	2	US-08-753-750B-11
27	64.5	13.7	225	2	US-10-104-047-3107

28	64.5	13.7	502	2	US-09-904-615-69	Sequence 69, Appl
29	64.5	13.7	502	2	US-10-054-988-69	Sequence 69, Appl
30	64	13.6	125	2	US-09-640-211A-762	Sequence 762, App
31	64	13.6	313	2	US-09-513-151A-68	Sequence 68, Appl
32	63.5	13.5	600	2	US-09-540-236-2965	Sequence 2965, Ap
33	63	13.4	162	2	US-09-248-796A-21408	Sequence 21408, A
34	63	13.4	452	2	US-09-284-768A-22	Sequence 22, Appl
35	63	13.4	608	2	US-09-284-768A-4	Sequence 4, Appl
36	63	13.4	657	2	US-09-284-768A-7	Sequence 7, Appl
37	62.5	13.3	225	2	US-09-107-532A-5865	Sequence 5865, Ap
38	62.5	13.3	259	2	US-09-134-000C-4934	Sequence 4934, Ap
39	62.5	13.3	672	2	US-09-949-016-9511	Sequence 9511, Ap
40	62	13.2	1047	2	US-09-902-540-11147	Sequence 11147, A
41	62	13.2	1047	2	US-10-104-047-2408	Sequence 2408, Ap
42	61.5	13.0	680	2	US-09-252-991A-29223	Sequence 29223, A
43	61	13.0	582	2	US-09-902-540-11161	Sequence 11161, A
44	60.5	12.8	425	2	US-09-252-991A-32805	Sequence 32805, A
45	60.5	12.8	1244	2	US-08-938-281A-5	Sequence 5, Appl
46	60.5	12.8	1244	2	US-09-589-619-5	Sequence 5, Appl
47	60	12.7	347	2	US-09-489-039A-8503	Sequence 8503, Ap
48	60	12.7	347	2	US-09-252-991A-25606	Sequence 25606, A
49	59.5	12.6	407	2	US-09-583-110-4694	Sequence 4694, Ap
50	59.5	12.6	436	2	US-09-107-433-8819	Sequence 3819, Ap
51	59.5	12.6	2005	2	US-08-836-325-7	Sequence 7, Appl
52	59.5	12.6	2005	2	US-09-457-571-7	Sequence 7, Appl
53	59	12.5	510	1	US-08-097-829-2	Sequence 2, Appl
54	59	12.5	510	1	US-08-577-403-2	Sequence 2, Appl
55	59	12.5	837	1	US-09-564-805-228	Sequence 228, App
56	58.5	12.4	230	2	US-09-270-767-46697	Sequence 46697, A
57	58.5	12.4	401	2	US-09-543-681A-5084	Sequence 5084, Ap
58	58.5	12.4	444	2	US-10-104-047-2690	Sequence 2690, Ap
59	58.5	12.4	510	2	US-09-852-067-2	Sequence 2, Appl
60	58.5	12.4	510	2	US-10-1338-691-2	Sequence 2, Appl
61	58.5	12.4	526	2	US-09-949-016-6263	Sequence 6263, Ap
62	58	12.3	145	2	US-09-902-540-13774	Sequence 13774, A
63	58	12.3	506	2	US-08-888-998-2	Sequence 2, Appl
64	58	12.3	506	2	US-09-362-633-2	Sequence 2, Appl
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66	58	12.3	506	2	US-09-877-476-24	Sequence 24, Appl
67	58	12.3	506	2	US-09-877-476-26	Sequence 26, Appl
68	58	12.3	506	2	US-09-877-476-30	Sequence 30, Appl
69	58	12.3	506	2	US-09-877-476-36	Sequence 36, Appl
70	58	12.3	506	2	US-09-877-476-38	Sequence 38, Appl
71	58	12.3	506	2	US-09-877-476-40	Sequence 40, Appl
72	58	12.3	1302	1	US-08-232-537-2	Sequence 2, Appl
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74	57.5	12.2	393	2	US-09-634-238-774	Sequence 274, App
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RESULT 1
US-09-252-991A-23355
Sequence 23355, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABBUCCINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196, 136
CURRENT FILING DATE: 1999-02-18
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23355
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23355

Query Match 51.4%; Score 242; DB 2; Length 122;
Best Local Similarity 51.7%; Pred. No. 2.6e-24;
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Db 33 MSRTVTCRKTHBELPGLDPPYPGAKGEDITNNVSRKAMDEWKHQTMLINERLNMNA 92

Qy 61 KSRTFLKOMEAYFFGDAQSPGEGYVP 87
Db 93 EDRKLEQEMDKFLSGEDYAKADGYVP 119

RESULT 2
US-09-328-352-5456
Sequence 5456, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328.352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5456
LENGTH: 92
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 47.9%; Score 225.5; DB 2; Length 92;
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Matches 44; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

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Db 4 MSROVPCRKXKQEMEGLPAPPGAKGQGFENNVSKQMOEWLQHTTLINERKLNVPEP 63

Qy 61 KSRTFLKOMEAYFFGDAQSPGEGYVP 87
Db 64 BAKKFLBQREKRFNDESVKABGKWP 91

RESULT 3
US-09-543-681A-5443
Sequence 5443, Application US/09543681A
Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128.706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5443
LENGTH: 93
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 44.2%; Score 208; DB 2; Length 93;
Best Local Similarity 47.1%; Pred. No. 6.2e-20;
Matches 41; Conservative 13; Mismatches 33; Indels 0; Gaps 0;

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Qy 61 KSRTFLKOMEAYFFGDAQSPGEGYVP 87
Db 64 DDKRLBQEMVRFPLBSGHVHIDGYTP 90

RESULT 4
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489.039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117.747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Matches 43; Conservative 10; Mismatches 34; Indels 0; Gaps 0;

Qy 1 MSRWQCVKLGHEABGLDRPPYPGALGARIYQEVSKAMQGMWKHQTMLINERYLSPIDP 60
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Qy 61 KSRTFLKOMEAYFFGDAQSPGEGYVP 87
Db 77 EHRKLEQEMVQFLFEGKDVHIEGYTP 103

RESULT 5
US-09-540-236-2859
Sequence 2859, Application US/09540236
Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540.236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2859
LENGTH: 110
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 37.6%; Score 177; DB 2; Length 110;
Best Local Similarity 41.7%; Pred. No. 1.1e-15;
Matches 35; Conservative 11; Mismatches 38; Indels 0; Gaps 0;

Qy 4 MVQCVKLGHEABGLDRPPYPGALGARIYQEVSKAMQGMWKHQTMLINERYLSPIDP 63
Db 24 MVQCVKLGHEABGLDRPPYPGALGARIYQEVSKAMQGMWKHQTMLINERYLSPIDP 63

Qy 64 TFLKOMEAYFFGDAQSPGEGYVP 87
Db 84 KYLBQREKFLDNGDYKPKGYP 107

RESULT 6
US-09-252-991A-31074
Sequence 31074, Application US/09252991A

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:24:18 ; Search time 54.8952 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-31
Perfect score: 471
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	294	62.4	88	US-09-955-502-27	Sequence 27, Appl
6	294	62.4	88	US-09-955-502-28	Sequence 28, Appl
7	291	61.8	87	US-09-955-502-32	Sequence 32, Appl
8	286	60.7	88	US-09-955-502-33	Sequence 33, Appl
9	275	58.4	87	US-09-955-502-2	Sequence 2, Appl
10	275	58.4	87	US-09-955-502-3	Sequence 3, Appl
11	257.5	54.7	86	US-09-955-502-4	Sequence 4, Appl
12	242	51.4	87	US-09-955-502-25	Sequence 25, Appl
13	237	50.3	87	US-09-955-502-24	Sequence 24, Appl
14	219	46.5	90	US-09-955-502-23	Sequence 23, Appl
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16	213	45.2	88	US-09-955-502-9	Sequence 9, Appl
17	211	44.8	87	US-09-955-502-8	Sequence 8, Appl
18	208	44.2	91	US-09-955-502-5	Sequence 5, Appl
19	204	43.3	90	US-09-955-502-10	Sequence 10, Appl
20	202	42.9	87	US-09-955-502-7	Sequence 7, Appl
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28	197	41.8	91	US-09-955-502-17	Sequence 17, Appl
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36	166	35.2	76	US-09-955-502-25	Sequence 25, Appl
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56	166	35.2	76	US-09-955-502-45	Sequence 45, Appl
57	166	35.2	76	US-09-955-502-46	Sequence 46, Appl
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59	166	35.2	76	US-09-955-502-48	Sequence 48, Appl
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62	166	35.2	76	US-09-955-502-51	Sequence 51, Appl
63	166	35.2	76	US-09-955-502-52	Sequence 52, Appl
64	166	35.2	76	US-09-955-502-53	Sequence 53, Appl
65	166	35.2	76	US-09-955-502-54	Sequence 54, Appl
66	166	35.2	76	US-09-955-502-55	Sequence 55, Appl
67	166	35.2	76	US-09-955-502-56	Sequence 56, Appl
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69	166	35.2	76	US-09-955-502-58	Sequence 58, Appl
70	166	35.2	76	US-09-955-502-59	Sequence 59, Appl
71	166	35.2	76	US-09-955-502-60	Sequence 60, Appl
72	166	35.2	76	US-09-955-502-61	Sequence 61, Appl
73	166	35.2	76	US-09-955-502-62	Sequence 62, Appl
74	166	35.2	76	US-09-955-502-63	Sequence 63, Appl
75	166	35.2	76	US-09-955-502-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1
US-09-955-502-31
Sequence 31, Application US/09955502
Parent No. US2002072118A1
GENERAL INFORMATION:
APPLICANT: Dowm, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.9/559
CURRENT FILING DATE: 2001-09-18
PRIORITY FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 87
TYPE: PRT
ORGANISM: Thibacillus ferrooxidans

US-09-955-502-31

Query Match 100.0%; Score 471; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 8,6e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSRWOCVKLGHEABGLDRPPYPGALGARITYQEVSKKAWGMLKHQTMLINEYRLSPIDP 60
Qy 61 KSRTFLEKOMEAYFFGDAQSPBGYVP 87
Db 61 KSRTFLEKOMEAYFFGDAQSPBGYVP 87

RESULT 2
US-09-955-502-29
Sequence 29, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia mallei
US-09-955-502-29

Query Match 65.8%; Score 310; DB 3; Length 87;
Best Local Similarity 64.4%; Pred. No. 5,3e-30;
Matches 56; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

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Db 1 MARWICAKLGEABGLDRPPYPGALGARITYQEVSKKAWGMLKHQTMLINEYRLSPIDP 60
Qy 61 KSRTFLEKOMEAYFFGDAQSPBGYVP 87
Db 61 RARQYLMKQTEKYFFGDAQSPBGYVP 87

RESULT 3
US-09-955-502-30
Sequence 30, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

Query Match 65.8%; Score 310; DB 3; Length 87;

Best Local Similarity 64.4%; Pred. No. 5,3e-30;
Matches 56; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MSRWOCVKLGHEABGLDRPPYPGALGARITYQEVSKKAWGMLKHQTMLINEYRLSPIDP 60
Db 1 MARWICAKLGEABGLDRPPYPGALGARITYQEVSKKAWGMLKHQTMLINEYRLSPIDP 60
Qy 61 KSRTFLEKOMEAYFFGDAQSPBGYVP 87
Db 61 RARQYLMKQTEKYFFGDAQSPBGYVP 87

RESULT 4
US-09-955-502-26
Sequence 26, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 86
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-09-955-502-26

Query Match 62.4%; Score 294; DB 3; Length 88;
Best Local Similarity 62.1%; Pred. No. 5e-28;
Matches 54; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MSRWOCVKLGHEABGLDRPPYPGALGARITYQEVSKKAWGMLKHQTMLINEYRLSPIDP 60
Db 1 MARWICAKLGEABGLDRPPYPGALGARITYQEVSKKAWGMLKHQTMLINEYRLSPIDP 60
Qy 61 KSRTFLEKOMEAYFFGDAQSPBGYVP 87
Db 61 RARQYLMKQTEKYFFGDAQSPBGYVP 87

RESULT 5
US-09-955-502-27
Sequence 27, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria meningitidis B
US-09-955-502-27

Query Match 62.4%; Score 294; DB 3; Length 88;
Best Local Similarity 62.1%; Pred. No. 5e-28;
Matches 54; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.75626 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502A-31

Perfect score: 471

Sequence: 1 MSRWVCVKLGHEAEGIDRP.....KQMEAYFRGDGASQSPGVYP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications_AA_New:*
1: /cgm2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgm2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /cgm2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /cgm2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	62.4	88	6	US-10-467-657-968
2	67	14.2	907	7	US-11-103-957-82
3	65	13.8	912	6	US-10-467-657-7142
4	64.5	13.7	225	7	US-11-072-512-3107
5	64	13.6	313	7	US-11-237-600-68
6	62	13.2	316	7	US-11-156-084-193
7	62	13.2	316	7	US-11-156-084-287
8	62	13.2	1047	7	US-11-072-512-2408
9	61	13.0	216	7	US-11-156-084-244
10	61	13.0	216	7	US-11-156-084-322
11	61	13.0	316	7	US-11-156-084-210
12	61	13.0	316	7	US-11-156-084-280
13	60.5	12.8	1244	6	US-10-531-036-36
14	60	12.7	521	6	US-10-467-657-1344
15	59	12.5	306	6	US-11-052-554A-222
16	59	12.5	645	6	US-10-510-386-32
17	58.5	12.4	444	7	US-11-186-284-226
18	58.5	12.4	444	7	US-11-072-512-2690
19	58.5	12.4	509	6	US-10-131-826A-108
20	58.5	12.4	553	7	US-11-205-109-25
21	58	12.3	506	7	US-11-010-239-38
22	57	12.1	304	7	US-11-156-084-291
23	57	12.1	315	7	US-11-156-084-313
24	57	12.1	315	7	US-11-156-084-353
25	57	12.1	336	7	US-11-165-226-125

26	56.5	12.0	1981	6	US-10-374-954-23	Sequence 23, Appl
27	56.5	12.0	1998	6	US-10-374-954-21	Sequence 21, Appl
28	56.5	12.0	2009	6	US-10-374-954-2	Sequence 2, Appl
29	56	11.9	313	7	US-11-156-084-208	Sequence 208, Appl
30	56	11.9	421	7	US-11-226-701-11	Sequence 11, Appl
31	55.5	11.8	295	7	US-11-072-512-3285	Sequence 3285, Ap
32	55	11.7	470	6	US-10-979-821-14	Sequence 14, Appl
33	55	11.7	470	6	US-11-114-922-14	Sequence 14, Appl
34	54.5	11.6	237	6	US-10-467-657-570	Sequence 570, Appl
35	54.5	11.6	328	6	US-10-848-375-1	Sequence 1, Appl
36	54.5	11.6	352	7	US-11-018-868-13	Sequence 13, Appl
37	54.5	11.6	697	7	US-11-103-957-39	Sequence 39, Appl
38	54	11.5	316	7	US-11-156-084-213	Sequence 213, Appl
39	54	11.5	316	7	US-11-156-084-214	Sequence 214, Appl
40	54	11.5	348	7	US-11-156-084-303	Sequence 303, Appl
41	54	11.5	348	7	US-11-156-084-267	Sequence 267, Appl
42	54	11.5	462	7	US-11-055-822-956	Sequence 956, Appl
43	54	11.5	523	7	US-11-055-822-954	Sequence 954, Appl
44	53.5	11.4	205	7	US-11-072-512-3387	Sequence 3387, Ap
45	53.5	11.4	290	6	US-10-131-826A-222	Sequence 222, Appl
46	53.5	11.4	559	6	US-10-873-528-158	Sequence 158, Appl
47	53.5	11.4	2871	7	US-11-124-367A-264	Sequence 264, Appl
48	53	11.3	589	7	US-11-072-512-2914	Sequence 2914, Ap
49	52.5	11.1	222	7	US-11-156-084-121	Sequence 121, Appl
50	52.5	11.1	296	6	US-10-467-657-7994	Sequence 7994, Ap
51	52.5	11.1	329	6	US-10-981-873-29	Sequence 29, Appl
52	52.5	11.1	352	6	US-10-981-873-28	Sequence 28, Appl
53	52.5	11.1	380	6	US-10-525-674-28	Sequence 28, Appl
54	52.5	11.1	393	7	US-11-111-239-11	Sequence 11, Appl
55	52.5	11.1	520	6	US-10-131-826A-144	Sequence 144, Appl
56	52.5	11.1	726	7	US-11-052-554A-127	Sequence 127, Appl
57	52.5	11.1	1242	7	US-11-124-367A-338	Sequence 338, Appl
58	52.5	11.1	1242	7	US-11-124-367A-339	Sequence 339, Appl
59	52.5	11.1	1717	7	US-11-182-016-20	Sequence 20, Appl
60	52	11.0	296	7	US-11-072-512-2977	Sequence 2977, Ap
61	52	11.0	310	7	US-11-156-084-301	Sequence 301, Appl
62	52	11.0	380	6	US-10-517-939-140	Sequence 140, Appl
63	52	11.0	881	7	US-11-077-550-132	Sequence 124, Appl
64	52	11.0	902	7	US-11-077-550-132	Sequence 132, Appl
65	52	11.0	912	7	US-11-077-550-116	Sequence 116, Appl
66	52	11.0	914	7	US-11-077-550-120	Sequence 120, Appl
67	52	11.0	944	7	US-11-077-550-122	Sequence 122, Appl
68	52	11.0	950	7	US-11-077-550-118	Sequence 118, Appl
69	52	11.0	1187	7	US-11-098-686-10523	Sequence 10523, A
70	52	11.0	1254	6	US-10-528-031-47	Sequence 47, Appl
71	52	11.0	1467	6	US-10-507-966-1	Sequence 1, Appl
72	52	11.0	3353	7	US-11-037-243-64	Sequence 64, Appl
73	51.5	10.9	264	7	US-11-214-199-46	Sequence 46, Appl
74	51.5	10.9	345	6	US-10-467-657-252	Sequence 252, Appl
75	51.5	10.9	345	6	US-10-467-657-3086	Sequence 3086, Ap

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 62.4%; Score 294; DB 6; Length 88;
Best Local Similarity 62.1%; Pred. No. 1.3e-29;
Matches 54; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSRWQCVKLGHEAEGLDRPPYALGARIYQEVSKEMQGLKHQTMLINEYRLSPIDP 60
DB 1 MARWFCVKNLKEABGKMFPLPNEIGKRIFENVSQEMAMATRHQTMLINEYRLSPIDP 60

QY 61 KSRTPLEKQMEAYFFGDAQSPG 87
DB 61 RAREYLAQMEQYFFGDAQSPG 87

RESULT 2
US-11-103-957-82
Sequence 82, Application US/11103957
Publication No. US20050281847A1

GENERAL INFORMATION:
APPLICANT: Berthet, Francois-Xavier Jacques
APPLICANT: Lobet, Yves
APPLICANT: Poolman, Jan
APPLICANT: Verliant, Vincent Georges Christian Louis
TITLE OF INVENTION: Vaccine Composition
FILE REFERENCE: B45261
CURRENT APPLICATION NUMBER: US/11/103,957
CURRENT FILING DATE: 2005-04-12
PRIOR APPLICATION NUMBER: US/10/467,534
PRIOR FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: PCT/EP02/01356
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: GB 0103169.9
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 108
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 82
LENGTH: 907
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-11-103-957-82

Query Match 14.2%; Score 67; DB 7; Length 907;
Best Local Similarity 31.2%; Pred. No. 3.1;
Matches 30; Conservative 7; Mismatches 37; Indels 22; Gaps 6;

QY 11 GHEAE---GLDR---PPYPALGARI--YQEVSKEMQGLKHQTMLINEYRL 55
DB 699 GYEAKIKNGKQAKGAPAYLNAQSRITGINILGKIDNNGWVKLPEGWSTFAYNRV 758

QY 56 SPI-----DPKSRTPLEKQMEAYFFGDAQSPG 84
DB 759 RDIKKRADRTDIQSHLFDALQPSRYVGSYDQPEG 794

RESULT 3
US-10-467-657-7142
Sequence 7142, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 7142
LENGTH: 912
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7142

Query Match 13.8%; Score 65; DB 6; Length 912;
Best Local Similarity 30.2%; Pred. No. 5.5;
Matches 29; Conservative 6; Mismatches 39; Indels 22; Gaps 5;

QY 11 GHEAEGLD---PPYPALGARI--YQEVSKEMQGLKHQTMLINEYRL 55
DB 704 GYEAKIKNGKQAKGAPAYLNAQSRITGINILGKIDNNGWVKLPEGWSTFAYNRV 763

QY 56 SPI-----DPKSRTPLEKQMEAYFFGDAQSPG 84
DB 764 RDIKKRADRTDIQSHLFDALQPSRYVGSYDQPEG 799

RESULT 4
US-11-072-512-3107
Sequence 3107, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: YAMACHIKI, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3107
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3107

Query Match 13.7%; Score 64.5; DB 7; Length 225;
Best Local Similarity 27.9%; Pred. No. 1.1;
Matches 24; Conservative 13; Mismatches 28; Indels 21; Gaps 5;

QY 10 LGHEAE-GLDRPPY-----GALGARIYQEVSKEMQGLKHQTMLINEYRLSPID 59
DB 44 LVHQSIFADRPCPLPMKHTKMGGLNSR-----GKGWVDRRLANVSFRYGYG 95

QY 60 PKSRTPLEKQMEAYFFGDAQSPG 84
DB 96 QKS--FSKILIEETKFFNDALETYGK 119

GenCore version 5.1.7
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OW protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 70.7181 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502a-32
Perfect score: 466
Sequence: 1 MARRIKAKLGIRADGLDAP.....QERKFLPGGTSPTGVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21.*
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2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	100.0	87	5	ABB78177 Amino aci
2	291	62.4	87	5	ABB78176 Amino aci
3	276	59.2	87	5	ABB78175 Amino aci
4	270	57.9	87	5	ABB78174 Amino aci
5	268	57.5	88	5	ABB78178 Amino aci
6	260	55.8	87	5	ABB78148 Amino aci
7	260	55.8	87	5	ABB78147 Amino aci
8	250	53.6	89	9	ABE41576 Amino aci
9	250	53.6	95	9	ABE38294 Amino aci
10	243	52.1	88	5	ABB78171 Amino aci
11	243	52.1	88	5	ABB78172 Amino aci
12	243	52.1	88	5	ABB78173 Amino aci
13	243	52.1	88	6	ABP77219 Amino aci
14	242.5	52.0	86	5	ABB78149 Amino aci
15	239	51.3	87	5	ABB78169 Amino aci
16	235.5	50.5	92	6	ADA34169 Amino aci
17	235	50.4	87	5	ABB78170 Amino aci
18	235	50.4	122	7	ABO74609 Pseudomon
19	226	48.5	90	5	ABB78168 Amino aci
20	224	48.1	87	5	ABB78152 Amino aci
21	223	47.9	87	5	ABB78150 Amino aci
22	219	47.0	87	5	ABB78151 Amino aci
23	215	46.1	88	5	ABB78154 Amino aci
24	215	46.1	90	5	ABB78155 Amino aci

25	214	45.9	93	7	ADP05158 Bacterial
26	205	44.0	87	5	ABB78153 Amino aci
27	201	43.1	107	7	ABO65445 Klebsiell
28	200	42.9	91	5	ABB78158 Amino aci
29	200	42.9	91	5	ABB78157 Amino aci
30	200	42.9	91	5	ABB78156 Amino aci
31	195	41.8	88	5	ABB78160 Amino aci
32	195	41.8	91	5	ABB78161 Amino aci
33	195	41.8	91	5	ABB78159 Amino aci
34	195	41.8	91	5	ABB78162 Amino aci
35	193	41.4	110	8	ADU05173 M. catarr
36	191.5	41.1	90	5	ABB78167 Amino aci
37	189	40.6	78	5	ABB78164 Amino aci
38	188	40.3	91	5	ABB78163 Amino aci
39	186	39.9	90	5	ABB78165 Amino aci
40	154	33.0	76	5	ABB78166 Amino aci
41	74	15.9	603	8	ADU91918 Plant ful
42	73.5	15.8	364	3	AA39023 Arabidops
43	73.5	15.8	388	3	AA39022 Arabidops
44	73.5	15.8	436	3	AA39021 Arabidops
45	73.5	15.8	474	7	ABO75727 Pseudomon
46	73	15.7	582	9	ABM91962 M. xanthu
47	71.5	15.3	268	8	ADU95150 Plant ful
48	71.5	15.3	683	8	ADU96168 Plant ful
49	71	15.2	287	4	AA94116 Human pro
50	71	15.2	329	4	AA85750 Human imm
51	71	15.2	321	3	AA843482 Human imm
52	71	15.2	427	3	AA843107 Human ORF
53	71	15.2	566	5	ABP97401 Novel hum
54	71	15.2	591	8	ABM82407 Tumour-as
55	71	15.1	615	7	ADJ71113 Human hea
56	70.5	15.1	491	3	AA808899 Human hea
57	70.5	15.1	534	5	AA668347 Human zin
58	70.5	15.1	840	8	ADM87322 Human pro
59	70	15.0	485	3	AA646903 Arabidops
60	70	15.0	584	6	AA646902 Arabidops
61	69.5	14.9	438	6	ABO14402 Novel hum
62	69.5	14.9	438	8	ADG78792 Human sec
63	69.5	14.9	438	8	ADN61100 Human sec
64	69.5	14.9	507	6	ABU41973 Protein e
65	69.5	14.9	564	8	ADM87771 Human BST
66	69.5	14.9	972	4	ABB70158 Drosophil
67	68.5	14.7	295	8	AD124548 Human mod
68	68.5	14.7	393	8	AD167182 Lactobaci
69	68.5	14.7	507	6	ABU40210 Protein e
70	68.5	14.7	646	8	ADU60267 Plant pol
71	68.5	14.7	704	9	AD214794 Human tum
72	68	14.6	76	9	AEA27813 Rat ortho
73	68	14.6	405	7	AD671390 Novel hum
74	67.5	14.5	287	4	ABE46739 C. tracho
75	67.5	14.5	436	9	ADW17810 Pinus rad

ALIGNMENTS

RESULT 1	ABB78177	standard; protein; 87 AA.
XX	ABB78177;	
AC	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
XX	hydroxyl radical; DNA damage; YggX homologue.	
OS	Methylococcus capsulatus.	
XX		
PN	US2002072118-A1.	
XX		

```
PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YgX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YgX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YgX homologues
XX
SQ Sequence 87 AA;
XX
XX Query Match 100.0%; Score 466; DB 5; Length 87;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-48;
XX Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MARRIICAKGIBADGIDAPPFGPGQRIFEHYSKEMQDWLKLQTMLINEHRLTPPEA 60
Db 1 MARRIICAKGIBADGIDAPPFGPGQRIFEHYSKEMQDWLKLQTMLINEHRLTPPEA 60
XX
QY 61 SARKELEBEREKFLFGGISTPGGYVP 87
Db 61 SARKELEBEREKFLFGGISTPGGYVP 87
XX
XX RESULT 2
XX ABB78176 standard; protein; 87 AA.
XX
XX ABB78176;
XX
XX 29-AUG-2003 (revised)
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YgX homologue.
XX
XX Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
XX
XX Acidithiobacillus ferrooxidans.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
PI
```

```
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YgX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YgX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YgX homologues. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
SQ Sequence 87 AA;
XX
XX Query Match 62.4%; Score 291; DB 5; Length 87;
XX Best Local Similarity 58.6%; Pred. No. 3.1e-27;
XX Matches 51; Conservative 15; Mismatches 21; Indels 0; Gaps 0;
XX
QY 1 MARRIICAKGIBADGIDAPPFGPGQRIFEHYSKEMQDWLKLQTMLINEHRLTPPEA 60
Db 1 MSRWVCVKLGHEAEGLDRPPYFGALGARIVQEVSKEMQDWLKLQTMLINEHRLSPIDP 60
XX
QY 61 SARKELEBEREKFLFGGISTPGGYVP 87
Db 61 KSRTLEKQMEAYFFGDAQSPGIVP 87
XX
XX RESULT 3
XX ABB78175 standard; protein; 87 AA.
XX
XX ABB78175;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YgX homologue.
XX
XX Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
XX
XX Unidentified.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
```

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:22:21 / Search time 9.41601 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-32
Perfect score: 466
Sequence: 1 MARRIICAKLIGIADGLDAP.....QEREKPLFGGCTSPGQVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: PIR_80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	52.1	88	2	H81014 conserved hypotet
2	235	50.4	90	2	H83003 conserved hypotet
3	224	48.1	90	2	C64013 hypotetrical prote
4	215	46.1	90	2	C82320 conserved hypotet
5	201	43.1	105	2	C82624 conserved hypotet
6	200	42.9	91	2	A85954 hypotetrical prote
7	200	42.9	91	2	A65082 hypotetrical prote
8	200	42.9	91	2	P91108 hypotetrical prote
9	195	41.8	91	2	AH0879 conserved hypotet
10	186	39.9	90	2	A10116 conserved hypotet
11	154	33.0	93	2	E84994 hypotetrical prote
12	73.5	15.8	507	2	A83105 hypotetrical prote
13	72.5	15.6	313	2	D69756 conserved hypotet
14	71	15.2	427	2	T46255 hypotetrical prote
15	70	15.0	499	2	T04433 hypotetrical prote
16	70	15.0	499	2	A85216 hypotetrical prote
17	68.5	14.7	520	2	B96517 hypotetrical prote
18	68	14.6	374	2	B86198 hypotetrical prote
19	67.5	14.5	261	2	T13932 gag protein - frui
20	67.5	14.5	472	2	H81665 replicative DNA he
21	67.5	14.5	472	2	H81665 replicative DNA he
22	67	14.4	353	1	FOMVOR gag polypoteine -
23	67	14.4	512	2	C96517 hypotetrical prote
24	66	14.2	611	2	C84863 hypotetrical prote
25	66	14.2	639	2	C86455 hypotetrical prote
26	65	13.9	165	1	XUBSNI methylated-DNA-lpr
27	65	13.9	391	1	FOMVAM gag polypoteine -
28	65	13.9	603	2	F86442 unknown protein (1
29	65	13.9	802	2	G89893 Pr1A, primosomal p

30	65	13.9	994	2	B82843 valyl-tRNA synthet
31	65	13.9	1324	2	T00366 hypotetrical prote
32	64.5	13.8	1475	2	S42718 nuclear pore compl
33	64	13.7	424	2	H84295 glycine hydroxymet
34	64	13.7	732	2	S23001 tral protein - Esc
35	63.5	13.6	3187	2	JCS837 364K Golgi complex
36	63.5	13.6	439	2	B96520 hypotetrical prote
37	63.5	13.6	439	1	OKF71 hypotetrical 51K p
38	63.5	13.6	2201	2	AH0095 probable sideropho
39	63	13.5	198	2	AF0968 hypotetrical prote
40	63	13.5	387	2	T25452 hypotetrical prote
41	63	13.5	634	2	G34638 gag protein - frui
42	63	13.5	633	2	T04179 hypotetrical prote
43	62.5	13.4	158	2	AD2410 hypotetrical prote
44	62.5	13.4	283	2	P82779 hypotetrical prote
45	62.5	13.4	482	2	A12259 site-specific DNA-
46	62.5	13.4	482	2	S72471 site-specific DNA-
47	62.5	13.4	970	2	A13605 potassium efflux s
48	62	13.3	168	2	AD2450 hypotetrical prote
49	62	13.3	306	1	JQ1395 phosphoribosylamin
50	62	13.3	488	2	AH2792 l-serine dehydrata
51	62	13.3	488	2	G97571 l-serine dehydrata
52	62	13.3	537	2	T04745 hypotetrical prote
53	62	13.3	619	2	C83168 heat shock protein
54	62	13.3	661	2	AG2842 DNA primase (Impor
55	62	13.3	661	2	H97619 DNA primase (Ap299
56	62	13.3	2033	2	T30849 actin binding prot
57	61.5	13.2	609	2	B81385 probable ATP /GTP
58	61	13.1	371	2	F90581 hypotetrical prote
59	61	13.1	401	2	G84392 homoserine O-acety
60	61	13.1	523	1	I64055 GMP synthase (glut
61	61	13.1	686	2	T25743 hypotetrical prote
62	61	13.1	956	2	H81654 conserved hypotet
63	60.5	13.0	236	2	AH1936 internalin homolog
64	60.5	13.0	300	2	AE1380 probable GMP synth
65	60.5	13.0	368	2	T31103 oligopeptidase (EC
66	60.5	13.0	601	1	A55485 oligoendopeptidase
67	60.5	13.0	601	2	G86840 NADPH-ferritinoporo
68	60.5	13.0	692	2	S37159 6-phosphofructokin
69	60.5	13.0	780	1	K1RBF WD-repeat protein
70	60.5	13.0	1551	2	AB2410 probable amino aci
71	60	12.9	333	2	D95968 translation elonga
72	60	12.9	447	2	S39505 probable membrane
73	60	12.9	602	2	S58336 conjugal transfer
74	60	12.9	815	2	G82861 conserved hypotet
75	59.5	12.8	185	1	B69374

ALIGNMENTS

RESULT 1
H81014
conserved hypotetrical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: H81014, F81958
R:Retelien, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, J.A
Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:2015755; PMID:10710307
A:Accession: H81014
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <Trp>
A:Cross-references: UNIPARC:UP100000C4E7F; GB:AB002552; GB:AB002098; NID:G7227279; PTDN:
A:Experimental source: serogroup B, strain MC58
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 / Search time 63.2638 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502a-32

Perfect score: 466

Sequence: 1 MARRITCAKLGIEADGLDAP.....QERKFLRGGSFPGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	466	100.0	90	1	FETP_METCA
2	276	59.2	91	1	FETP_BURMA
3	276	59.2	91	1	FETP_BURPS
4	275	59.0	91	2	QALISL_9BURK
5	268	57.5	90	1	FETP_COXBU
6	261	56.0	90	1	FETP_CHRYO
7	261	56.0	90	1	FETP_NITRU
8	260	55.8	90	1	FETP_BORBR
9	260	55.8	90	1	FETP_BORBA
10	260	55.8	90	1	FETP_BORPE
11	250	53.6	89	1	FETP_LEGPA
12	250	53.6	89	1	FETP_LEGPH
13	250	53.6	89	1	FETP_LEGPL
14	248	53.2	91	1	FETP_RALSO
15	243	52.1	88	1	FETP_NEIC1
16	243	52.1	88	1	FETP_NEIC1
17	243	52.1	88	1	FETP_NEIC1
18	239	51.3	90	1	FETP_PSEBK
19	235	50.4	90	1	FETP_PSEAB
20	232	49.8	92	1	FETP_XANOR
21	230	49.4	90	2	Q4J258_AZOV1
22	229.5	49.2	90	1	FETP_ACTAD
23	227	48.7	91	1	FETP_XANAC
24	226	48.5	90	1	FETP_PSEAM
25	226	48.5	90	2	Q4ZLJ3_PSEBSY
26	226	48.5	90	2	Q4KJ72_PSEBSY
27	224	48.1	90	1	FETP_HAEN1
28	224	48.1	90	2	Q4QMBD_HAEN1
29	222	47.6	90	2	Q6T7F6_PSEFL
30	221	47.4	92	1	FETP_XANCP
31	221	47.4	92	2	Q4UW14_XANCP

32	219	47.0	90	1	FETP_PASMU	Q6C1b9 paeteurella
33	219	47.0	91	1	FETP_MANSM	Q65ct7 mannheimia
34	218	46.8	90	1	FETP_IDILO	Q5qy58 idiomarina
35	218	46.8	90	1	FETP_VIBPL	Q5qy70 vibrio fusc
36	216	46.4	90	1	FETP_VIBVU	Q8dccc vibrio vuln
37	216	46.4	90	1	FETP_VIBVY	Q7m144 vibrio vuln
38	215	46.1	90	1	FETP_VIBCH	Q9kru4 vibrio chol
39	215	46.1	92	1	FETP_SHEON	Q8ebx6 shewanella
40	214	45.9	90	1	FETP_PHOHL	Q7n111 photorhabd
41	207	44.4	90	1	FETP_PHOPR	Q6lmk7 photobacter
42	207	44.4	90	1	FETP_VIBPA	Q7vnb6 haemophilus
43	205	44.0	94	1	FETP_HAEDU	Q87d06 xyella fas
44	204	43.8	90	1	FETP_XYLFT	Q9pc73 xyella fas
45	201	43.1	90	1	FETP_XYLTA	Q6d6j9 erynia car
46	199	42.7	90	1	FETP_ERMCT	Q4nwa4 anaeromyxob
47	198	42.5	92	2	Q4NWQ4_9DELT	P0a8p4 escherichia
48	195	41.8	90	1	FETP_ECO57	P0a8p5 escherichia
49	195	41.8	90	1	FETP_ECOLI	P0a8p5 shigella fl
50	195	41.8	90	1	FETP_SHITL	Q66fm3 yersinia ps
51	194	41.6	90	1	FETP_YERPS	Q8fe19 escherichia
52	191	41.0	90	1	FETP_ECOL6	Q57K04 salmonella
53	190	40.8	90	1	FETP_SALCH	Q5pmu1 salmonella
54	190	40.8	90	1	FETP_SALPA	P67617 salmonella
55	190	40.8	90	1	FETP_SALTY	Q8zhe7 yersinia pe
56	190	40.8	90	1	FETP_SALTY	Q5nhj7 francisella
57	186	39.9	90	1	FETP_YERPE	Q8K925 buchiera ap
58	183	39.3	87	1	FETP_FRATT	P57618 buchiera ap
59	183	39.3	96	2	Q4FVU7_9GAMM	Q7rv99 candidatus
60	165	35.4	78	1	FETP_BUCAP	Q8a3c5 wigleswort
61	154	33.0	77	1	FETP_BUCAI	Q8a244 buchiera ap
62	154	33.0	79	1	FETP_CANBR	Q4urx4 xanthomonas
63	152	32.6	78	1	FETP_WICBR	Q8bhm5 xanthomonas
64	130	27.9	87	1	FETP_BUCBP	Q4ntr3 anaeromyxob
65	77	16.5	443	2	Q4URX4_XANCP	Q9hw68 pseudomonas
66	77	16.5	443	2	Q8BPM5_XANCP	Q4efx7 terradon n
67	75	15.1	387	2	Q4NTM3_9DELT	Q6f6q2 candida gla
68	73.5	15.8	507	2	Q9HMG8_PSEAB	Q34504 bacillus su
69	73	15.7	306	2	Q6FQO2_CANCA	Q5fvv83 homo sapien
70	72.5	15.6	313	1	YCEB_BACSU	Q8f1f0 brachydario
71	72.5	15.6	313	1	YCEB_BACSU	Q8fp12 bartonella
72	72.5	15.6	917	2	Q5FV83_HUMAN	Q5sm51 candida alb
73	72	15.5	333	2	Q8JFX0_BRARE	
74	71.5	15.3	294	2	Q8KPI2_BAROU	
75	71.5	15.3	491	2	Q5AM51_CANAL	

ALIGNMENTS

RESULT 1				
FETP_METCA				
ID	FETP_METCA	STANDARD;	PRT;	90 AA.
AC	Q60AJ7;			
DT	13-SEP-2005 (Rel. 48, Created)			
DT	13-SEP-2005 (Rel. 48, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	OrderedLocustNames=MCA0856;			
OS	Methylococcus capsulatus.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;			
OC	Methylococcaceae; Methylococcus.			
OX	NCBI_TaxID=414;			
OX	[1]			
RN				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=Bath / NCIMB 11132;			
RX	PubMed=15383840; DOI=10.1371/journal.pbio.0020303;			
RA	Ward N.L., Larsen O., Sakwa J., Bruseth L., Knouri H.M., Durkin A.S.,			
RA	Dahlrot G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.B.,			
RA	Mehe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,			
RA	Ravel J., Tettelin H., Ren O., Read T.D., DeBoy R.T., Seshadri R.,			
RA	Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,			
RA	Grindhaug S.H., Holt I.B., Bidhammer I., Jonassen I., Vanaken S.,			
RA	Utterback T.V., Feldblyum T.V., Fraser C.M., Lilienhaug J.R.,			

```

RA Eisen J.A.;
RT "Genomic insights into methanotrophy: the complete genome sequence of
RL Methylococcus capsulatus (Bath).";
CC CC
CC -1- FUNCTION: Could be a mediator in iron transacations between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE017282; AAU93044.1; -; Genomic_DNA.
DR TIGR; MCA0856; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10225 MW; 867B7FC9B21CBD01 CRC64;

Query Match          100.0%; Score 466; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 5.5e-46;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRIICAKLGIEADGLDAPPFGPGQGRIFEHVSKKAMQDWLKLQTMLINEHRLTPPEA 60
DB 1 MARRIICAKLGIEADGLDAPPFGPGQGRIFEHVSKKAMQDWLKLQTMLINEHRLTPPEA 60
QY 61 SARFPLEGRERKPLFGGGSITPGGYVP 87
DB 61 SARFPLEGRERKPLFGGGSITPGGYVP 87

RESULT 2
PFTP_BURMA          STANDARD;          PRT;          91 AA.
AC Q62IU9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BML1752;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.040306101;
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Rensing C.M., Brinkac L.M.,
RA Daugherty S.C., Davidsen T.D., Deboy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarrisa S., Selengut J., Shambhlin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RL "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
CC -1- FUNCTION: Could be a mediator in iron transacations between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
DR EMBL; CP000010; AAU48201.1; -; Genomic_DNA.
DR TIGR; BMA1752; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;

Query Match          59.2%; Score 276; DB 1; Length 91;
Best Local Similarity 59.8%; Pred. No. 6.2e-24;
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QY 61 SARFPLEGRERKPLFGGGSITPGGYVP 87
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RESULT 3
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AC Q63SJ4;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BSL2326;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.040302101;
RA Holden M.T.G., Tittball R.W., Peacock S.J., Cerdano-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., Deshazer D.,
RA Feltham T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagers K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Veeraratchaveest M.,
RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parkhill J.;
RL "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
CC -1- FUNCTION: Could be a mediator in iron transacations between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX571965; CAH36329.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.4589 Seconds
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Title: US-09-955-502A-32

Perfect score: 466

Sequence: 1 MARRIKAKGIGRADGADP.....QERKFLFGGTSTPGYVP 87

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Issued Patents_Aa.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	235.5	50.5	92	2	US-09-328-352-5456
2	235	50.4	122	2	US-09-252-991A-53355
3	214	45.9	93	2	US-09-543-681A-5443
4	201	43.1	107	2	US-09-489-039A-11962
5	193	41.4	110	2	US-09-540-236-2859
6	73.5	15.8	474	2	US-09-252-991A-24473
7	73	15.7	582	2	US-09-902-540-11161
8	68.5	14.7	393	2	US-09-634-238-274
9	67.5	14.5	287	2	US-09-585-858-48
10	67.5	14.5	287	2	US-10-270-878-48
11	66	14.2	196	1	US-08-900-407-1
12	65	13.9	591	2	US-09-370-368-8
13	64.5	13.8	1475	2	US-09-538-092-1160
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15	63	13.5	586	2	US-08-964-268-3
16	63	13.5	586	2	US-09-105-254-3
17	63	13.5	586	2	US-10-413-536-3
18	63	13.5	606	2	US-09-618-425-5
19	62.5	13.4	482	2	US-09-135-639-2
20	62.5	13.4	795	2	US-09-328-352-6143
21	62	13.3	623	2	US-09-252-991A-22906
22	62	13.3	1130	2	US-09-976-594-280
23	61.5	13.2	395	2	US-09-593-828-13
24	61.5	13.2	395	2	US-09-593-828-13
25	61	13.1	343	2	US-09-252-991A-22307
26	61	13.1	586	2	US-09-252-991A-27398
27	61	13.1	908	2	US-09-623-326-9

28	61	13.1	908	2	US-09-623-326-10	Sequence 10, Appl
29	60.5	13.0	632	2	US-09-902-540-11147	Sequence 1147, A
30	60	12.9	329	2	US-09-602-787A-306	Sequence 306, App
31	60	12.9	459	2	US-09-602-787A-302	Sequence 302, App
32	60	12.9	601	1	US-08-458-477A-2	Sequence 2, Appl1
33	60	12.9	601	1	US-09-033-153-2	Sequence 2, Appl1
34	60	12.9	601	2	US-09-325-430B-2	Sequence 2, Appl1
35	59.5	12.8	358	2	US-09-252-991A-13333	Sequence 3133, A
36	59.5	12.8	705	1	US-08-456-647B-4	Sequence 4, Appl1
37	59.5	12.8	705	1	US-08-237-401A-2	Sequence 4, Appl1
38	59.5	12.8	839	2	US-09-758-282B-232	Sequence 232, App
39	59.5	12.8	839	2	US-09-577-304A-232	Sequence 232, App
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41	59	12.7	390	2	US-09-949-016-6813	Sequence 6813, Ap
42	59	12.7	390	2	US-09-593-828-8	Sequence 8, Ap
43	59	12.7	431	2	US-09-949-016-8893	Sequence 8893, Ap
44	59	12.7	519	2	US-10-113-794A-2	Sequence 2, Appl
45	59	12.7	520	2	US-09-949-016-9918	Sequence 9918, Ap
46	59	12.7	618	2	US-09-252-991A-22418	Sequence 22418, A
47	59	12.7	1455	1	US-08-726-012B-2	Sequence 2, Appl1
48	58.5	12.6	170	2	US-09-270-767-60691	Sequence 60691, A
49	58.5	12.6	204	2	US-09-270-767-45195	Sequence 45195, A
50	58.5	12.6	254	2	US-09-270-767-41684	Sequence 41684, A
51	58.5	12.6	1493	2	US-09-538-092-1263	Sequence 1263, Ap
52	58.5	12.6	2867	2	US-09-902-540-12593	Sequence 12593, A
53	58	12.4	561	2	US-09-489-039A-11625	Sequence 11625, A
54	57.5	12.3	289	2	US-09-105-697-2	Sequence 2, Appl1
55	57.5	12.3	300	2	US-09-585-858-42	Sequence 42, Appl
56	57.5	12.3	300	2	US-10-270-878-42	Sequence 42, Appl
57	57.5	12.3	310	1	US-08-484-956-88	Sequence 88, Appl
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65	57.5	12.3	320	1	US-08-757-653-163	Sequence 163, App
66	57.5	12.3	320	1	US-08-823-516-61	Sequence 61, Appl
67	57.5	12.3	320	2	US-08-753-038-102	Sequence 102, App
68	57.5	12.3	320	2	US-08-758-314-102	Sequence 102, App
69	57.5	12.3	320	2	US-09-684-938-102	Sequence 102, App
70	57.5	12.3	320	2	US-09-308-825A-102	Sequence 102, App
71	57.5	12.3	320	2	US-09-940-244-61	Sequence 61, Appl
72	57.5	12.3	320	2	US-09-381-212-61	Sequence 61, Appl
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ALIGNMENTS

RESULT 1
US-09-328-352-5456
Sequence 5456, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-039A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5456
LENGTH: 92
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Matches 47; Conservative 14; Mismatches 25; Indels 3; Gaps 2;

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Qy 61 SARFLEQERREKFLFGGGSSTP-PQGYVP 87
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RESULT 2
US-09-252-991A-23355

; Sequence 23355, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 23355

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23355

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Best Local Similarity 50.6%; Pred. No. 3.2e-22;
Matches 44; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

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Qy 61 SARFLEQERREKFLFGGGSSTP-PQGYVP 87
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RESULT 3
US-09-543-681A-5443

; Sequence 5443, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 5443

; LENGTH: 93

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-5443

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Qy 61 SARFLEQERREKFLFGGGSSTP-PQGYVP 87
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RESULT 4
US-09-489-039A-11962

; Sequence 11962, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 11962

; LENGTH: 107

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11962

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Qy 61 SARFLEQERREKFLFGGGSSTP-PQGYVP 87
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RESULT 5
US-09-540-236-2859

; Sequence 2859, Application US/09540236

; Patent No. 6673910

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 2859

; LENGTH: 110

; TYPE: PRT

; ORGANISM: M.catarrhalis

US-09-540-236-2859

Query Match 41.4%; Score 193; DB 2; Length 110;
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Qy 65 FLQERREKFLFGGGSSTP-PQGYVP 87
Db 85 YLNGRERKFLDNGDYKPKAGYKP 107

RESULT 6
US-09-252-991A-24473
; Sequence 24473, Application US/09252991A



GenCore version 5.1.7
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Run on: March 1, 2006, 00:34:35 ; Search time 54.4363 Seconds
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667.774 Million cell updates/sec

Title: US-09-955-502A-32

Perfect score: 466
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	268	57.5	88	US-09-955-502-33	Sequence 33, Appl
6	260	55.8	87	US-09-955-502-2	Sequence 2, Appl
7	260	55.8	87	US-09-955-502-3	Sequence 3, Appl
8	243	52.1	88	US-09-955-502-26	Sequence 26, Appl
9	243	52.1	88	US-09-955-502-27	Sequence 27, Appl
10	243	52.1	88	US-09-955-502-28	Sequence 28, Appl
11	242.5	52.0	86	US-09-955-502-4	Sequence 4, Appl
12	239	51.3	87	US-09-955-502-24	Sequence 24, Appl
13	235	50.4	87	US-09-955-502-25	Sequence 25, Appl
14	226	48.5	90	US-09-955-502-23	Sequence 23, Appl
15	224	48.1	87	US-09-955-502-7	Sequence 7, Appl
16	223	47.9	91	US-09-955-502-5	Sequence 5, Appl
17	219	47.0	87	US-09-955-502-6	Sequence 6, Appl
18	215	46.1	88	US-09-955-502-9	Sequence 9, Appl
19	215	46.1	90	US-09-955-502-10	Sequence 10, Appl
20	205	44.0	87	US-09-955-502-8	Sequence 8, Appl
21	201	43.1	89	US-09-955-502-22	Sequence 22, Appl
22	200	42.9	91	US-09-955-502-11	Sequence 11, Appl
23	200	42.9	91	US-09-955-502-12	Sequence 12, Appl
24	200	42.9	91	US-09-955-502-13	Sequence 13, Appl
25	195	41.8	88	US-09-955-502-15	Sequence 15, Appl
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27	195	41.8	91	US-09-955-502-16	Sequence 16, Appl

28	195	41.8	91	US-09-955-502-17	Sequence 17, Appl
29	189	40.6	78	US-09-955-502-19	Sequence 19, Appl
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35	73	15.7	200	US-10-424-599-191247	Sequence 191247, A
36	71.5	15.3	142	US-10-767-701-57742	Sequence 57742, A
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38	71.5	15.3	621	US-10-437-963-132015	Sequence 132015, A
39	71.5	15.3	683	US-10-425-114-58832	Sequence 58832, A
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46	69.5	14.9	438	US-09-974-879-570	Sequence 570, App
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58	69	14.8	328	US-10-437-963-174979	Sequence 174979, A
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61	68.5	14.7	507	US-10-282-122A-68134	Sequence 68134, A
62	68.5	14.7	646	US-10-739-930-10344	Sequence 10344, A
63	68.5	14.7	829	US-10-437-963-156165	Sequence 156165, A
64	68.5	14.7	1141	US-10-732-923-18071	Sequence 18071, A
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67	67.5	14.5	287	US-10-270-786-48	Sequence 48, Appl
68	67.5	14.5	287	US-10-270-710-48	Sequence 48, Appl
69	67.5	14.5	287	US-10-270-859-48	Sequence 48, Appl
70	67.5	14.5	287	US-10-270-846-48	Sequence 48, Appl
71	67.5	14.5	365	US-10-437-963-107715	Sequence 107715, A
72	67.5	14.5	472	US-10-282-122A-55283	Sequence 55283, A
73	67.5	14.5	526	US-10-437-963-156176	Sequence 156176, A
74	67.5	14.5	4498	US-10-732-923-15008	Sequence 15008, A
75	67	14.4	151	US-10-767-701-44295	Sequence 44295, A

ALIGNMENTS

RESULT 1
US-09-955-502-32
Sequence 32, Application US/09955502
Patent No. US2002072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.9/559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 32
LENGTH: 87
TYPE: PRT
ORGANISM: Methylococcus capsulatus

US-09-955-502-32

Query Match 100.0%; Score 466; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.2e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARRIICAKGIEADGIDAPPFGGQRIFEHVSKEAMODWLKQOTMLINEHRLTPPEA 60
DB 1 MARRIICAKGIEADGIDAPPFGGQRIFEHVSKEAMODWLKQOTMLINEHRLTPPEA 60
QY 61 SARKELEBEREKFLFGGISTPGGYVP 87
DB 61 SARKELEBEREKFLFGGISTPGGYVP 87

RESULT 2

US-09-955-502-31

; Sequence 31, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955.502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Thiobacillus ferrooxidans
US-09-955-502-31

Query Match 62.4%; Score 291; DB 3; Length 87;
Best Local Similarity 58.6%; Pred. No. 1.5e-28;
Matches 51; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MARRIICAKGIEADGIDAPPFGGQRIFEHVSKEAMODWLKQOTMLINEHRLTPPEA 60
DB 1 MSRWQCCKVLGHEAGLDPPTPGALGARITQVSKKANQCKLQOTMLINEHRLSPIDP 60
QY 61 SARKELEBEREKFLFGGISTPGGYVP 87
DB 61 KSRTFLKQMEAYFFGDGQSPGEGYVP 87

RESULT 3

US-09-955-502-29

; Sequence 29, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955.502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-09-955-502-29

Query Match 59.2%; Score 276; DB 3; Length 87;

Best Local Similarity 59.8%; Pred. No. 1.1e-26;
Matches 52; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 MARRIICAKGIEADGIDAPPFGGQRIFEHVSKEAMODWLKQOTMLINEHRLTPPEA 60
DB 1 MARRIICAKGIEADGIDAPPFGGQRIFEHVSKEAMODWLKQOTMLINEHRLTPPEA 60
QY 61 SARKELEBEREKFLFGGISTPGGYVP 87
DB 61 SARKELEBEREKFLFGGISTPGGYVP 87

RESULT 4

US-09-955-502-30

; Sequence 30, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955.502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

Query Match 59.2%; Score 276; DB 3; Length 87;
Best Local Similarity 59.8%; Pred. No. 1.1e-26;
Matches 52; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 MARRIICAKGIEADGIDAPPFGGQRIFEHVSKEAMODWLKQOTMLINEHRLTPPEA 60
DB 1 MARRIICAKGIEADGIDAPPFGGQRIFEHVSKEAMODWLKQOTMLINEHRLTPPEA 60
QY 61 SARKELEBEREKFLFGGISTPGGYVP 87
DB 61 SARKELEBEREKFLFGGISTPGGYVP 87

RESULT 5

US-09-955-502-33

; Sequence 33, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955.502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Coxiella burnetii
US-09-955-502-33

Query Match 57.5%; Score 268; DB 3; Length 88;
Best Local Similarity 58.8%; Pred. No. 1.2e-25;
Matches 50; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

GenCore version 5.1.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.60992 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-32

Perfect score: 466
Sequence: 1 MARRIICAKLGIADGLDAP.....QERKFLPGGTFPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	243	52.1	88	US-10-467-657-968	Sequence 968, App
2	66	14.2	199	US-10-821-234-950	Sequence 950, App
3	65	13.9	3803	US-10-995-561-773	Sequence 773, App
4	65	13.9	3960	US-10-995-561-771	Sequence 771, App
5	65	13.9	5335	US-10-995-561-777	Sequence 777, App
6	65	13.9	5406	US-10-995-561-774	Sequence 774, App
7	65	13.9	5415	US-10-995-561-779	Sequence 779, App
8	65	13.9	5464	US-10-995-561-775	Sequence 775, App
9	61.5	13.2	395	US-11-072-175-159	Sequence 159, App
10	60.5	13.0	619	US-11-156-953-5	Sequence 5, App11
11	59.5	12.8	549	US-11-085-185-2	Sequence 2, App11
12	57.5	12.3	177	US-09-995-493-124	Sequence 124, App
13	57.5	12.3	310	US-11-198-746-88	Sequence 88, App1
14	57.5	12.3	310	US-11-198-794-88	Sequence 88, App1
15	57.5	12.3	315	US-11-198-746-91	Sequence 91, App1
16	57.5	12.3	315	US-11-198-794-91	Sequence 91, App1
17	57.5	12.3	322	US-11-198-746-89	Sequence 89, App1
18	57.5	12.3	322	US-11-198-746-89	Sequence 89, App1
19	57.5	12.3	528	US-11-198-794-90	Sequence 90, App1
20	57.5	12.3	528	US-11-198-794-90	Sequence 90, App1
21	57.5	12.3	548	US-11-198-746-86	Sequence 86, App1
22	57.5	12.3	548	US-11-198-746-86	Sequence 86, App1
23	57.5	12.3	695	US-11-198-794-87	Sequence 87, App1
24	57.5	12.3	695	US-11-198-794-87	Sequence 87, App1
25	57.5	12.3	832	US-11-065-943-100	Sequence 100, App

26	57.5	12.3	832	7	US-11-007-797A-11	Sequence 11, App1
27	57.5	12.3	832	7	US-11-007-642B-11	Sequence 11, App1
28	57.5	12.3	832	7	US-11-198-746-4	Sequence 4, App11
29	57.5	12.3	832	7	US-11-198-794-4	Sequence 4, App11
30	57.5	12.3	833	7	US-11-242-730-1	Sequence 1, App11
31	57.5	12.3	833	7	US-11-198-746-85	Sequence 85, App1
32	57.5	12.3	833	7	US-11-198-794-85	Sequence 85, App1
33	57	12.2	264	7	US-11-072-512-3606	Sequence 3606, App
34	56	12.0	418	6	US-10-512-325-3	Sequence 3, App11
35	56	12.0	418	7	US-11-196-919-2	Sequence 2, App11
36	56	12.0	776	7	US-11-072-512-3117	Sequence 3117, App
37	56	12.0	833	7	US-11-076-187-5	Sequence 5, App11
38	55.5	11.9	264	7	US-11-214-199-46	Sequence 46, App1
39	55.5	11.9	893	7	US-11-072-512-3504	Sequence 3504, App
40	55	11.8	449	7	US-11-010-239-65	Sequence 65, App1
41	55	11.8	2455	7	US-11-186-999-14	Sequence 14, App1
42	55	11.8	2455	7	US-11-186-999-16	Sequence 16, App1
43	54	11.6	532	7	US-11-147-915-24	Sequence 24, App1
44	54	11.6	532	7	US-11-147-915-26	Sequence 26, App1
45	54	11.6	674	7	US-11-167-048-1	Sequence 1, App11
46	54	11.6	832	7	US-11-098-686-10182	Sequence 10182, App
47	53.5	11.5	285	6	US-10-467-657-222	Sequence 222, App
48	53.5	11.5	285	6	US-10-467-657-8230	Sequence 8230, App
49	53.5	11.5	447	7	US-11-072-512-2123	Sequence 2123, App
50	53.5	11.5	636	6	US-10-516-587-2	Sequence 2, App11
51	53	11.4	256	6	US-10-877-346-72	Sequence 72, App1
52	53	11.4	256	7	US-11-113-424-183	Sequence 183, App
53	53	11.4	446	7	US-11-055-822-86	Sequence 86, App1
54	53	11.4	593	7	US-11-194-246-317	Sequence 317, App
55	52.5	11.3	521	6	US-10-467-657-1344	Sequence 1344, App
56	52.5	11.3	635	7	US-11-098-686-10433	Sequence 10433, App
57	52	11.2	181	6	US-10-467-657-6074	Sequence 6074, App
58	52	11.2	333	6	US-10-131-826A-132	Sequence 132, App
59	52	11.2	371	7	US-11-186-284-173	Sequence 173, App
60	52	11.2	361	7	US-11-198-685-8	Sequence 8, App11
61	52	11.2	432	7	US-11-198-069-8	Sequence 8, App11
62	52	11.2	462	6	US-10-454-437-112	Sequence 112, App
63	52	11.2	498	7	US-11-124-168A-254	Sequence 254, App
64	52	11.2	558	7	US-11-072-512-2054	Sequence 2054, App
65	52	11.2	963	6	US-10-467-657-2054	Sequence 2, App11
66	51.5	11.1	191	7	US-11-098-686-10672	Sequence 10672, App
67	51.5	11.1	379	7	US-11-144-833-11	Sequence 11, App1
68	51.5	11.1	462	7	US-11-055-822-956	Sequence 956, App
69	51.5	11.1	523	7	US-11-055-822-954	Sequence 954, App
70	51.5	11.1	766	6	US-10-821-234-1691	Sequence 1691, App
71	51.5	11.1	1315	6	US-10-453-372-1034	Sequence 1034, App
72	51.5	11.1	1335	6	US-10-453-372-1030	Sequence 1030, App
73	51	10.9	190	6	US-10-467-657-1426	Sequence 1426, App
74	51	10.9	246	6	US-10-523-503-18	Sequence 18, App1
75	51	10.9	289	7	US-11-010-239-59	Sequence 59, App1

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467, 657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 52.1%; Score 243; DB 6; Length 88;
Best Local Similarity 51.7%; Pred. No. 2,3e-22;
Matches 45; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 MARRLIACLGIBDGLDAPFPFGQGRIFEHVSKKAMQDMLKQTMLINEHRLTPFEA 60
DB 1 MARVVCVKLNKEKKGKFPPLPNELGKRIENVSQKMAATRHQTMLINEHRLSLADP 60

QY 61 SARKLEQERKFLFGGTSSTPGYVP 87
DB 61 RAREYLAQMEQYFFGGADAVQGYVP 87

RESULT 2
US-10-821-234-950
Sequence 950, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labac, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 950
LENGTH: 199
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-950

Query Match 14.2%; Score 66; DB 6; Length 199;
Best Local Similarity 24.1%; Pred. No. 0.99;
Matches 19; Conservative 7; Mismatches 17; Indels 36; Gaps 3;

QY 8 AKLGIEADGLDAPFPFGQGRIFEHVSKKAMQDMLKQTMLINEHRLTPFEASARKFLE 67
DB 80 ARPGVPAESGRTTPPPFG-----EPWK-----VCVVVHSFKPEELMYK----- 116

QY 68 QERKFLFGGTSSTPGYVP 86
DB 117 -----TKDGYV 122

RESULT 3
US-10-995-561-773
Sequence 773, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 773
LENGTH: 3803
TYPE: PRT
ORGANISM: Homo sapiens

US-10-995-561-773

Query Match 13.9%; Score 65; DB 6; Length 3803;
Best Local Similarity 19.9%; Pred. No. 42;
Matches 28; Conservative 19; Mismatches 32; Indels 62; Gaps 7;

QY 6 ICALGIGT-----EADGLDAPFPFGQGRIFEHVSK-----EAMQ 40
DB 261 VAERLGVTRLDDADVDV---PSPDEKSVITVSSIYDAPFKVPEGEGISATEVDSRWQ 317

QY 41 D-----WLKQTMLINEHRL--TPFEASA-----RKFLQERK----- 72
DB 318 EYQSRVDSLIPWIKQHTILMSDKTPPNPVELKALYNQYIHFKEITELAKEREKRIEEL 377

QY 73 -----FLFGGTSSTPGYVP 87
DB 378 YKLEVWIEFGRIKLPQGYHP 398

RESULT 4
US-10-995-561-771
Sequence 771, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 771
LENGTH: 3960
TYPE: PRT
ORGANISM: Homo sapiens
US-10-995-561-771

Query Match 13.9%; Score 65; DB 6; Length 3960;
Best Local Similarity 19.9%; Pred. No. 44;
Matches 28; Conservative 19; Mismatches 32; Indels 62; Gaps 7;

QY 6 ICALGIGT-----EADGLDAPFPFGQGRIFEHVSK-----EAMQ 40
DB 261 VAERLGVTRLDDADVDV---PSPDEKSVITVSSIYDAPFKVPEGEGISATEVDSRWQ 317

QY 41 D-----WLKQTMLINEHRL--TPFEASA-----RKFLQERK----- 72
DB 318 EYQSRVDSLIPWIKQHTILMSDKTPPNPVELKALYNQYIHFKEITELAKEREKRIEEL 377

QY 73 -----FLFGGTSSTPGYVP 87
DB 378 YKLEVWIEFGRIKLPQGYHP 398

RESULT 5
US-10-995-561-777
Sequence 777, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 777
LENGTH: 5335
TYPE: PRT

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using BW model

Run on: February 28, 2006, 19:26:45 ; Search time 71.531 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-33

Perfect score: 467
Sequence: 1 MTRRIICQKLGKKEADALNYS.....EMINFLFGTSERKAGYTSR 88

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	5	ABB78178 Amino aci
2	295	63.2	89	9	ABB41576 L. pneumo
3	295	63.2	95	9	ABB38294 L. pneumo
4	286	61.2	87	5	ABB78176 Amino aci
5	268	57.4	87	5	ABB78177 Amino aci
6	263	56.3	87	5	ABB78175 Amino aci
7	258	55.2	88	5	ABB78171 Amino aci
8	258	55.2	88	5	ABB78172 Amino aci
9	258	55.2	88	5	ABB78173 Amino aci
10	258	55.2	88	6	ABP77219 N. gonorr
11	257	55.0	87	5	ABB78174 Amino aci
12	241	51.6	90	5	ABB78155 Amino aci
13	237	50.7	87	5	ABB78153 Amino aci
14	235	50.3	93	7	ADP05158 Bacterial
15	233	49.9	90	5	ABB78165 Amino aci
16	232	49.7	107	7	ABO65445 Klebslell
17	230	49.3	87	5	ABB78148 Amino aci
18	230	49.3	87	5	ABB78147 Amino aci
19	230	49.3	91	5	ABB78150 Amino aci
20	227	48.6	78	5	ABB78164 Amino aci
21	227	48.6	91	5	ABB78158 Amino aci
22	227	48.6	91	5	ABB78157 Amino aci
23	227	48.6	91	5	ABB78156 Amino aci
24	224	48.0	87	5	ABB78152 Amino aci

ALIGNMENTS

25	223	47.8	86	5	ABB78149 Amino aci
26	223	47.8	87	5	ABB78151 Amino aci
27	220	47.1	87	5	ABB78170 Amino aci
28	220	47.1	122	7	ABO74609 Pseudomon
29	218	46.7	88	5	ABB78160 Amino aci
30	218	46.7	91	5	ABB78161 Amino aci
31	218	46.7	91	5	ABB78159 Amino aci
32	218	46.7	91	5	ABB78162 Amino aci
33	215.5	46.1	92	6	ADA34169 Amino aci
34	215	46.0	90	5	ABB78168 Amino aci
35	214	45.8	91	5	ABB78163 Amino aci
36	205.5	44.0	90	5	ABB78167 Amino aci
37	205	43.9	88	5	ABB78154 Amino aci
38	204	43.7	87	5	ABB78169 Amino aci
39	185	39.6	110	8	ADL05173 Amino aci
40	164	35.1	76	5	ABB78166 Amino aci
41	81	17.3	451	7	ADP07116 Bacterial
42	68	14.6	461	2	AAW10210 Mature en
43	68	14.6	490	2	AAW10209 Full leng
44	67.5	14.5	369	2	AAV35630 Chlamydia
45	67.5	14.5	375	8	ADS44184 Bacterial
46	67	14.3	283	5	ABBS5069 Lactococc
47	66.5	14.2	494	6	ABU17056 Protein e
48	66.5	14.2	495	6	ADA36816 Acinetoba
49	66.5	14.2	529	5	ABG71896 Human mac
50	66.5	14.2	719	4	AAH95255 Human pro
51	66.5	14.2	934	8	ADM87275 Human pro
52	66.5	14.2	2285	4	ABB63057 Drosophil
53	66	14.1	415	4	ABB30842 Amino aci
54	66	14.1	430	4	ABB30831 Amino aci
55	66	14.1	532	4	ABB30841 Amino aci
56	66	14.1	547	4	ABB30830 Amino aci
57	66	14.1	578	4	ABB30840 Amino aci
58	66	14.1	593	4	ABB30829 Amino aci
59	66	14.1	678	4	ABB30851 Amino aci
60	66	14.1	693	4	ABB30845 Amino aci
61	66	14.1	724	4	ABB30850 Amino aci
62	66	14.1	739	4	ABB30844 Amino aci
63	65.5	14.0	352	4	ABB64200 Amino aci
64	65.5	14.0	457	8	ADQ67016 Drosophil
65	65.5	14.0	1797	8	ADN17774 Bacterial
66	65	13.9	170	6	ABU28434 Protein e
67	65	13.9	1085	8	ADS43754 Bacterial
68	64.5	13.8	56	4	AAU46284 Propionib
69	64.5	13.8	56	6	ABM42803 Propionib
70	64.5	13.8	287	4	AAH46739 C. tricho
71	64.5	13.8	310	6	ABU40274 Protein e
72	64.5	13.8	472	2	AAV37727 Protein i
73	64.5	13.8	472	6	ABU27359 Protein e
74	64.5	13.8	898	9	ABE90973 Lantibiot
75	64	13.7	175	4	ABB30838 Amino aci

RESULT 1
ID ABB78178 standard; protein; 88 AA.

XX ABB78178;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;

KW hydroxyl radical; DNA damage; YggX homologue.

XX Coxiella burnetii.

OS US2002072118-A1.

XX

PD 13-JUN-2002.
 XX 18-SEP-2001; 2001US-009555502.
 XX 22-SEP-2000; 2000US-0234588P.
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC enterica serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 88 AA;

Query Match 100.0%; Score 467; DB 5; Length 88;
 Best Local Similarity 100.0%; Pred. No. 3.3e-50;
 Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRRIICOKLGEADALNYSYPGELGRIYNIHSEQAMQAMLSHOTMLINRYLSLIDP 60
 Db 1 MTRRIICOKLGEADALNYSYPGELGRIYNIHSEQAMQAMLSHOTMLINRYLSLIDP 60

Qy 61 KARQFLQEMINFLFGTSEKPKAGYTS 88
 Db 61 KARQFLQEMINFLFGTSEKPKAGYTS 88

RESULT 2
 AEB41576
 ID AEB41576 standard; protein; 89 AA.
 XX
 AC AEB41576;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE L. pneumophila protein SEQ ID NO 5908.
 XX
 KW detection; infection; Antibacterial; Vaccine.
 XX
 OS Legionella pneumophila.
 XX
 WO2005049642-A2.
 XX
 PD 02-JUN-2005.
 XX
 PF 23-SEP-2004; 2004WO-IB003578.
 XX
 PR 21-NOV-2003; 2003FR-00013687.
 XX
 PA (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;

PI Ruenick C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 PI Jarraud S;
 XX
 DR WPI; 2005-388305/40.
 XX
 PT New genome of *Legionella pneumophila* Paris strain and derived
 PT polypeptides, useful for detection or identification of the strain and
 PT for treatment and prevention of infections.
 XX
 PS Claim 3; SEQ ID NO 5908; 660pp; English.
 XX

CC The invention relates to an isolated or purified nucleotide sequences (I)
 CC from *Legionella pneumophila* Paris strain. (II), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of *Legionella pneumophila* and to prepare recombinant
 CC (hybrid) polypeptides (Ib). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC *Legionella*, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions. For treatment and prevention of infections by *L.*
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC *L. pneumophila* protein.

SQ Sequence 89 AA;

Query Match 63.2%; Score 295; DB 9; Length 89;
 Best Local Similarity 58.8%; Pred. No. 1.1e-28;
 Matches 50; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTRRIICOKLGEADALNYSYPGELGRIYNIHSEQAMQAMLSHOTMLINRYLSLIDP 60
 Db 1 MSRTVFCCKLKQEBKGEKOPFGEELGKVFNEVSKQAMNMWLSHOTMLINRYLSLIDP 60

Qy 61 KARQFLQEMINFLFGTSEKPKAGYTS 85
 Db 61 RAREFLKEWQKVFGESEKPKSGY 85

RESULT 3
 AEB38294
 ID AEB38294 standard; protein; 95 AA.
 XX
 AC AEB38294;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE L. pneumophila protein SEQ ID NO 2626.
 XX
 KW detection; infection; Antibacterial; Vaccine.
 XX
 OS Legionella pneumophila.
 XX
 WO2005049642-A2.
 XX
 PD 02-JUN-2005.
 XX
 PF 23-SEP-2004; 2004WO-IB003578.
 XX
 PR 21-NOV-2003; 2003FR-00013687.
 XX
 PA (INSP) INST PASTEUR.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 PI Ruenick C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 PI Jarraud S;
 XX
 DR WPI; 2005-388305/40.
 XX

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.52424 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-33
Perfect score: 467
Sequence: 1 MTRRIICQKLGKADALNYS.....EMINFLPGTSEKPGYTSR 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: PIR.80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	55.2	88	2	H81014 conserved hypochet
2	241	51.6	90	2	C82320 conserved hypochet
3	233	49.9	90	2	A10116 conserved hypochet
4	227	48.6	91	2	A85954 hypochetrical prote
5	227	48.6	91	2	A65082 hypochetrical prote
6	227	48.6	91	2	F91108 hypochetrical prote
7	224	48.0	90	2	C64013 hypochetrical prote
8	220	47.1	90	2	H83003 conserved hypochet
9	218	46.7	91	2	AH0879 conserved hypochet
10	214	45.8	105	2	C82624 conserved hypochet
11	164	35.1	93	2	B84994 hypochetrical prote
12	67.5	14.5	367	2	G81526 hypochetrical prote
13	67.5	14.5	368	2	D72011 hypochetrical prote
14	67.5	14.5	368	2	B86612 hypochetrical prote
15	67.5	14.5	375	2	T39364 hypochetrical prote
16	67	14.3	329	2	H86839 hypochetrical prote
17	67	14.3	329	2	T29862 hypochetrical prote
18	66.5	14.2	973	2	T50449 DNA repair and rec
19	65	13.9	1085	2	JC2227 probable helicase
20	64.5	13.8	472	2	H81665 replicative DNA he
21	64.5	13.8	472	2	G71503 probable replicati
22	64.5	13.8	554	2	G82272 DNA repair protein
23	64.5	13.8	701	2	S35313 T1P1 protein - Yea
24	64	13.7	609	2	S36569 BI protein - human
25	63.5	13.6	115	2	B86771 hypochetrical prote
26	63.5	13.6	243	2	A95064 conserved hypochet
27	63.5	13.6	264	2	C97931 conserved hypochet
28	63.5	13.6	312	2	D83539 conserved hypochet
29	63	13.5	419	2	AD2741 N-acetylmuramoyl-L

30	63	13.5	580	2	F75142 abc transporter AT
31	63	13.5	582	2	B71182 probable ABC trans
32	63	13.5	913	2	T35718 hypochetrical prote
33	62.5	13.4	841	2	B90244 ribonucleotide red
34	62	13.3	514	1	H0DV18 cytochrome-c3 hydr
35	62	13.3	644	2	AD0712 conserved hypochet
36	62	13.3	644	2	D90940 hypochetrical prote
37	62	13.3	644	2	G64938 hypochetrical prote
38	62	13.3	644	2	H85768 hypochetrical prote
39	62	13.3	967	2	F87678 DNA polymerase I l
40	62	13.3	997	2	S67697 probable membrane
41	61.5	13.2	260	2	AH1639 hypochetrical prote
42	61.5	13.2	909	2	C84965 oxoglutarate dehyd
43	61.5	13.2	918	2	T58178 glutamate receptor
44	61.5	13.2	3746	1	YGPLV3 alpha-aminoadipyl-
45	61.5	13.2	3770	2	A40889 delta-(L-alpha-ami
46	61.5	13.2	3791	1	YGPLV8 carboxylesterase (
47	61	13.1	215	2	S14287 phosphatidylglycer
48	61	13.1	253	2	AB0271 glycoyltransferas
49	61	13.1	263	2	E97189 hypochetrical prote
50	61	13.1	269	2	A69997 circular genome pr
51	61	13.1	407	2	S11479 carboxylesterase (
52	61	13.1	540	2	S53370 esterase B1 - sout
53	61	13.1	540	2	A35986 hypochetrical prote
54	61	13.1	703	2	B82355 ATP-dependent heli
55	61	13.1	703	2	B82148 nitrate reductase
56	61	13.1	830	2	AE0369 two-component sens
57	61	13.1	1131	2	AD2166 peptide synthetase
58	61	13.1	2459	2	AF2136 beta-lactamase (EC
59	60.5	13.0	249	2	A35263 probable modificat
60	60.5	13.0	309	2	D71173 conserved hypochet
61	60.5	13.0	327	2	G70402 probable beta-lact
62	60.5	13.0	498	2	A72725 hypochetrical prote
63	60.5	13.0	591	2	E71651 delta-(L-alpha-ami
64	60.5	13.0	3649	1	S18268 alpha-aminoadipyl-
65	60.5	13.0	3712	1	YGCEVC hypochetrical prote
66	60	12.8	167	2	C72763 secretory protein
67	60	12.8	234	2	JH0483 hypochetrical prote
68	60	12.8	413	2	B70573 leucine aminopepti
69	60	12.8	468	2	F87359 cytochrome P450 1A
70	60	12.8	518	2	A27821 hypochetrical prote
71	60	12.8	528	2	T22941 xpsr protein - Xan
72	60	12.8	531	2	T12056 xpsr protein - Xan
73	60	12.8	531	2	S17937 gag polyprotein -
74	60	12.8	591	1	ROMTMM conserved hypochet
75	60	12.8	644	2	AF0262

ALIGNMENTS

RESULT 1
H81014 conserved hypochetrical protein NMB2021 [Imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014, F81958
R/Retelin: H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maesigani, V.; Pizsa, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappunli, R.; Wei
A/Titile: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: AB1000; WMD:2015755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI000000487F; GB:AE002552; GB:AE002098; NID:97227279; PIDN:;
A/Experimental source: serogroup B, strain MC58
R/Parikhili, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Ugeles, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

A>Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A/Reference number: A81775; MUID:20222556; PMID:10761319
A/Accession: F81958
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <PAR>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:G7379120; PIDN:
A/Experimental source: serogroup A, strain Z2491
C/Genetics:
A/Gene: NMB2021; NMA0419
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 55.2%; Score 258; DB 2; Length 88;
Best Local Similarity 50.0%; Pred. No. 7.6e-22;
Matches 44; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MTRRIICQKLGKADALNYSPPYGLGRIYNIHISEQAWQAMLSHOTMLINERYLSLIDP 60
Db 1 MARVWPCVKLNKEABGKPPPLPNEIGKRIPEYNSQEMAMWTHQTMLINENKSLADP 60

Qy 61 KARQFLQEMINFLFGTSEKPAGYTSB 88
Db 61 RAREYLAQWMEQYFFGDGADAVQGYVPO 88

RESULT 2
C82320
conserved hypothetical protein VC0451 [imported] - *Vibrio cholerae* (strain N16961 serog
C/Species: *Vibrio cholerae*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82320
R/Heldelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Hardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Base, S.; Qin, H.; Dragoti, I.; Sellers, F
1, R.K.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <HE1>
A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:G9654871; PIDN:
A/Experimental source: serogroup O1, strain N16961, biotype El Tor
C/Genetics:
A/Gene: VC0451
A/Map position: 1
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 51.6%; Score 241; DB 2; Length 90;
Best Local Similarity 51.2%; Pred. No. 6.3e-20;
Matches 44; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MTRRIICQKLGKADALNYSPPYGLGRIYNIHISEQAWQAMLSHOTMLINERYLSLIDP 60
Db 1 MARVWPCVKLNKEADGADPQLYPGLGRIYNIHISEQAWQAMLSHOTMLINERYLSLIDP 60

Qy 61 KARQFLQEMINFLFGTSEKPAGYT 86
Db 61 EHRKLEQEMVNFLEFGKEVHIIGYT 86

RESULT 3
A10116
conserved hypothetical protein YP00953 [imported] - *Yersinia pestis* (strain CO92)
C/Species: *Yersinia pestis*
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: A10116
R/Parhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: A10116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <KUR>
A/Cross-references: UNIPARC:UPI00000DCC4; GB:AL590842; PIDN:CAC89796.1; PID:G15979022; C
C/Genetics:
A/Gene: YP00953
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 49.9%; Score 233; DB 2; Length 90;
Best Local Similarity 51.2%; Pred. No. 5e-19;
Matches 44; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MTRRIICQKLGKADALNYSPPYGLGRIYNIHISEQAWQAMLSHOTMLINERYLSLIDP 60
Db 1 MSRTIFCTPLQREABGDDPQLYPGLGRIYNIHISEQAWQAMLSHOTMLINERYLSLIDP 60

Qy 61 KARQFLQEMINFLFGTSEKPAGYT 86
Db 61 EDRKLEQEMVNFLEFGQDVHINGYT 86

RESULT 4
A85954
hypothetical protein y9gx [imported] - *Escherichia coli* (strain O157:H7, substrain EDL93;
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
11ler, L.; Grobeck, E.J.; Davis, N.W.; Llm, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <STD>
A/Cross-references: UNIPARC:PS2065; UNIPARC:UPI0000163A04; GB:AE005174; NID:G12517511; P
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: y9gx
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 48.6%; Score 227; DB 2; Length 91;
Best Local Similarity 50.0%; Pred. No. 2.4e-18;
Matches 44; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MTRRIICQKLGKADALNYSPPYGLGRIYNIHISEQAWQAMLSHOTMLINERYLSLIDP 60
Db 1 MSRTIFCTPLQREABGDDPQLYPGLGRIYNIHISEQAWQAMLSHOTMLINERYLSLIDP 60

Qy 61 KARQFLQEMINFLFGTSEKPAGYTSE 88
Db 61 EHRKLEQEMVNFLEFGKEVHIIGYTP 88

RESULT 5
A65082
hypothetical protein b2962 - *Escherichia coli* (strain K-12)
C/Species: *Escherichia coli*
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R/Blaetner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.V.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of *Escherichia coli* K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A65082
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPARC:PS2065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:G
A/Experimental source: strain K-12, substrain M61655

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.991 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502a-33

Perfect score: 467
Sequence: 1 MTRRIICQKLGKADALNYS.....EMINFLFGTSEKPGAYTSE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	100.0	90	1	FETP COXBU
2	295	63.2	89	1	FETP COXBU
3	295	63.2	89	1	FETP LEGPH
4	292	62.5	89	1	FETP LEGPH
5	271	58.0	90	1	FETP CHROV
6	268	57.4	90	1	FETP METCA
7	266	57.0	87	1	FETP PRATT
8	264	56.5	91	2	Q4LS19_9BURK
9	263	56.3	90	1	FETP NITBU
10	263	56.3	91	1	FETP BURMA
11	263	56.3	91	1	FETP BURPS
12	261	55.9	92	1	FETP XANOR
13	258	55.2	88	1	FETP NEIGA
14	258	55.2	88	1	FETP NEIGA
15	255	55.2	88	1	FETP NEIGA
16	255	54.6	91	1	FETP XANAC
17	250	53.5	92	1	FETP XANAC
18	250	53.5	92	2	Q4UM14_XANCP
19	245	52.5	90	1	FETP IDILO
20	241	51.6	90	1	FETP VIBCH
21	241	51.6	91	1	FETP BALSO
22	240	51.4	90	1	FETP VIBUV
23	240	51.4	90	1	FETP VIBUV
24	237	50.7	94	1	FETP VIBUV
25	234	50.1	90	1	FETP YERP
26	233	49.9	90	1	FETP YERP
27	232	49.7	90	1	FETP PHOIL
28	232	49.7	92	2	Q4W04_9DBLT
29	231	49.5	90	1	FETP VIBPA
30	230	49.3	90	1	FETP BORPA
31	230	49.3	90	1	FETP BORPA

32	230	49.3	90	1	FETP BORPE	Q7WC4 bordetella
33	226	48.4	90	1	FETP VIBF1	Q5ET0 vibrio fusc
34	224	48.0	90	1	FETP HAEB1	P4408 haemophilus
35	224	48.0	90	2	Q4QMD9_HAE18	Q4QMD9 haemophilus
36	223	47.8	90	1	FETP PASMU	Q9CDB paeteurella
37	222	47.5	90	1	FETP ECO57	Q9CDB paeteurella
38	222	47.5	90	1	FETP ECO11	P0A83 escherichia
39	222	47.5	90	1	FETP SHIFL	P0A83 escherichia
40	222	47.5	90	1	FETP XYLFT	Q8706 xyella fas
41	220	47.1	90	1	FETP PSBAE	Q9H36 pseudomonas
42	218	46.7	90	1	FETP ECO16	Q8F19 escherichia
43	218	46.7	91	1	FETP MANSI	Q65VC7 manheimia
44	216	46.3	90	1	FETP PHOPR	Q61MK7 photobacter
45	215.5	46.1	90	1	FETP ACIAD	Q66B3 acinetobact
46	215	46.0	90	1	FETP ERWCT	Q66B3 acinetobact
47	215	46.0	90	1	FETP PSEBM	Q66B3 acinetobact
48	215	46.0	90	2	Q4ZLP3_PSEBSY	Q8715 pseudomonas
49	214	45.8	90	1	FETP XYLTA	Q4ZLP3 pseudomonas
50	214	45.8	90	2	Q4U228_AZOVI	Q9PC73 xyella fas
51	213	45.6	90	1	FETP SALCH	Q57K04 azotobacter
52	213	45.6	90	1	FETP SALPA	Q57K04 azotobacter
53	213	45.6	90	1	FETP SALTY	Q57K04 azotobacter
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55	205	43.9	92	1	FETP SHEON	Q88149 pseudomonas
56	204	43.7	90	1	FETP PSEBK	Q88149 pseudomonas
57	202	43.3	90	2	Q6T7F6_PSEFL	Q88149 pseudomonas
58	201	43.0	78	1	FETP WIGER	Q88149 pseudomonas
59	195	41.8	90	2	Q4K1T2_PSEFS	Q88149 pseudomonas
60	189	40.5	96	2	Q4FVJ7_9GAMM	Q4F12 pseudomonas
61	179	38.3	78	1	FETP BUCBP	Q4F12 pseudomonas
62	176	37.7	87	1	FETP BUCBP	Q4F12 pseudomonas
63	173	37.0	79	1	FETP CANBP	Q88944 buchiera ap
64	164	35.1	77	1	FETP BUCAT	Q88944 buchiera ap
65	81	17.3	2492	2	Q8UJN1_9CLOS	Q88944 buchiera ap
66	80	17.1	458	2	Q6G0N1_BAROU	Q88944 buchiera ap
67	79	16.9	458	2	Q6G4V6_BAROU	Q88944 buchiera ap
68	77	16.5	282	2	Q97TLO_CLOAB	Q88944 buchiera ap
69	75.5	16.2	263	2	Q4JZK9_STRPN	Q88944 buchiera ap
70	72	15.4	263	2	Q871N6_NEUCR	Q88944 buchiera ap
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73	71	15.2	804	2	Q74KX1_LACJO	Q88944 buchiera ap
74	70.5	15.1	264	2	Q4K2D9_STRPN	Q88944 buchiera ap
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ALIGNMENTS

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ID FETP_COXBU	STANDARD:	PRT:	90 AA.		
AC Q83D06;					
DT 10-OCT-2003 (Rel. 42, Created)					
DR 10-OCT-2003 (Rel. 42, Last sequence update)					
DT 13-SEP-2005 (Rel. 48, Last annotation update)					
DE Probable Pe(2+) trafficking protein.					
GN OrderedLocNames=CB00941;					
OS Coxiella burnetii.					
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;					
CC Coxiellaceae; Coxiella.					
OX NCBI_TaxID=777;					
RM [1]					
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).					
RC STRAIN=Nine Mile phase I / RSA 493;					
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931179100;					
RA Sebnadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.B.,					
RA Nelson W.C., Ward N.L., Tettein H., Davidson T.M., Beaman M.J.,					
RA Deboy R.T., Daugherty S.C., Brinkac L.W., Madupu R., Dodson R.V.,					
RA Kohnert H.M., Lee K.H., Carthy H.A., Scanlan D., Heinzen R.A.,					
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.,					
RT "Complete genome sequence of the Q-fever pathogen, Coxiella					
burnetii.";					

```

RL  Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
CC  -1- FUNCTION: Could be a mediator in iron transactions between iron
CC  acquisition and iron-requiring processes, such as synthesis and/or
CC  repair of Fe-S clusters in biosynthetic enzymes (by similarity).
CC  -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
DR  EMBL: AB016962; AA090467.1; -; Genomic_DNA.
DR  TIGR: CB09041; -.
DR  HAMAP: MF_00686; -, 1.
DR  InterPro: IPR007457; YggX.
DR  Pfam: PF04362; DUF495; 1.
DR  PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR  ProDom: PD029191; DUF495; 1.
KW  Complete proteome; Iron.
SQ  SEQUENCE 90 AA; 10482 MW; 70354D317942C9AE CRC64;

Query Match
Best Local Similarity 100.0%; Score 467; DB 1; Length 90;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTRRIICQKLGKADALNYSYPGELGERIYNHISEQAWQAWLSHOTMLINERYSLIDP 60

Qy 61 KARQFLQEMINFLFGTSGEKAGYTSR 88
Db 61 KARQFLQEMINFLFGTSGEKAGYTSR 88

RESULT 2
FETP LEGPA STANDARD; PRT; 89 AA.
ID 05X3X9;
AC 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Ordered locus Names=lp1902;
OS Legionella pneumophila (strain Paris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467720; DOI=10.1038/ng1447;
RA Cazalec C., Rusnolk C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarrard S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaeser P., Buchrieser C.;
RT "Evidence in the Legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR  EMBL: CR628336; CAH13054.1; -; Genomic_DNA.
DR  LegiOLaSL: lpi1902; -.
DR  HAMAP: MF_00686; -, 1.
DR  InterPro: IPR007457; YggX.
DR  Pfam: PF04362; DUF495; 1.
DR  PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR  ProDom: PD029191; DUF495; 1.
KW  Complete proteome; Iron.
SQ  SEQUENCE 89 AA; 10539 MW; F4B7C711D9F5A1 CRC64;

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DR  PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR  ProDom: PD029191; DUF495; 1.
KW  Complete proteome; Iron.
SQ  SEQUENCE 89 AA; 10539 MW; F4B7C711D9F5A1 CRC64;

Query Match
Best Local Similarity 58.8%; Score 295; DB 1; Length 89;
Matches 50; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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Db 1 MSRTVFCCKLQKQAEAGLEKQPPGELGKRVNEVSKQAMNWLSHOTMLINERYSLIDP 60

Qy 61 KARQFLQEMINFLFGTSGEKAGYTSR 85
Db 61 KARQFLQEMINFLFGTSGEKAGYTSR 85

RESULT 3
FETP LEGPA STANDARD; PRT; 89 AA.
ID 05Z080;
AC 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Ordered locus Names=lp91927;
OS Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
OS ATCC 33152).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=272624;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asanani G., Hill K., Nara J., Feder M., Rineer J., Greenberg J.J.,
RA Stehenko V., Park S.H., Zhao B., Tepilskeya B., Edwards J.R.,
RA Pampou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cayani E., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila.";
RL Science 305:1966-1968(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR  EMBL: AB017354; AAU27997.1; -; Genomic_DNA.
DR  HAMAP: MF_00686; -, 1.
DR  InterPro: IPR007457; YggX.
DR  Pfam: PF04362; DUF495; 1.
DR  PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR  ProDom: PD029191; DUF495; 1.
KW  Complete proteome; Iron.
SQ  SEQUENCE 89 AA; 10539 MW; F4B7C711D9F5A1 CRC64;

Query Match
Best Local Similarity 63.2%; Score 295; DB 1; Length 89;
Matches 50; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTRRIICQKLGKADALNYSYPGELGERIYNHISEQAWQAWLSHOTMLINERYSLIDP 60
Db 1 MSRTVFCCKLQKQAEAGLEKQPPGELGKRVNEVSKQAMNWLSHOTMLINERYSLIDP 60

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.6595 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-33

Perfect score: 467

Sequence: 1 MTRRIICXKLGKADALNYS.....EMINFLFGSGEKDAGTSE 88

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Issued Patents AA:*
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5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	235	50.3	93	US-09-543-681A-5443	Sequence 5443, Ap
2	232	49.7	107	US-09-489-039A-11962	Sequence 11962, A
3	220	47.1	122	US-09-252-991A-23355	Sequence 23355, A
4	215.5	46.1	92	US-09-328-352-5456	Sequence 5456, Ap
5	185	39.6	110	US-09-540-236-2859	Sequence 2859, Ap
6	81	17.3	451	US-09-543-681A-7401	Sequence 7401, Ap
7	68	14.6	461	US-08-672-571A-3	Sequence 1, Appl1
8	68	14.6	490	US-09-198-452A-1048	Sequence 1048, Ap
9	67.5	14.5	369	US-09-438-185A-977	Sequence 977, Ap
10	67.5	14.5	369	US-09-328-352-8103	Sequence 8103, Ap
11	66.5	14.2	495	US-09-585-858-48	Sequence 48, Appl
12	64.5	13.8	287	US-10-270-878-48	Sequence 48, Appl
13	64.5	13.8	287	US-09-538-092-303	Sequence 303, App
14	64.5	13.6	701	US-09-583-110-2877	Sequence 2877, Ap
15	63.5	13.6	220	US-09-415-260A-7	Sequence 7, Appl1
16	63.5	13.6	309	US-09-248-786A-19920	Sequence 19920, A
17	63.5	13.6	374	US-09-252-991A-29855	Sequence 29855, A
18	63.5	13.6	390	US-09-543-681A-7295	Sequence 7295, Ap
19	62.5	13.4	419	US-09-489-039A-7892	Sequence 7892, Ap
20	62	13.3	651	US-09-538-092-113	Sequence 113, Appl
21	62	13.3	997	US-09-962-834A-2	Sequence 2, Appl1
22	61.5	13.2	521	US-09-851-873-103	Sequence 103, App
23	61.5	13.2	524	US-09-248-796A-18975	Sequence 18975, A
24	61.5	13.2	758	US-08-222-617A-6	Sequence 6, Appl1
25	61.5	13.2	938	US-10-104-047-3855	Sequence 3855, Ap
26	61.5	13.2	3666	US-08-222-617A-12	Sequence 12, Appl1
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28	61.5	13.2	3727	1	US-08-222-617A-27	Sequence 27, Appl1
29	61.5	13.2	3778	1	US-08-222-617A-2	Sequence 2, Appl1
30	61	13.1	157	2	US-09-543-681A-5227	Sequence 5227, Ap
31	61	13.1	507	2	US-09-248-786A-19164	Sequence 19164, A
32	61	13.1	944	2	US-09-107-532A-4864	Sequence 4864, Ap
33	60.5	13.0	249	1	US-08-459-264-2	Sequence 2, Appl1
34	60.5	13.0	249	1	US-08-459-264-3	Sequence 2, Appl1
35	60.5	13.0	249	1	US-08-459-264-2	Sequence 2, Appl1
36	60.5	13.0	249	1	US-08-459-264-3	Sequence 3, Appl1
37	60.5	13.0	329	2	US-09-602-787A-306	Sequence 306, App
38	60.5	13.0	356	2	US-09-270-767-46120	Sequence 46120, A
39	60.5	13.0	459	2	US-09-602-787A-302	Sequence 302, App
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41	60.5	13.0	3665	1	US-08-222-617A-13	Sequence 13, Appl1
42	60.5	13.0	3712	1	US-08-222-617A-4	Sequence 4, Appl1
43	60.5	13.0	3712	1	US-08-222-617A-25	Sequence 25, Appl1
44	60	12.8	263	2	US-09-252-991A-22230	Sequence 22230, A
45	60	12.8	591	2	US-09-370-368-8	Sequence 8, Appl1
46	59.5	12.7	262	2	US-09-134-000C-4842	Sequence 4842, Ap
47	59.5	12.7	339	2	US-09-107-532A-7148	Sequence 7148, Ap
48	59.5	12.7	417	2	US-09-543-681A-7845	Sequence 7845, Ap
49	59.5	12.7	473	2	US-09-543-681A-6170	Sequence 6170, Ap
50	59.5	12.7	600	2	US-09-270-767-45242	Sequence 45242, A
51	59	12.6	192	2	US-09-540-236-3508	Sequence 3508, Ap
52	59	12.6	225	2	US-09-543-681A-6406	Sequence 6406, Ap
53	59	12.6	328	1	US-08-637-759B-447	Sequence 447, App
54	59	12.6	328	2	US-08-871-355A-447	Sequence 447, App
55	59	12.6	328	2	US-09-201-945-447	Sequence 447, App
56	59	12.6	541	2	US-09-417-251A-8	Sequence 8, Appl1
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58	59	12.6	711	2	US-09-711-164-456	Sequence 456, App
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60	58.5	12.5	309	2	US-09-415-260A-1	Sequence 1, Appl1
61	58.5	12.5	309	2	US-09-415-260A-2	Sequence 2, Appl1
62	58.5	12.5	309	2	US-09-415-260A-3	Sequence 3, Appl1
63	58.5	12.5	309	2	US-09-415-260A-4	Sequence 4, Appl1
64	58.5	12.5	329	2	US-09-189-527-4	Sequence 4, Appl1
65	58.5	12.5	503	2	US-09-058-260-26	Sequence 26, Appl
66	58.5	12.5	617	2	US-09-902-540-14388	Sequence 14388, A
67	58.5	12.5	937	2	US-09-543-681A-5513	Sequence 5513, Ap
68	58	12.4	243	2	US-09-270-767-31727	Sequence 31727, A
69	58	12.4	581	2	US-09-713-273A-12	Sequence 12, Appl1
70	58	12.4	675	2	US-09-634-238-228	Sequence 228, App
71	58	12.4	1477	2	US-08-492-459-10	Sequence 10, Appl
72	58	12.4	1477	2	US-08-423-752-10	Sequence 10, Appl
73	58	12.4	1477	2	US-08-945-994-3	Sequence 3, Appl1
74	58	12.4	1477	2	US-08-716-873-24	Sequence 24, Appl1
75	58	12.4	1477	2	US-08-716-873-24	Sequence 24, Appl1

ALIGNMENTS

RESULT 1
US-09-543-681A-5443
Sequence 5443, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709,1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5443
LENGTH: 93
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Best Local Similarity 52.3%; Pred. No. 1.1e-23;
Matches 45; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

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Db 4 MSRTIFCTPLNKRGADGDFOLYPGLGRIYNIHQWQWMLSHQTMLINEYRLSLIDP 63

Qy 61 KARQFLQEMINFLFGTSGSEKPGAYT 86
Db 64 DRRKLFQEMVRFLEGHVDHIDYT 89

RESULT 2
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 49.7%; Score 232; DB 2; Length 107;
Best Local Similarity 52.3%; Pred. No. 3.2e-23;
Matches 45; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

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Db 17 MSRTIFCTPLNKRGADGDFOLYPGLGRIYNIHQWQWMLSHQTMLINEYRLSLIDP 76

Qy 61 KARQFLQEMINFLFGTSGSEKPGAYT 86
Db 77 EHRKLFQEMVRFLEGHVDHIDYT 102

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 47.1%; Score 220; DB 2; Length 122;
Best Local Similarity 48.2%; Pred. No. 1.6e-21;
Matches 41; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MTRRIICQKLGKADALNYSPPYGLGRIYNIHQWQWMLSHQTMLINEYRLSLIDP 60

Db 33 MSRTWCRKRYHEELPGIDRPPYGAKEGDIYNNVSKAWDEWQHQTMLINERLNNMNA 92

Qy 61 KARQFLQEMINFLFGTSGSEKPGAY 85
Db 93 EDRKFLQEMDKFLSGDYAKADGY 117

RESULT 4
US-09-328-352-5456
; Sequence 3456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 46.1%; Score 215.5; DB 2; Length 92;
Best Local Similarity 42.7%; Pred. No. 4.3e-21;
Matches 38; Conservative 23; Mismatches 27; Indels 1; Gaps 1;

Qy 1 MTRRIICQKLGKADALNYSPPYGLGRIYNIHQWQWMLSHQTMLINEYRLSLIDP 60
Db 4 MSRTWCRKRYHEELPGIDRPPYGAKEGDIYNNVSKAWDEWQHQTMLINERLNNMNA 92

Qy 61 KARQFLQEMINFLFGTSGSEKPGAYT 88
Db 64 EAKKFLQEMDKFLSGDYAKADGY 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540, 236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 39.6%; Score 185; DB 2; Length 110;
Best Local Similarity 44.4%; Pred. No. 6.8e-17;
Matches 36; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

Qy 5 IICQKLGKADALNYSPPYGLGRIYNIHQWQWMLSHQTMLINEYRLSLIDP 64
Db 25 VFCRKYQGNLPLKPNPFPAKAGELIDTISAKAMNMLEQTMLINEYRLSLIDP 84

Qy 65 FLQEMINFLFGTSGSEKPGAY 85
Db 85 YLNEQREKFLDNGDYKADGY 105

RESULT 6
US-09-543-681A-7401
; Sequence 7401, Application US/09543681A

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 55.062 Seconds
(without alignments)
667.774 Million cell updates/sec

Title: US-09-955-502a-33

Perfect score: 467

Sequence: 1 MTRRIICQKLGKADALNYS.....EMINPLFGTSGSEKAGYTSE 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published_Applications_AA_Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	467	100.0	88	3	US-09-955-502-33
2	286	61.2	87	3	US-09-955-502-31
3	268	57.4	87	3	US-09-955-502-32
4	263	56.3	87	3	US-09-955-502-29
5	263	56.3	87	3	US-09-955-502-30
6	258	55.2	88	3	US-09-955-502-26
7	258	55.2	88	3	US-09-955-502-27
8	258	55.2	88	3	US-09-955-502-28
9	241	51.6	90	3	US-09-955-502-10
10	237	50.7	87	3	US-09-955-502-8
11	233	49.9	90	3	US-09-955-502-20
12	230	49.3	87	3	US-09-955-502-2
13	230	49.3	87	3	US-09-955-502-3
14	230	49.3	87	3	US-09-955-502-5
15	227	48.6	91	3	US-09-955-502-19
16	227	48.6	91	3	US-09-955-502-11
17	227	48.6	91	3	US-09-955-502-12
18	227	48.6	91	3	US-09-955-502-13
19	224	48.0	87	3	US-09-955-502-7
20	223	47.8	86	3	US-09-955-502-4
21	223	47.8	87	3	US-09-955-502-6
22	220	47.1	87	3	US-09-955-502-25
23	218	46.7	88	3	US-09-955-502-15
24	218	46.7	91	3	US-09-955-502-14
25	218	46.7	91	3	US-09-955-502-16
26	218	46.7	91	3	US-09-955-502-17
27	215	46.0	90	3	US-09-955-502-23

ALIGNMENTS

28	214	45.8	89	3	US-09-955-502-22	Sequence 22, Appl
29	214	45.8	91	3	US-09-955-502-18	Sequence 18, Appl
30	205	43.9	88	3	US-09-955-502-9	Sequence 9, Appl
31	204	43.7	87	3	US-09-955-502-24	Sequence 24, Appl
32	164	35.1	76	3	US-09-955-502-21	Sequence 21, Appl
33	67.5	14.5	369	4	US-10-289-762-1048	Sequence 1048, Ap
34	67.5	14.5	375	4	US-10-369-493-22614	Sequence 22614, A
35	66.5	14.2	494	4	US-10-289-122A-44980	Sequence 44980, A
36	66.5	14.2	666	4	US-10-156-761-9189	Sequence 9189, Ap
37	66.5	14.2	934	5	US-10-112-944-468	Sequence 368, Ap
38	66.5	14.2	973	5	US-10-732-923-8581	Sequence 8581, Ap
39	66.5	14.2	2285	6	US-11-097-143-15963	Sequence 15963, A
40	65.5	14.0	352	6	US-11-097-143-19392	Sequence 19392, A
41	65.5	14.0	1588	4	US-10-437-963-189741	Sequence 189741, A
42	65.5	14.0	1630	4	US-10-437-963-122660	Sequence 122660, A
43	65.5	14.0	1797	4	US-10-369-493-427	Sequence 427, App
44	65	13.9	170	4	US-10-282-122A-56358	Sequence 56358, A
45	65	13.9	1085	4	US-10-369-493-22184	Sequence 22184, A
46	65	13.9	1085	5	US-10-732-923-8616	Sequence 8616, Ap
47	65	13.9	1085	5	US-10-732-923-8617	Sequence 8617, Ap
48	64.5	13.8	287	4	US-10-270-875-48	Sequence 48, Appl
49	64.5	13.8	287	4	US-10-270-878-48	Sequence 48, Appl
50	64.5	13.8	287	4	US-10-270-786-48	Sequence 48, Appl
51	64.5	13.8	287	4	US-10-270-710-48	Sequence 48, Appl
52	64.5	13.8	287	4	US-10-270-859-48	Sequence 48, Appl
53	64.5	13.8	287	4	US-10-270-846-48	Sequence 48, Appl
54	64.5	13.8	310	4	US-10-282-122A-68198	Sequence 68198, A
55	64.5	13.8	472	4	US-10-282-122A-55283	Sequence 55283, A
56	64.5	13.8	852	4	US-10-437-963-189743	Sequence 189743, A
57	64.5	13.8	898	6	US-11-034-275-21	Sequence 21, Appl
58	64	13.7	484	5	US-10-220-335-185	Sequence 185, App
59	64	13.7	839	3	US-09-738-269-23	Sequence 23, Appl
60	64	13.7	839	4	US-10-023-437-23	Sequence 23, Appl
61	63.5	13.6	145	4	US-10-437-963-131602	Sequence 131602, A
62	63.5	13.6	219	4	US-10-424-599-223697	Sequence 223697, A
63	63.5	13.6	243	5	US-10-472-928-968	Sequence 968, App
64	63.5	13.6	264	4	US-10-282-122A-57082	Sequence 7082, A
65	63.5	13.6	272	4	US-10-282-122A-57082	Sequence 7082, A
66	63.5	13.6	285	3	US-09-815-242-10713	Sequence 10713, A
67	63.5	13.6	312	3	US-09-815-242-11806	Sequence 11806, A
68	63.5	13.6	312	4	US-10-282-122A-66219	Sequence 66219, A
69	63.5	13.6	952	4	US-10-437-963-144288	Sequence 144288, A
70	63	13.5	580	4	US-10-369-493-21555	Sequence 21555, A
71	63	13.5	582	4	US-10-369-493-13377	Sequence 13377, A
72	63	13.5	1066	4	US-10-369-493-20392	Sequence 20392, A
73	63	13.5	1374	4	US-10-437-963-189670	Sequence 189670, A
74	62.5	13.4	230	4	US-10-437-963-133569	Sequence 133569, A
75	62.5	13.4	1990	4	US-10-437-963-199073	Sequence 199073, A

RESULT 1
US-09-955-502-33
Sequence 33, Application US/09955502
Patent No. US2002072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentn Ver. 2.1
SEQ ID NO 33
LENGTH: 88
TYPE: PRT
ORGANISM: Coxiteella burnetii

US-09-955-502-33

Query Match 100.0%; Score 467; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRRIICQKGEKADALNYSYPGELGRIYNIHSQAWQAWLSHOTMLINEYRLSLIDP 60
Db 1 MTRRIICQKGEKADALNYSYPGELGRIYNIHSQAWQAWLSHOTMLINEYRLSLIDP 60
Qy 61 KARQFLQEMINFLFGTSGSEKPAGYTSR 88
Db 61 KARQFLQEMINFLFGTSGSEKPAGYTSR 88

RESULT 2

US-09-955-502-31
Sequence 31, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 87
TYPE: PRT
ORGANISM: Thiobacillus ferrooxidans
US-09-955-502-31

Query Match 61.2%; Score 286; DB 3; Length 87;
Best Local Similarity 60.0%; Pred. No. 9.7e-28;
Matches 51; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MTRRIICQKGEKADALNYSYPGELGRIYNIHSQAWQAWLSHOTMLINEYRLSLIDP 60
Db 1 MSRWQCYKLGHEAGLDLRRPPLGALGARIQVBSKEMQWMLKQOTMLINEYRLSLIDP 60
Qy 61 KARQFLQEMINFLFGTSGSEKPAGY 85
Db 61 KSRFLQKQEMAYFPDGAQSPGEGY 85

RESULT 3

US-09-955-502-32
Sequence 32, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 32
LENGTH: 87
TYPE: PRT
ORGANISM: Methylococcus capsulatus
US-09-955-502-32

Query Match 57.4%; Score 268; DB 3; Length 87;

Best Local Similarity 58.8%; Pred. No. 1.8e-25;
Matches 50; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MTRRIICQKGEKADALNYSYPGELGRIYNIHSQAWQAWLSHOTMLINEYRLSLIDP 60
Db 1 MARRIICAKLGIEADLDLAPPPGQORIFEHVSKQAWQDWIKQOTMLINEYRLTPFEA 60
Qy 61 KARQFLQEMINFLFGTSGSEKPAGY 85
Db 61 SARRFLQERKFLFGGISTPGGY 85

RESULT 4

US-09-955-502-29
Sequence 29, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia mallei
US-09-955-502-29

Query Match 56.3%; Score 263; DB 3; Length 87;
Best Local Similarity 54.1%; Pred. No. 7.5e-25;
Matches 46; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MTRRIICQKGEKADALNYSYPGELGRIYNIHSQAWQAWLSHOTMLINEYRLSLIDP 60
Db 1 MARRIICAKLGIEAGLDLPPPLPEELGKRLYESVSKQAWQDWIKQOTMLINEYRLNADP 60
Qy 61 KARQFLQEMINFLFGTSGSEKPAGY 85
Db 61 RARQYLMKQYTKYRFGGADQASGY 85

RESULT 5

US-09-955-502-30
Sequence 30, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

Query Match 56.3%; Score 263; DB 3; Length 87;
Best Local Similarity 54.1%; Pred. No. 7.5e-25;
Matches 46; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using SW model

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280.957 Million cell updates/sec

Title: US-09-955-502A-33

Perfect score: 467
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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3	61.5	13.2	938 7 US-11-072-512-3855	Sequence 3855, App
4	61.5	13.2	7968 7 US-11-186-731-5	Sequence 5, App
5	58.5	12.5	329 6 US-10-981-873-29	Sequence 29, App
6	58	12.4	375 6 US-10-517-939-272	Sequence 27, App
7	57.5	12.3	338 6 US-10-914-165-37	Sequence 16, App
8	56	12.0	1046 7 US-11-120-308-186	Sequence 87, App
9	56	12.0	1176 6 US-10-821-234-897	Sequence 44, App
10	55.5	11.9	210 7 US-11-194-246-441	Sequence 245, App
11	55.5	11.9	335 7 US-11-072-175-245	Sequence 9, App
12	55.5	11.9	1579 7 US-11-052-554A-9	Sequence 24, App
13	55.5	11.9	4868 7 US-11-044-111-24	Sequence 339, App
14	55	11.8	318 7 US-11-234-786-339	Sequence 10124, App
15	55	11.8	625 7 US-11-098-686-10124	Sequence 1, App
16	55	11.8	1560 7 US-11-059-982-1	Sequence 5376, App
17	55	11.8	1841 7 US-11-057-058-63	Sequence 1025, App
18	54.5	11.7	360 6 US-10-467-657-5376	Sequence 1019, App
19	54.5	11.7	638 6 US-10-995-561-1025	Sequence 1024, App
20	54.5	11.7	1160 6 US-10-995-561-1019	Sequence 1027, App
21	54.5	11.7	1302 6 US-10-995-561-1024	Sequence 12, App
22	54.5	11.7	1306 6 US-10-995-561-1027	Sequence 127, App
23	54	11.6	739 7 US-11-078-189-12	Sequence 486, App
24	53.5	11.5	350 5 US-09-978-360A-486	Sequence 786, App
25	53.5	11.5	388 6 US-10-467-657-786	

26	53	11.3	368 6 US-10-689-742-100	Sequence 100, App
27	53	11.3	382 7 US-11-134-795-19	Sequence 19, App
28	52.5	11.2	268 7 US-11-098-686-10958	Sequence 10958, App
29	52.5	11.2	381 7 US-11-143-984A-111	Sequence 111, App
30	52.5	11.2	406 6 US-10-995-561-748	Sequence 748, App
31	52.5	11.2	406 6 US-10-995-561-749	Sequence 749, App
32	52.5	11.2	406 6 US-10-995-561-750	Sequence 750, App
33	52.5	11.2	406 6 US-10-995-561-751	Sequence 751, App
34	52.5	11.2	406 6 US-10-995-561-752	Sequence 752, App
35	52.5	11.2	479 7 US-11-152-366-48	Sequence 48, App
36	52.5	11.2	492 6 US-10-821-234-1108	Sequence 1108, App
37	52.5	11.2	522 7 US-11-152-366-51	Sequence 51, App
38	52.5	11.2	644 7 US-11-072-512-1945	Sequence 2945, App
39	52	11.1	163 6 US-10-467-657-2662	Sequence 2662, App
40	52	11.1	194 5 US-09-978-360A-608	Sequence 608, App
41	52	11.1	247 6 US-10-838-616-46	Sequence 46, App
42	52	11.1	380 6 US-10-525-674-28	Sequence 28, App
43	52	11.1	638 7 US-11-072-512-2626	Sequence 2626, App
44	52	11.1	856 6 US-10-510-947-8	Sequence 8, App
45	52	11.1	856 7 US-11-042-988-13	Sequence 13, App
46	52	11.1	856 7 US-11-135-235-1	Sequence 1, App
47	52	11.1	898 7 US-11-174-150-43	Sequence 43, App
48	51.5	11.0	277 6 US-10-821-234-1435	Sequence 1435, App
49	51.5	11.0	318 6 US-10-793-626-1600	Sequence 1600, App
50	51.5	11.0	462 7 US-11-072-512-3571	Sequence 3571, App
51	51.5	11.0	574 7 US-11-098-686-11000	Sequence 11000, App
52	51.5	11.0	923 7 US-11-057-058-66	Sequence 66, App
53	51	10.9	196 7 US-11-098-686-10972	Sequence 10972, App
54	51	10.9	200 6 US-10-793-626-1186	Sequence 1186, App
55	51	10.9	200 6 US-10-793-626-1390	Sequence 1390, App
56	51	10.9	209 6 US-09-995-493-94	Sequence 94, App
57	51	10.9	351 6 US-10-981-873-27	Sequence 27, App
58	51	10.9	383 6 US-10-513-759-4	Sequence 4, App
59	51	10.9	383 7 US-11-129-143-76	Sequence 76, App
60	51	10.9	871 6 US-10-933-025-3	Sequence 3, App
61	51	10.8	3011 6 US-10-985-205-3	Sequence 10697, App
62	50.5	10.8	268 7 US-11-098-686-10697	Sequence 1190, App
63	50.5	10.8	456 6 US-10-793-626-1190	Sequence 968, App
64	50.5	10.8	724 6 US-10-793-626-968	Sequence 9, App
65	50	10.7	180 6 US-10-665-455-8	Sequence 5848, App
66	50	10.7	244 7 US-11-098-686-11294	Sequence 2, App
67	50	10.7	336 6 US-10-467-657-5848	Sequence 2186, App
68	50	10.7	421 6 US-10-858-730-2	Sequence 128, App
69	50	10.7	508 7 US-11-072-512-2186	Sequence 67, App
70	50	10.7	561 7 US-11-031-206-138	Sequence 103, App
71	50	10.7	651 6 US-10-770-726-67	Sequence 48, App
72	50	10.7	651 7 US-11-177-138-10	Sequence 10, App
73	50	10.7	786 6 US-10-467-962B-103	Sequence 58, App
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75	50	10.7	870 7 US-11-165-226-58	

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 55.2%; Score 258; DB 6; Length 88;
Best Local Similarity 50.0%; Pred. No. 1.9e-24;
Matches 44; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 1 MTRRIICQKLGKADALNYSYPGELGRIYNNHISEQAWQAMLSHOTMLINERYLSLIDP 60
DB 1 MARWVFCVTKLKEAGKPKPLPFLGKRIPEVNSQEMAWMTHTQMTLINENRSLADP 60

QY 61 KARQFLQEMINFLFGGSEKPAQYTS 88
DB 61 RAREYLAQWQWQYFEGDADAVQGYVQ 88

RESULT 2
US-11-152-366-49
Sequence 49, Application US/11152366
Publication No. US20060014184A1
GENERAL INFORMATION:

APPLICANT: Brys, Reginald
APPLICANT: Vandeghinste, Nick
APPLICANT: Tomme, Peter H. M.
TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The
TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases
FILE REFERENCE: P27,880-A USA
CURRENT APPLICATION NUMBER: US/11/152,366
CURRENT FILING DATE: 2005-06-14
PRIOR APPLICATION NUMBER: 60/579,307
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 295
SOFTWARE: PatentIn version 3.3
SEQ ID NO 49
LENGTH: 521
TYPE: PRT
ORGANISM: Homo sapiens
US-11-152-366-49

Query Match 13.2%; Score 61.5; DB 7; Length 521;
Best Local Similarity 25.6%; Pred. No. 9.3;
Matches 20; Conservative 10; Mismatches 19; Indels 29; Gaps 3;

QY 13 EADALNYSYPGELGRIYNNHISEQAWQAMLSHOTMLINERYLSLIDP 52
DB 413 EADALNYSYPGELGRIYNNHISEQAWQAMLSHOTMLINERYLSLIDP 470

QY 53 YRLSLIDPKARQFLQEM 70
DB 471 -----PRMLKFLKTM 481

RESULT 3
US-11-072-512-3855
Sequence 3855, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO

APPLICANT: SEKI, NAOTIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3855
LENGTH: 938
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3855

Query Match 13.2%; Score 61.5; DB 7; Length 938;
Best Local Similarity 30.4%; Pred. No. 1.9;
Matches 24; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

QY 5 IICQKLGKADALNYSYPGELGRIYNNHISEQAWQAMLSHOTMLINERYLSLIDPKARQ 64
DB 453 IICD---QVSNVILIPSEAGSQT-HVS-----LPLSQVANSRSLPMSSEVSEF 499

QY 65 FLEQEMINFLFGGSEKPA 83
DB 500 FDAQEVLTLSASSSENEA 516

RESULT 4
US-11-186-731-5
Sequence 5, Application US/11186731
Publication No. US20050255521A1
GENERAL INFORMATION:

APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Acton, Susan L.
TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
TITLE OF INVENTION: Members and Uses Therefor
FILE REFERENCE: MP12001-0471RCP1(M)
CURRENT APPLICATION NUMBER: US/11/186,731
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/077,130
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/269201
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 7968
TYPE: PRT
ORGANISM: Homo sapiens
US-11-186-731-5

Query Match 13.2%; Score 61.5; DB 7; Length 7968;
Best Local Similarity 26.8%; Pred. No. 2.5e+02;
Matches 19; Conservative 16; Mismatches 11; Indels 25; Gaps 4;

QY 2 TRRIICQKLGKADALNYSYPGELGRIYNNHISEQAWQAMLSHOTMLINERYLSLIDPK 61
DB 1220 TRRLVQVQVK-ADAGYSCGAG--GQRV-----SFQHLITEPK 1255

QY 62 AROFLQEMIN 72
DB 1256 A-VFAKQQLVA 1265

RESULT 5
US-10-981-873-29

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 73.9696 seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502a-34

Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFRGKDVHLEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21.*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*
9: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	100.0	91	5	ABB78161 Amino aci
2	488	100.0	91	5	ABB78159 Amino aci
3	488	100.0	91	5	ABB78162 Amino aci
4	472	97.1	91	5	ABB78163 Amino aci
5	472	96.7	88	5	ABB78160 Amino aci
6	469	96.1	91	5	ABB78158 Amino aci
7	469	96.1	91	5	ABB78157 Amino aci
8	469	96.1	91	5	ABB78156 Amino aci
9	445	91.2	107	7	ABO65445 Kiebsiell
10	393	80.5	90	5	ABB78165 Amino aci
11	389	79.7	90	5	ABB78155 Amino aci
12	389	79.1	78	5	ABB78164 Amino aci
13	385	78.9	87	5	ABB78152 Amino aci
14	383	78.5	91	5	ABB78150 Amino aci
15	383	78.5	93	7	ADP05158 Bacteri
16	377	77.3	87	5	ABB78151 Amino aci
17	371	76.0	87	5	ABB78153 Amino aci
18	336	68.9	88	5	ABB78154 Amino aci
19	259	53.1	76	5	ABB78166 Amino aci
20	249	51.0	87	5	ABB78148 Amino aci
21	249	51.0	87	5	ABB78147 Amino aci
22	235	48.2	86	5	ABB78149 Amino aci
23	228	46.7	87	5	ABB78170 Amino aci
24	228	46.7	122	7	ABO74609 Pseudomon

ALIGNMENTS

25	224.5	46.0	89	9	ABB41576	Aeb41576 L. pneumo
26	224.5	46.0	90	9	ABB38294	Aeb38294 L. pneumo
27	222.5	45.6	95	5	ABB78167	Abb78167 Amino aci
28	222	45.5	90	5	ABB78168	Abb78168 Amino aci
29	218	44.7	87	5	ABB78169	Abb78169 Amino aci
30	218	44.7	88	5	ABB78178	Abb78178 Amino aci
31	211	43.2	88	5	ABB78171	Abb78171 Amino aci
32	211	43.2	88	5	ABB78172	Abb78172 Amino aci
33	211	43.2	88	5	ABB78173	Abb78173 Amino aci
34	211	43.2	88	5	ABB77219	Abb77219 N. gonorr
35	206	42.2	87	5	ABB78175	Abb78175 Amino aci
36	200	41.0	87	5	ABB78174	Abb78174 Amino aci
37	197	40.4	87	5	ABB78176	Abb78176 Amino aci
38	195.5	40.1	92	6	ADJ34169	Ada34169 Acinetoba
39	195	40.0	87	5	ABB78177	Abb78177 Amino aci
40	130	26.6	110	8	ADP05173	Adp05173 M. catarr
41	77	15.8	1647	8	ABG10750	Abg10750 Novel hum
42	72	14.8	309	8	ADN46828	Adn46828 Thermococ
43	72	14.8	506	6	AAV74371	Aav74371 Neisseria
44	72	14.8	507	6	ABU40210	Abu40210 Protein e
45	71.5	14.7	184	3	ABJ16290	Abj16290 Rat N-ace
46	71	14.5	447	2	AAR52657	Aar52657 Rat N-ace
47	71	14.5	447	7	ADJ55944	Adj55944 Rat Prote
48	71	14.5	507	3	AAV74372	Aav74372 Neisseria
49	71	14.5	507	3	AAV74373	Aav74373 Neisseria
50	71	14.5	546	6	ABU38097	Abu38097 Protein e
51	71	14.5	548	6	AAR04737	Aar04737 Bruglia ma
52	70.5	14.4	184	4	AAE16325	Aae16325 Pinus rad
53	70.5	14.4	184	4	AAE65734	Aae65734 Amexin-1
54	70.5	14.4	184	7	ADB94702	Adb94702 Programme
55	70.5	14.4	593	4	ABG19947	Abg19947 Novel hum
56	70	14.3	257	3	AAJ31203	Aaj31203 Arabidops
57	70	14.3	297	3	AAJ31202	Aaj31202 Arabidops
58	70	14.3	324	3	AAJ31201	Aaj31201 Arabidops
59	70	14.3	758	9	ADW71760	Adw71760 Salmonell
60	69.5	14.2	227	3	AAJ38052	Aaj38052 Arabidops
61	69.5	14.2	1377	8	ADV81847	Adv81847 Streptoco
62	69.5	14.2	1387	8	ADV88434	Adv88434 Streptoco
63	69.5	14.2	1387	8	ADV79687	Adv79687 Streptoco
64	69	14.1	503	4	ABG16577	Abg16577 Novel hum
65	69	14.1	679	9	ADJ85056	Adj85056 Partial F
66	68.5	14.0	608	5	ABP73745	Abp73745 Candida a
67	68.5	14.0	632	8	ADS29711	Ads29711 Bacteri
68	68	13.9	239	8	ADP07537	Adp07537 Human col
69	68	13.9	280	5	AAJ54294	Aaj54294 Amino aci
70	68	13.9	280	5	ABG93805	Abg93805 Lactuca s
71	68	13.9	280	8	ADJ50292	Adj50292 Oll -asoc
72	68	13.9	285	4	AAJ92683	Aaj92683 Human pro
73	68	13.9	302	4	AAJ88379	Aaj88379 Human mem
74	68	13.9	302	9	ADJ63123	Adj63123 Human cto
75	68	13.9	414	6	ABU11747	Abu11747 Human MDP

RESULT 1
ABB78161
ID ABB78161 standard; protein; 91 AA.

AC ABB78161; 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;

KV hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

XX US2002072118-A1.

PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnicks JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgX homologues
 SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.3e-49;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTFCTYLORDAEGDQFOLYPGELGKRIYNEISKDAWAQOMHKQTLINKEKLNMANNA 60
 DB 1 MSRTFCTYLORDAEGDQFOLYPGELGKRIYNEISKDAWAQOMHKQTLINKEKLNMANNA 60

QY 61 EHRKLLBQEMVSPLEFGKDVHIEGYTPEDKK 91
 DB 61 EHRKLLBQEMVSPLEFGKDVHIEGYTPEDKK 91

RESULT 2
 ABB78159 standard; protein; 91 AA.

AC ABB78159;
 XX

DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgX homologue.

DE Superoxide damage; cell; YgX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YgX homologue.
 XX

OS Unidentified.
 XX

PN US2002072118-A1.
 XX

PD 13-JUN-2002.
 XX

PF 18-SEP-2001; 2001US-00955502.
 XX

PR 22-SEP-2000; 2000US-0234588P.
 XX

PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnicks JA;
 XX

DR WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgX homologues
 SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.3e-49;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTFCTYLORDAEGDQFOLYPGELGKRIYNEISKDAWAQOMHKQTLINKEKLNMANNA 60
 DB 1 MSRTFCTYLORDAEGDQFOLYPGELGKRIYNEISKDAWAQOMHKQTLINKEKLNMANNA 60

QY 61 EHRKLLBQEMVSPLEFGKDVHIEGYTPEDKK 91
 DB 61 EHRKLLBQEMVSPLEFGKDVHIEGYTPEDKK 91

RESULT 3
 ABB78162 standard; protein; 91 AA.

AC ABB78162;
 XX

DT 05-NOV-2002 (first entry)
 XX

DE Amino acid sequence of a YgX homologue.

DE Superoxide damage; cell; YgX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YgX homologue.
 XX

OS *Salmonella* typhi.
 XX

PN US2002072118-A1.
 XX

PD 13-JUN-2002.
 XX

PF 18-SEP-2001; 2001US-00955502.
 XX

PR 22-SEP-2000; 2000US-0234588P.
 XX

PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnicks JA;
 XX

DR WPI; 2002-589476/63.
 XX

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX

PS Example; Fig 1A; 16pp; English.
 XX

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgX protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21, Search time 9.84893 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502a-34

Perfect score: 488
Sequence: 1 MSRTTCTTYLQPDAGQDPQ.....SFLPEGKDVHIEGTTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	100.0	91	2 AH0879	conserved hypothet
2	469	96.1	91	2 AB5954	hypothetical prote
3	469	96.1	91	2 AB5082	hypothetical prote
4	469	96.1	91	2 F91108	hypothetical prote
5	393	80.5	90	2 A10116	conserved hypothet
6	389	79.7	90	2 C82320	conserved hypothet
7	385	78.9	90	2 C64013	hypothetical prote
8	259	53.1	93	2 B84994	hypothetical prote
9	232	47.5	105	2 C82624	conserved hypothet
10	228	46.7	90	2 H83003	conserved hypothet
11	211	43.2	88	2 H81014	conserved hypothet
12	179.5	16.3	1638	2 D87749	protein unc-73b [i
13	79.5	16.3	2488	2 T42739	guanine nucleotide
14	78	16.0	1260	2 T04440	hypothetical prote
15	73.5	15.1	495	2 AH0985	probable zinc-prot
16	71.5	14.7	209	2 J64172	hypothetical prote
17	71	14.5	447	2 JC2076	alpha-1,3-mannosyl
18	71	14.5	507	2 C81063	funarate hydratase
19	71	14.5	546	2 AB1807	funarate hydratase
20	70	14.5	548	2 AB5510	63k antigen - nema
21	70	14.3	324	2 T05429	hypothetical prote
22	70	14.3	758	2 AD0763	thiosulfate reduct
23	69.5	14.3	859	2 AS7143	thiosulfate-dithio
24	69.5	14.2	859	2 T29630	hypothetical prote
25	69	14.1	265	2 T46013	hypothetical prote
26	69	14.1	447	2 T15527	hypothetical prote
27	68.5	14.0	683	2 AC2256	hypothetical prote
28	68	13.9	445	1 XDHUMB	alpha-1,3-mannosyl
29	68	13.9	689	2 F83902	beta-galactosidase

30	67.5	13.8	166	2 F70562	hypothetical prote
31	67	13.7	447	1 A38561	alpha-1,3-mannosyl
32	67	13.7	1111	2 T23047	hypothetical prote
33	66.5	13.6	410	1 KEMSD	cathepsin D (EC 3.
34	66	13.5	447	1 A42500	alpha-1,3-mannosyl
35	66	13.5	703	2 B82148	ATP-dependent heli
36	66	13.5	1085	2 B82148	hypothetical colle
37	65.5	13.4	287	2 F82265	conserved hypothet
38	65.5	13.4	365	2 B54128	PC-binding hypothet
39	65	13.3	433	2 A70465	probable GTP bindi
40	65	13.3	507	2 AB3105	probable fumarate
41	65	13.3	511	2 AB9574	ABC transporter at
42	65	13.3	593	2 C64097	probable soluble l
43	65	13.3	1230	2 S56850	SMC1 protein homol
44	64.5	13.2	327	2 AD2129	transcription regu
45	64.5	13.2	385	2 D87723	hypothetical prote
46	64.5	13.2	401	2 AE1978	hypothetical prote
47	64.5	13.2	544	2 T40058	probable chromatin
48	64.5	13.2	1197	2 S26947	DNA-directed DNA p
49	64	13.1	251	2 B90428	hypothetical prote
50	64	13.1	548	2 A28209	60k filarial antig
51	64	13.1	643	2 A43647	parasporeal crystal
52	63.5	13.0	379	2 S70709	type II site-speci
53	63.5	13.0	438	2 T37786	probable RNA-bindi
54	63.5	13.0	2672	2 A48126	translational activa
55	63	12.9	205	2 C26135	keratin, 50K type
56	63	12.9	235	2 G65212	hypothetical prote
57	63	12.9	258	2 AB7991	hypothetical prote
58	63	12.9	258	2 B5121	phosphoesterase, p
59	63	12.9	483	2 G64799	yeav protein - Bsc
60	63	12.9	543	2 T16016	hypothetical prote
61	63	12.9	549	2 T16016	hypothetical prote
62	63	12.9	1119	2 T15842	hypothetical prote
63	63	12.9	1166	2 H71609	hypothetical prote
64	63	12.9	1209	2 T46027	hypothetical prote
65	63	12.9	1327	2 T14594	guanine nucleoti
66	63	12.9	1572	2 S45251	SNF2alpha protei
67	63	12.9	1586	2 S39580	HBM protein - hum
68	62.5	12.8	165	2 AB1382	shikimate kinase (
69	62.5	12.8	259	2 C83203	conserved hypothet
70	62.5	12.8	305	2 A75211	asparaginase (EC 3
71	62.5	12.8	375	2 T37245	GTP-binding regula
72	62.5	12.8	498	2 G91179	hypothetical prote
73	62.5	12.8	498	2 H86025	hypothetical prote
74	62.5	12.8	498	2 S47748	53.1k protein prec
75	62.5	12.8	629	2 B83107	chemotactic transd

ALIGNMENTS

RESULT 1

Conserved hypothetical protein STY3266 [imported] - *Salmonella enterica* subsp. *enterica*
C/Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

A/Note: this species has also been called *Salmonella typhi*
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004

C/Accession: AH0879
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AH0879

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-91 <PAR>

A/Cross-references: UNIPARC:UP100000544C; GB:AL513382; PTDN:CADO2936.1; PTD:gl6504189;

A/Genetics: C/Genetics: A/Gene: STY3266

C/Superfamily: Fe(II) trafficking protein YggX

Query Match 100.0%; Score 488; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.1e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60
1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91
61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91

Db 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 2
A:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
Hiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ysgX
C:Superfamily: fe(II) trafficking protein YsgX

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60
1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91
61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91

Db 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 3
A:Species: Escherichia coli (strain K-12)
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65082
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:G
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein YsgX

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60
1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60
1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91
61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91

Db 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 4
A:Species: Escherichia coli (strain O157:H7, substrain R11
P1108
hypoetical protein EC63838 [imported]
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C:Accession: F91108
R:Hayashi, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <HAY>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA837261.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: EC63838
C:Superfamily: fe(II) trafficking protein YsgX

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60
1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91
61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91

Db 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 5
A:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: A10116
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
H., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A10116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <KUR>
A:Cross-references: UNIPARC:UPI00000DCC4; GB:A1590842; PIDN:CAC69796.1; PID:g15979022;
C:Genetics:
A:Gene: YPO0953
C:Superfamily: fe(II) trafficking protein YsgX

Query Match 80.5%; Score 393; DB 2; Length 90;
Best Local Similarity 81.1%; Pred. No. 8.1e-33;
Matches 73; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60
1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDABEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 90
61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 90

Db 61 EHRKLLBQEMVSLFPEGKDVHIEGYTPEDKK 90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 66.1725 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502a-34

Perfect score: 488
Sequence: 1 MSRTIFCTYLQDAEGQDFQ.....SFLFKGVHIEGYTPDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	99.0	90	1	PERP_SALCH
2	483	99.0	90	1	PERP_SALPA
3	483	99.0	90	1	PERP_SALTI
4	483	99.0	90	1	PERP_SALTY
5	464	95.1	90	1	PERP_ECOLI
6	464	95.1	90	1	PERP_ECOLI
7	464	95.1	90	1	PERP_ECOLI
8	460	94.3	90	1	PERP_ECOLI
9	416	85.2	90	1	PERP_ECOLI
10	401	82.2	90	1	PERP_ECOLI
11	393	80.5	90	1	PERP_ECOLI
12	393	80.5	90	1	PERP_ECOLI
13	389	79.7	90	1	PERP_ECOLI
14	389	79.7	90	1	PERP_ECOLI
15	389	79.7	90	1	PERP_ECOLI
16	387	79.3	90	1	PERP_ECOLI
17	385	78.9	90	1	PERP_ECOLI
18	385	78.9	90	1	PERP_ECOLI
19	383	78.5	90	1	PERP_ECOLI
20	377	77.3	90	1	PERP_ECOLI
21	376	77.0	90	1	PERP_ECOLI
22	371	76.0	90	1	PERP_ECOLI
23	365	74.8	90	1	PERP_ECOLI
24	341	69.9	90	1	PERP_ECOLI
25	336	68.9	90	1	PERP_ECOLI
26	259	53.1	90	1	PERP_ECOLI
27	249	51.0	90	1	PERP_ECOLI
28	249	51.0	90	1	PERP_ECOLI
29	249	51.0	90	1	PERP_ECOLI
30	243	49.8	90	1	PERP_ECOLI
31	239	49.0	90	1	PERP_ECOLI

32	232	47.5	90	1	PERP_XYTRA	09pC73 xylella fas
33	232	47.5	90	1	PERP_XANOR	05gY22 xanthomonas
34	228.5	46.8	89	1	PERP_LEGPL	05wvc4 legionella
35	228	46.7	90	1	PERP_PSEAF	09nu36 pseudomonas
36	228	46.7	90	1	PERP_XYLEF	087d06 xylella fas
37	228	46.7	90	1	PERP_XANCP	08p829 xanthomonas
38	228	46.7	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
39	225	46.1	78	1	PERP_WIGBR	08d3c5 wiglesworth
40	224.5	46.0	89	1	PERP_LEGPA	05x380 legionella
41	224.5	46.0	89	1	PERP_NITRU	082x62 nitrosomona
42	222	45.5	90	1	PERP_PSEBM	087lf5 pseudomonas
43	222	45.5	90	1	Q4ZLP3_PSEBSY	Q4ZLP3 pseudomonas
44	222	45.5	90	2	PERP_COXBU	083d06 coxiella bu
45	218	44.7	90	1	PERP_PSEBK	043228 azotobacter
46	218	44.7	90	1	Q4J228_AZOVI	Q4J228 azotobacter
47	218	44.7	90	2	Q6Y7F6_PSEFL	Q6Y7F6 pseudomonas
48	215	44.1	90	1	PERP_CHROO	07n84 chromobacter
49	213	43.6	90	1	PERP_CANBR	07v39 candidatus
50	212	43.2	88	1	PERP_NEIGI	05f553 neisseria g
51	211	43.2	88	1	PERP_NEIMA	05f553 neisseria m
52	211	43.2	88	1	PERP_NEIMA	05f553 neisseria m
53	211	43.2	88	1	PERP_NEIMA	05f553 neisseria m
54	207	42.4	87	1	PERP_BURPA	089a44 buchnera ap
55	206	42.2	91	1	PERP_BURPA	0621p3 burkholderi
56	206	42.2	91	1	PERP_BURPA	0621p3 burkholderi
57	205	42.0	90	2	Q4KJ22_PSEBF5	Q4KJ22 pseudomonas
58	205	42.0	90	1	PERP_RALSO	08y010 ralstonia s
59	203	41.6	91	2	Q4LS19_9BURK	Q4LS19 burkholderi
60	195	40.0	90	1	PERP_METCA	060a17 methylococc
61	192	39.3	87	1	PERP_FRATT	05nuj8 francisella
62	190.5	39.0	90	1	PERP_ACIDN	04f713 psychrobact
63	146	29.9	96	2	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
64	145	29.7	92	2	Q4NMQ4_9DELT	Q4NMQ4 anaeromyxob
65	82.5	16.9	482	2	Q5NUY1_9BURK	Q5NUY1 ralstonia m
66	82.5	16.9	514	2	Q6A1Z9_DSPPS	Q6A1Z9 desulfoale
67	79.5	16.3	1638	2	Q7KPP4_CAEEL	Q7KPP4 caenorhabdi
68	79.5	16.3	2140	2	Q6BEM2_CAEEL	Q6BEM2 caenorhabdi
69	79.5	16.3	2488	2	Q6L528_CAEEL	Q6L528 caenorhabdi
70	78.5	16.1	337	2	Q81A88_BACCR	Q81A88 bacillus ce
71	78	16.0	1260	2	Q49677_ARATH	Q49677 arabidopsis
72	77.5	15.9	1047	2	Q5CJ53_CRYHO	Q5CJ53 cryptospori
73	76.5	15.7	486	2	Q7WX51_ALCEU	Q7WX51 alcaligenes
74	75.5	15.5	1278	2	Q5CYM7_CRYPV	Q5CYM7 cryptospori
75	75	15.4	385	2	Q734A2_BACCI	Q734A2 bacillus ce

ALIGNMENTS

RESULT 1
ID PERP_SALCH STANDARD; PRT; 90 AA.
AC Q57K04;
DT 13-SEP-2005 (Rel. 48; Created)
DT 13-SEP-2005 (Rel. 48; Last sequence update)
DE Probable Fe(2+) trafficking protein.
GN Name=ygkx; Ordered locus names=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_Taxid=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gk1297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
RT "The genome sequence of *Salmonella enterica* serovar *Choleraesuis*, a
highly invasive and resistant zoonotic pathogen."
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-regulating processes, such as synthesis and/or

```

CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB017220; AAX66958.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Prodom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT_MET 0
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1BE2255E3C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTYLQDASGDFQLYPGELGKRIYNEISKDAAQWQHQTMLINEKLNMMNAE 61
DB 1 SRTIFCTYLQDASGDFQLYPGELGKRIYNEISKDAAQWQHQTMLINEKLNMMNAE 60
QY 62 HRKLEQEMVSLFPGKOVHIEGYTPEDCK 91
DB 61 HRKLEQEMVSLFPGKOVHIEGYTPEDCK 90

RESULT 2
PEPT_SALPA STANDARD; PRT; 90 AA.
ID Q5PMW1;
AC 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gx; OrderedLocustNames=SP2974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_Taxid=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozeraky P., McCellan M.,
RA Hartline C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Mink P.,
RA Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Flores L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
DR SMR; Q5PMW1; 1-91.
DR HAMAP; MF_00686; -; 1.

```

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DR InterPro; IPR007457; Y9GX.
DR Prodom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT INIT_MET 0
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1BE2255E3C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTYLQDASGDFQLYPGELGKRIYNEISKDAAQWQHQTMLINEKLNMMNAE 61
DB 1 SRTIFCTYLQDASGDFQLYPGELGKRIYNEISKDAAQWQHQTMLINEKLNMMNAE 60
QY 62 HRKLEQEMVSLFPGKOVHIEGYTPEDCK 91
DB 61 HRKLEQEMVSLFPGKOVHIEGYTPEDCK 90

RESULT 3
PEPT_SALTI STANDARD; PRT; 90 AA.
ID P67618; O8XFW6;
AC P67618; O8XFW6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gx; OrderedLocustNames=STY3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_Taxid=601;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parthill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Iyou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blatner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
DR EMBL; AB016844; AAO70576.1; -; Genomic_DNA.
DR SMR; P67618; 1-90.
DR HAMAP; MF_00686; -; 1.

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 18.2616 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502a-34

Perfect score: 488

Sequence: 1 MSRTTFCYTLQRDAEGQDFQ.....SFLFGKGVHIGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5-COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/6-COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/7-COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/8-COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/9-COMB.pep.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	71	14.5	548	2	US-09-167-299-3
7	70.5	14.4	184	2	US-09-325-932A-66
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9	68	13.9	280	2	US-09-323-998E-37
10	68	13.9	337	2	US-09-270-767-41746
11	68	13.9	1214	2	US-10-164-595-24
12	66.5	13.6	325	2	US-09-134-000C-4346
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21	65.5	13.4	546	2	US-08-798-841-2
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23	65.5	13.4	982	2	US-09-565-501A-95
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49	62	12.7	448	2	US-09-270-767-42959	Sequence 42959, A
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US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709 20040001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using SW model

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Title: US-09-955-502A-34

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Scoring table: BLOSUM62
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Minimum DB seq length: 0
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
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SUMMARIES

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6	469	96.1	91	US-09-955-502-11	Sequence 11, Appl
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16	336	68.9	88	US-09-955-502-9	Sequence 9, Appl
17	259	53.1	76	US-09-955-502-21	Sequence 21, Appl
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21	232	47.5	89	US-09-955-502-22	Sequence 22, Appl
22	228	46.7	87	US-09-955-502-25	Sequence 25, Appl
23	222	45.5	90	US-09-955-502-23	Sequence 23, Appl
24	218	44.7	87	US-09-955-502-24	Sequence 24, Appl
25	218	44.7	88	US-09-955-502-33	Sequence 33, Appl
26	211	43.2	88	US-09-955-502-26	Sequence 26, Appl
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43	69	14.1	679	US-10-805-684-105	Sequence 105, Appl
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49	68	13.9	445	US-10-844-874-14	Sequence 14, Appl
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69	66	13.5	459	US-10-087-192-375	Sequence 375, Appl
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ALIGNMENTS

RESULT 1
US-09-955-502-14
Sequence 14, Application US/09955502
Parent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 91
TYPE: PRT
ORGANISM: Salmonella paratyphi

US-09-955-502-14

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Best Local Similarity 100.0%; Pred. No. 6.8e-49;
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Qy 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91
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RESULT 2
US-09-955-502-16

; Sequence 16, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 16

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella dublin

US-09-955-502-16

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RESULT 3
US-09-955-502-17

; Sequence 17, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 17

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella typhi CT18

US-09-955-502-17

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Db 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 4
US-09-955-502-18

; Sequence 18, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 18

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella typhimurium

US-09-955-502-18

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Qy 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 5
US-09-955-502-15

; Sequence 15, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 15

; LENGTH: 88

; TYPE: PRT

; ORGANISM: Salmonella enteritidis

US-09-955-502-15

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Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
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Title: US-09-955-502a-34

Perfect score: 488
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Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22	58.5	12.0	749	US-11-098-686-10505	Sequence 10505, App
23	58.5	12.0	782	US-10-793-626-2352	Sequence 2352, App
24	58.5	12.0	782	US-10-793-626-2352	Sequence 25, App1
25	58	11.9	448	US-10-618-320A-25	

26	58	11.9	480	US-10-510-386-12	Sequence 12, App1
27	58	11.9	1501	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.8	242	US-11-023-562-220	Sequence 220, App
29	57.5	11.8	336	US-10-453-372-640	Sequence 640, App
30	57.5	11.8	577	US-11-072-175-187	Sequence 187, App
31	57.5	11.8	752	US-11-072-512-3003	Sequence 3003, App
32	57.5	11.8	775	US-10-453-372-656	Sequence 656, App
33	57.5	11.8	793	US-10-995-561-925	Sequence 925, App
34	57.5	11.8	804	US-10-453-372-650	Sequence 650, App
35	57.5	11.8	847	US-10-453-372-654	Sequence 654, App
36	57.5	11.8	857	US-10-453-372-652	Sequence 652, App
37	57.5	11.8	905	US-10-453-372-658	Sequence 633, App
38	57.5	11.8	905	US-10-453-372-662	Sequence 662, App
39	57.5	11.8	905	US-10-453-372-664	Sequence 664, App
40	57.5	11.8	963	US-10-995-561-923	Sequence 923, App
41	57.5	11.8	963	US-10-453-372-660	Sequence 660, App
42	57.5	11.8	1012	US-10-453-372-666	Sequence 646, App
43	57.5	11.8	3803	US-10-995-561-773	Sequence 773, App
44	57.5	11.8	3960	US-10-995-561-771	Sequence 771, App
45	57.5	11.8	5335	US-10-995-561-777	Sequence 779, App
46	57.5	11.8	5406	US-10-995-561-774	Sequence 779, App
47	57.5	11.8	5415	US-10-995-561-779	Sequence 779, App
48	57.5	11.8	5464	US-10-995-561-775	Sequence 779, App
49	57.5	11.8	5935	US-10-995-561-776	Sequence 779, App
50	57	11.7	234	US-10-524-972-120	Sequence 120, App
51	57	11.7	234	US-10-821-234-1463	Sequence 1463, App
52	57	11.7	432	US-11-072-512-3856	Sequence 3856, App
53	57	11.7	440	US-11-000-463-722	Sequence 722, App
54	56.5	11.6	1254	US-10-528-031-47	Sequence 47, App1
55	56.5	11.6	1897	US-10-821-234-1635	Sequence 1635, App
56	56.5	11.6	1907	US-11-000-463-250	Sequence 250, App
57	56.5	11.6	3433	US-10-714-781A-67	Sequence 67, App1
58	56	11.5	206	US-11-124-367A-316	Sequence 316, App
59	55.5	11.4	136	US-10-793-626-580	Sequence 580, App
60	55.5	11.4	279	US-11-098-686-10812	Sequence 10812, App
61	55.5	11.4	1188	US-11-115-639-42	Sequence 42, App1
62	55.5	11.4	1188	US-11-115-639-43	Sequence 43, App1
63	55.5	11.4	189	US-11-071-262-1	Sequence 1, App1
64	55	11.3	667	US-10-793-626-198	Sequence 198, App
65	55	11.3	692	US-11-038-284-33	Sequence 33, App1
66	55	11.3	783	US-11-037-243-67	Sequence 67, App1
67	55	11.3	873	US-11-038-284-35	Sequence 35, App1
68	55	11.3	889	US-11-038-284-15	Sequence 15, App1
69	55	11.3	1142	US-11-109-156-22	Sequence 22, App1
70	55	11.3	2665	US-11-124-368A-214	Sequence 214, App
71	55	11.3	317	US-11-124-368A-215	Sequence 215, App
72	55	11.2	450	US-10-523-503-74	Sequence 74, App1
73	54.5	11.2	6	US-10-618-320A-26	Sequence 26, App1
74	54.5	11.2	496	US-11-069-642-20	Sequence 20, App1
75	54.5	11.2			

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTRANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 / Search time 73.9696 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502a-35

Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFKGVHLEGYTPDKK 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database: A_Geneseq_21:*

1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*
9: geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	100.0	91	5	ABE78161 Amino aci
2	488	100.0	91	5	ABE78159 Amino aci
3	488	100.0	91	5	ABE78162 Amino aci
4	474	97.1	91	5	ABE78163 Amino aci
5	472	96.7	88	5	ABE78160 Amino aci
6	469	96.1	91	5	ABE78158 Amino aci
7	469	96.1	91	5	ABE78157 Amino aci
8	469	96.1	91	5	ABE78156 Amino aci
9	445	91.2	107	7	ABO65445 Amino aci
10	393	80.5	90	5	ABE78165 Amino aci
11	389	79.7	90	5	ABE78155 Amino aci
12	386	79.1	78	5	ABE78164 Amino aci
13	385	78.9	87	5	ABE78152 Amino aci
14	383	78.5	91	5	ABE78150 Amino aci
15	383	78.5	93	7	ADP05158 Bacterial
16	377	77.3	87	5	ABE78151 Amino aci
17	371	76.0	87	5	ABE78153 Amino aci
18	336	68.9	88	5	ABE78154 Amino aci
19	259	53.1	76	5	ABE78166 Amino aci
20	249	51.0	87	5	ABE78148 Amino aci
21	249	51.0	87	5	ABE78147 Amino aci
22	235	48.2	86	5	ABE78149 Amino aci
23	228	46.7	87	5	ABE78170 Amino aci
24	228	46.7	122	7	ABO74609 Pseudomon

25	224.5	46.0	89	9	ABE41576	Abd41576 L. pneumo
26	224.5	46.0	95	9	ABE38294	Abd38294 L. pneumo
27	222.5	45.6	90	5	ABE78167	Abd78167 Amino aci
28	222	45.5	90	5	ABE78168	Abd78168 Amino aci
29	218	44.7	87	5	ABE78169	Abd78169 Amino aci
30	218	44.7	88	5	ABE78178	Abd78178 Amino aci
31	211	43.2	88	5	ABE78171	Abd78171 Amino aci
32	211	43.2	88	5	ABE78172	Abd78172 Amino aci
33	211	43.2	88	5	ABE78173	Abd78173 Amino aci
34	211	43.2	88	5	ABE77219	Abp77219 N. gonorr
35	206	42.2	87	5	ABE78175	Abd78175 Amino aci
36	200	41.0	87	5	ABE78174	Abd78174 Amino aci
37	197	40.4	87	5	ABE78176	Abd78176 Amino aci
38	195.5	40.1	92	5	ADA34169	Ada34169 Acinetoba
39	195	40.0	87	5	ABE78177	Abd78177 Amino aci
40	130	26.6	110	8	ADP05173	Adp05173 M. catarr
41	77	15.8	1647	4	ABG10750	Abg10750 Novel hum
42	72	14.8	309	8	ADN46828	Adn46828 Thermococ
43	72	14.8	506	3	AAV74371	AAV74371 Neisseria
44	72	14.8	507	6	ABU40210	Abu40210 Protein e
45	71.5	14.7	184	3	AAH16290	AAH16290 Pirus rad
46	71	14.5	447	2	AAE52657	AAE52657 Rat N-ace
47	71	14.5	447	7	AAE55944	AAE55944 Rat Prote
48	71	14.5	507	3	AAV74372	AAV74372 Neisseria
49	71	14.5	507	3	AAV74373	AAV74373 Neisseria
50	71	14.5	546	6	ABU38097	Abu38097 Protein e
51	71	14.5	546	6	AAE04737	AAE04737 Brugia ma
52	70.5	14.4	184	4	AAH16325	AAH16325 Pirus rad
53	70.5	14.4	184	4	AAH65734	AAH65734 Annexin-I
54	70.5	14.4	184	7	ADB94702	ADB94702 Programme
55	70.5	14.4	593	4	ABG19947	Abg19947 Novel hum
56	70	14.3	257	3	AAH31203	AAH31203 Arabidops
57	70	14.3	297	3	AAH31202	AAH31202 Arabidops
58	70	14.3	324	3	AAH31201	AAH31201 Arabidops
59	69.5	14.2	758	9	ADW71760	Adw71760 Salmonell
60	69.5	14.2	227	3	AAH38052	AAH38052 Arabidops
61	69.5	14.2	1377	8	ADH81847	Adh81847 Streptoco
62	69.5	14.2	1387	8	ADH88434	Adh88434 Streptoco
63	69.5	14.2	1387	8	ADH79687	Adh79687 Streptoco
64	69	14.1	503	4	ABG16577	Abg16577 Novel hum
65	69	14.1	679	9	ADH85056	Adh85056 Partial F
66	68.5	14.0	608	5	ABP73745	Abp73745 Candida a
67	68.5	14.0	632	8	ADS29711	Ads29711 Bacterial
68	68	13.9	239	8	ADT07537	Adt07537 Human col
69	68	13.9	280	3	AAH54294	AAH54294 Amino aci
70	68	13.9	280	5	ABG93505	Abg93505 Lactuca s
71	68	13.9	280	8	ADJ50292	Adj50292 Oil - asoc
72	68	13.9	285	4	AAH92683	AAH92683 Human pro
73	68	13.9	302	4	AAH88379	AAH88379 Human mem
74	68	13.9	302	9	ADY63123	Ady63123 Human cto
75	68	13.9	414	6	ABU11747	Abu11747 Human MDD

ALIGNMENTS

RESULT 1	ABE78161	standard; protein; 91 AA.
ID	ABE78161	
XX	ABE78161;	
AC	05-NOV-2002	(first entry)
DT		
XX		
DR		Amino acid sequence of a YggX homologue.
XX		
KV		Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX		hydroxyl radical; DNA damage; YggX homologue.
OS		Unidentified.
XX		
PN		
XX		US2002072118-A1.

PD 13-JUN-2002.
 XX 18-SEP-2001; 2001US-00955502.
 PF 22-SEP-2000; 2000US-0234588P.
 PR
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 PI Downs D, Gralnick JA;
 XX WPI, 2002-589476/63.
 DR
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgX protein, a
 PR protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgX homologues
 XX
 SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.3e-49;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTFCYTLORDAEGODPOLYPGELGKRIYNEISKDAMAOHOKQTMLINEKLNMMNA 60
 DB 1 MSRTTFCYTLORDAEGODPOLYPGELGKRIYNEISKDAMAOHOKQTMLINEKLNMMNA 60
 QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91
 DB 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 2
 ABB78159
 ID ABB78159 standard; protein; 91 AA.
 XX
 AC ABB78159;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgX homologue.
 XX
 DE Superoxide damage; cell; YgX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YgX homologue.
 XX
 OS Unidentified.
 OS
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 PD
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX

XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 PI Downs D, Gralnick JA;
 XX

DR WPI, 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgX protein, a
 PR protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgX homologues
 XX

SQ Sequence 91 AA;
 Query Match 100.0%; Score 488; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.3e-49;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTFCYTLORDAEGODPOLYPGELGKRIYNEISKDAMAOHOKQTMLINEKLNMMNA 60
 DB 1 MSRTTFCYTLORDAEGODPOLYPGELGKRIYNEISKDAMAOHOKQTMLINEKLNMMNA 60
 QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91
 DB 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 3
 ABB78162
 ID ABB78162 standard; protein; 91 AA.
 XX
 AC ABB78162;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgX homologue.
 XX
 DE Superoxide damage; cell; YgX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YgX homologue.
 XX
 OS *Salmonella* typhi.
 OS
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 PD
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX

XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 PI Downs D, Gralnick JA;
 XX
 DR WPI, 2002-589476/63.
 DR

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgX protein (a protein identified from *Salmonella*

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.84893 Seconds
(without alignments)

889.003 Million cell updates/sec

Title: US-09-955-502A-35

Perfect score: 1 MSRTICTYVIGRDASGDDFQ.....SFLFEKGVHIEGYTPEDRK 91

Sequence:

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR 80.*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	100.0	91	2	AH0879 conserved hypotet
2	469	96.1	91	2	A85954 hypothetical prote
3	469	96.1	91	2	A65082 hypothetical prote
4	469	96.1	91	2	F91108 hypothetical prote
5	393	80.5	90	2	A10116 conserved hypotet
6	389	79.7	90	2	C82320 conserved hypotet
7	385	78.9	90	2	C64013 hypothetical prote
8	259	53.1	93	2	E84994 hypothetical prote
9	232	47.5	105	2	C82624 conserved hypotet
10	228	46.7	90	2	H83003 conserved hypotet
11	211	43.2	88	2	H81014 conserved hypotet
12	79.5	16.3	1638	2	D87749 protein unc-73b (i
13	79.5	16.3	2468	2	T42739 guanine nucleotide
14	78	16.0	1260	2	T04440 hypothetical prote
15	73.5	15.1	495	2	AH0985 probable zinc-prot
16	71.5	14.7	209	2	I64172 hypothetical prote
17	71	14.5	447	2	JC2076 alpha-1,3-mannosyl
18	71	14.5	507	2	C81063 fumarate hydratase
19	71	14.5	546	2	A81807 fumarate hydratase
20	71	14.5	548	2	A54510 63K antigen - nema
21	70	14.3	324	2	T05429 chitosulfate reduct
22	70	14.3	758	2	AD0763 chitosulfate reduct
23	70	14.3	758	2	A57143 thiosulfate-dithio
24	69.5	14.2	859	2	T29630 hypothetical prote
25	69	14.1	265	2	T46013 hypothetical prote
26	69	14.1	447	2	T16527 hypothetical prote
27	68.5	14.0	445	1	AC2256 alpha-1,3-mannosyl
28	68	13.9	445	1	XUH0MB beta-galactosidase
29	68	13.9	689	2	F83902

30	67.5	13.8	166	2	F70562	hypothetical prote
31	67	13.7	447	1	A38561	alpha-1,3-mannosyl
32	67	13.7	1111	2	T23047	hypothetical prote
33	66.5	13.6	410	1	KHMSD	cathepsin D (BC 3)
34	66	13.5	447	1	A42500	alpha-1,3-mannosyl
35	66	13.5	703	2	B82148	ATP-dependent heli
36	66	13.5	1085	2	S62516	hypothetical coile
37	65.5	13.4	287	2	F82265	conserved hypotet
38	65.5	13.4	365	2	B54128	Fe-binding protein
39	65	13.3	433	2	A70465	probable GTP bindi
40	65	13.3	507	2	A83105	probable fumarase
41	65	13.3	511	2	A99574	ABC transporter at
42	65	13.3	593	2	C64097	probable soluble l
43	65	13.3	1230	2	S56850	SMC1 protein homol
44	64.5	13.2	327	2	AD2129	transcription regu
45	64.5	13.2	385	2	D87723	protein R06A10.2 (
46	64.5	13.2	401	2	AE1978	hypothetical prote
47	64.5	13.2	544	2	T40058	probable chromatin
48	64.5	13.2	1197	2	S26947	DNA-directed DNA p
49	64	13.1	251	2	B90428	hypothetical prote
50	64	13.1	548	2	A28209	60K filarial antig
51	64	13.1	643	2	A43647	parasporeal crystal
52	63.5	13.0	379	2	S70709	type II site-speci
53	63.5	13.0	438	2	T37786	probable RNA-bindi
54	63.5	13.0	2672	2	A48126	translation activa
55	63	12.9	205	2	C26135	keratin, 50K type
56	63	12.9	235	2	G65212	hypothetical 26.7K
57	63	12.9	258	2	A97991	hypothetical prote
58	63	12.9	258	2	E95121	hypothetical prote
59	63	12.9	483	2	G64799	phosphoserine, p
60	63	12.9	543	2	T16015	ybeV protein - Bac
61	63	12.9	549	2	T16016	hypothetical prote
62	63	12.9	1119	2	T15842	hypothetical prote
63	63	12.9	1166	2	H71609	hypothetical prote
64	63	12.9	1209	2	T46027	hypothetical prote
65	63	12.9	1327	2	T14594	guanine nucleoti
66	63	12.9	1572	2	S45251	SNF2alpha protein
67	63	12.9	1586	2	S39580	HNRN protein - hum
68	62.5	12.8	165	2	A81382	shikimate kinase (
69	62.5	12.8	259	2	G83203	conserved hypotet
70	62.5	12.8	305	2	A75211	asparaginase (BC 3
71	62.5	12.8	375	2	T37245	GTP-binding regula
72	62.5	12.8	498	2	G91179	hypothetical prote
73	62.5	12.8	498	2	H86025	hypothetical prote
74	62.5	12.8	498	2	S47748	53.1K protein prec
75	62.5	12.8	629	2	B83107	chemotactic transd

ALIGNMENTS

RESULT 1
AH0879 conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Doad, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parkhill, J.; Wain, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Doad, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:21534947; PMID:11677608
A:Accession: AH0879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 (PAR)
A:Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;
C:Genetics:
A:Gene: STY3266
C:Superfamily: fel(II) trafficking protein YggX

Query Match 100.0%; Score 488; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 2,1e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60
1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60

Qy 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91
61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91

Db 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91

RESULT 2
A65954
hypothetical protein y9gx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A65954
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, R.J.; Davis, N.W.; Lam, A.; Dinalanta, E.; Potamouais, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A65480; MUID:21074935; PMID:11206551
A/Accession: A65954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <ENO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: Y9GX
A/Superfamily: fe(ii) trafficking protein Y9gx

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60
1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60

Qy 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91
61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91

Db 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R./Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A65082
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:G
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: fe(ii) trafficking protein Y9gx

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60
1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60

Db 1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60
1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60

Qy 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91
61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91

Db 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91

RESULT 4
F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain RI
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R./Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: F91108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <HAY>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA037261.1;
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECs3838
A/Superfamily: fe(ii) trafficking protein Y9gx

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60
1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60

Qy 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91
61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91

Db 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 91

RESULT 5
A10116
conserved hypothetical protein YP00953 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: A10116
R./Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tillett, R.M.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: A10116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <KUR>
A/Cross-references: UNIPARC:UPI00000DCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022;
C/Genetics:
A/Gene: YP00953
A/Superfamily: fe(ii) trafficking protein Y9gx

Query Match 80.5%; Score 393; DB 2; Length 90;
Best Local Similarity 81.1%; Pred. No. 8.1e-33;
Matches 73; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Db 1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60
1 MSRTICTYLGORDAEGODPOLYPGELGKRIYNEISKDAWAQOHQOTMLINEKKLMMNNA 60

Qy 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 90
61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 90

Db 61 EHRKLEQEMVNFLEPGKDVHIEGYTPEDKK 90

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 66.1725 Seconds

(without alignments)
970.238 Million cell updates/sec

Title: us-09-955-502a-35

Perfect score: 488
Sequence: 1 MSRTICTYLPDAAGQDFQ.....SFLFGKDVHTEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	99.0	90	1	FETP_SALCH
2	483	99.0	90	1	FETP_SALCH
3	483	99.0	90	1	FETP_SALCH
4	483	99.0	90	1	FETP_SALCH
5	464	95.1	90	1	FETP_SALCH
6	464	95.1	90	1	FETP_SALCH
7	464	95.1	90	1	FETP_SALCH
8	460	94.3	90	1	FETP_SALCH
9	460	94.3	90	1	FETP_SALCH
10	401	82.2	90	1	FETP_SALCH
11	393	80.5	90	1	FETP_SALCH
12	393	80.5	90	1	FETP_SALCH
13	389	79.7	90	1	FETP_SALCH
14	389	79.7	90	1	FETP_SALCH
15	389	79.7	90	1	FETP_SALCH
16	387	79.3	90	1	FETP_SALCH
17	385	78.9	90	1	FETP_SALCH
18	385	78.9	90	1	FETP_SALCH
19	383	78.5	90	1	FETP_SALCH
20	377	77.3	90	1	FETP_SALCH
21	376	77.0	90	1	FETP_SALCH
22	371	76.0	90	1	FETP_SALCH
23	365	74.8	90	1	FETP_SALCH
24	341	69.9	90	1	FETP_SALCH
25	336	66.9	90	1	FETP_SALCH
26	259	53.1	90	1	FETP_SALCH
27	249	51.0	90	1	FETP_SALCH
28	249	51.0	90	1	FETP_SALCH
29	249	51.0	90	1	FETP_SALCH
30	243	49.8	90	1	FETP_SALCH
31	239	49.0	90	1	FETP_SALCH

32	232	47.5	90	1	FETP_XYLRA
33	232	47.5	90	1	FETP_XANOR
34	228.5	46.8	92	1	FETP_LEGPL
35	228	46.7	90	1	FETP_PSEAR
36	228	46.7	90	1	FETP_XYLFT
37	228	46.7	92	1	FETP_XANCP
38	228	46.7	92	2	Q4UW14_XANCP
39	225	46.1	78	1	FETP_WIGBR
40	224.5	46.0	89	1	FETP_LEGPA
41	224.5	46.0	89	1	FETP_LEGPA
42	222	45.5	90	1	FETP_NITRU
43	222	45.5	90	1	FETP_PSEBM
44	222	45.5	90	2	Q4ZLP3_PSEBY
45	218	44.7	90	1	FETP_COXBU
46	218	44.7	90	1	FETP_PSEBK
47	218	44.7	90	2	Q4J28_AZOV1
48	215	44.1	90	2	Q6T7F6_PSRFL
49	213	43.6	90	1	FETP_CHROO
50	212	43.4	79	1	FETP_CANBR
51	211	43.2	88	1	FETP_NEIGI
52	211	43.2	88	1	FETP_NEIMA
53	211	43.2	88	1	FETP_NEIMA
54	207	42.4	87	1	FETP_BUCBP
55	206	42.2	91	1	FETP_BURPA
56	206	42.2	91	1	FETP_BURPS
57	205	42.0	90	2	Q4KJ22_PSEF5
58	205	42.0	91	1	FETP_RALSO
59	203	41.6	91	2	Q4L819_9BURK
60	195	40.0	90	1	FETP_METCA
61	192	39.3	87	1	FETP_FRATT
62	190.5	39.0	90	1	FETP_AC1AD
63	146	29.9	96	2	Q4FVJ7_9GAMM
64	145	29.7	92	2	Q4NM04_9DELT
65	82.5	16.9	482	2	Q5NVI1_9BURK
66	82.5	16.9	514	2	Q6A1Z9_DSPPS
67	79.5	16.3	1638	2	Q6BHW2_CABEL
68	79.5	16.3	2140	2	Q6BHW2_CABEL
69	79.5	16.3	2488	2	Q6L528_CABEL
70	78.5	16.1	337	2	Q6L1A8_BACCR
71	78	16.0	1260	2	Q49677_ARATH
72	77.5	15.9	1047	2	Q5CJ53_CRYHO
73	76.5	15.7	486	2	Q7WXS1_ALCEU
74	75.5	15.5	1278	2	Q5CYM7_CRYPV
75	75	15.4	385	2	Q734A2_BACCI

ALIGNMENTS

RESULT 1				
ID	FETP_SALCH	STANDARD:	PRT;	90 AA.
AC	Q57K04;			
DT	13-SEP-2005 (Rel. 48, Created)			
DT	13-SEP-2005 (Rel. 48, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	Name=yggX; OrderedLocustNames=SC3052;			
OS	Salmonella choleraesuis.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Salmonella.			
OX	NCBI_TaxID=591;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=SC-B67;			
RX	PubMed=15781495; DOI=10.1093/nar/gki297;			
RA	Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,			
RA	Wang H.-S., Lee Y.-S.;			
RT	"The genome sequence of salmonella enterica serovar Choleraesuis, a			
RT	highly invasive and resistant zoonotic pathogen.";			
RL	Nucleic Acids Res. 33:1690-1698(2005).			
CC	-1- FUNCTION: Could be a mediator in iron transactions between iron			
CC	acquisition and iron-regulating processes, such as synthesis and/or			

Q9PC73 xylElla fas
Q5GY22 xanthomonas
Q5WVC4 legionella
Q9HJ36 pseudomonas
Q87D06 xylElla fas
Q8P829 xanthomonas
Q4UW14 xanthomonas
Q8D3C5 wiglesworth
Q5XU80 legionella
Q82Xf5 nitrosomonas
Q87f15 pseudomonas
Q421P3 pseudomonas
Q8XJ06 coxiella bu
Q88439 pseudomonas
Q4J228 AZOV1
Q6T7F6_PSRFL
Q6T7F6_PSRFL
Q7WXS1_ALCEU
Q5CYM7_CRYPV
Q734A2_BACCI

```
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity). trafficking protein family.
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE017220; AAK66958.1; -; Genomic_DNA.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC ProDom; PD029191; DUP435; 1.
CC Complete proteome; Iron.
CC INIT MET 0 0
CC SEQUENCE 90 AA; 10768 MW; B3B6A1E2255E3C CRC64;

Query Match 99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SRTIFCTYLQDAEGQDFOLYPGELGKRIYNEISKDAMQOHKQTMLINEKLMNNAE 61
Db 1 SRTIFCTYLQDAEGQDFOLYPGELGKRIYNEISKDAMQOHKQTMLINEKLMNNAE 60

Oy 62 HRKLIQEMVSLFPEGKDVHIEGYTPEDKK 91
Db 61 HRKLIQEMVSLFPEGKDVHIEGYTPEDKK 90

RESULT 2
FETP_SALPA STANDARD; PRT; 90 AA.
ID FETP_SALPA
AC O5PMML;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=YggX; OrderedLocustNames=SPA2974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxID=54388;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.B., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozeresky P., McCellan M.,
RA Harting C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremliki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehanthy K., Fronick C., Magini V., Nhan M., Warren W., Flores L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity). trafficking protein family.
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
CC SMR; O5PMML; 1-91.
CC HAMAP; MF_00686; -; 1.
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DR InterPro; IPR007457; YggX.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
DR INIT MET 0 0
DR SEQUENCE 90 AA; 10768 MW; B3B6A1E2255E3C CRC64;

Query Match 99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 SRTIFCTYLQDAEGQDFOLYPGELGKRIYNEISKDAMQOHKQTMLINEKLMNNAE 61
Db 1 SRTIFCTYLQDAEGQDFOLYPGELGKRIYNEISKDAMQOHKQTMLINEKLMNNAE 60

Oy 62 HRKLIQEMVSLFPEGKDVHIEGYTPEDKK 91
Db 61 HRKLIQEMVSLFPEGKDVHIEGYTPEDKK 90

RESULT 3
FETP_SALTI STANDARD; PRT; 90 AA.
ID FETP_SALTI
AC P67618; Q8XFW6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=YggX; OrderedLocustNames=STY3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxID=601;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Baeham D., Brooke K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leach A., Moulé S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
DOI=10.1126/DB.185.7.2330-2337.2003;
RA Deng W., Ilyou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
CC EMBL; AE016844; AAO70576.1; -; Genomic_DNA.
CC SMR; P67618; 1-90.
CC HAMAP; MF_00686; -; 1.
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 18.2616 Seconds

(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-35

Perfect score: 488
Sequence: 1 MSRTTCTYLRDAGQDPQ.....SFLFGKDVHIEGYTPDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445	91.2	107	2	US-09-489-039A-11962
2	383	78.5	93	2	US-09-543-681A-5443
3	228	46.7	122	2	US-09-252-991A-23355
4	195.5	40.1	92	2	US-09-328-352-5456
5	130	26.6	110	2	US-09-540-236-2859
6	71	14.5	548	2	US-09-167-299-3
7	70.5	14.4	184	2	US-09-325-932A-66
8	68.5	14.0	544	2	US-09-248-796A-18911
9	68	13.9	280	2	US-09-323-998B-37
10	68	13.9	337	2	US-09-270-767-41746
11	68	13.9	1214	2	US-10-164-595-24
12	66.5	13.6	325	2	US-09-134-000C-4346
13	66	13.5	292	2	US-09-328-352-5836
14	65.5	13.4	546	1	US-08-533-669A-2
15	65.5	13.4	546	1	US-08-183-861-2
16	65.5	13.4	546	2	US-09-022-765-2
17	65.5	13.4	546	2	US-09-551-974A-2
18	65.5	13.4	546	2	US-09-565-501A-2
19	65.5	13.4	546	2	US-09-639-206A-2
20	65.5	13.4	546	2	US-09-874-923-2
21	65.5	13.4	546	2	US-08-798-841-2
22	65.5	13.4	982	2	US-09-551-974A-95
23	65.5	13.4	982	2	US-09-565-501A-95
24	65.5	13.4	982	2	US-09-639-206A-95
25	65.5	13.4	982	2	US-09-874-923-95
26	65.5	13.4	1427	2	US-09-551-974A-97
27	65.5	13.4	1427	2	US-09-565-501A-97

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709, 20040001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

28	65.5	13.4	1427	2	US-09-639-206A-97	Sequence 97, Appl
29	65.5	13.4	1427	2	US-09-874-923-97	Sequence 97, Appl
30	65.5	13.4	1641	2	US-09-551-974A-96	Sequence 96, Appl
31	65.5	13.4	1641	2	US-09-565-501A-96	Sequence 96, Appl
32	65.5	13.4	1641	2	US-09-639-206A-96	Sequence 96, Appl
33	65.5	13.4	1641	2	US-09-874-923-96	Sequence 96, Appl
34	65	13.3	474	2	US-09-252-991A-44473	Sequence 24473, A
35	64	13.1	98	2	US-09-270-767-41085	Sequence 41085, A
36	64	13.1	98	2	US-09-270-767-56301	Sequence 56301, A
37	64	13.1	569	2	US-09-107-532A-6689	Sequence 6689, Ap
38	64	13.1	644	2	US-08-793-331-7	Sequence 7, Appl
39	64	13.1	1176	2	US-09-489-039A-8879	Sequence 8879, Ap
40	63.5	13.0	921	2	US-09-248-796A-14950	Sequence 14950, A
41	63	12.9	1586	2	US-09-538-092-1171	Sequence 14958, A
42	62.5	12.8	260	2	US-09-252-991A-17498	Sequence 17498, A
43	62.5	12.8	419	2	US-09-543-681A-7295	Sequence 7295, Ap
44	62.5	12.8	662	2	US-09-583-110-5119	Sequence 5119, Ap
45	62.5	12.8	664	2	US-09-107-433-2775	Sequence 2775, Ap
46	62.5	12.8	701	2	US-09-252-991A-23288	Sequence 23288, A
47	62	12.7	227	2	US-09-270-767-58283	Sequence 58283, A
48	62	12.7	238	2	US-09-323-998B-41	Sequence 41, Appl
49	62	12.7	448	2	US-09-270-767-42959	Sequence 42959, A
50	62	12.7	604	2	US-09-008-097-4	Sequence 4, Appl
51	62	12.7	604	2	US-09-472-667-4	Sequence 4, Appl
52	62	12.7	898	2	US-09-583-110-3150	Sequence 3150, Ap
53	62	12.7	899	2	US-09-107-433-3196	Sequence 3196, Ap
54	62	12.7	1167	2	US-09-008-097-6	Sequence 6, Appl
55	62	12.7	1167	2	US-09-472-667-6	Sequence 6, Appl
56	61.5	12.6	591	2	US-09-370-368-8	Sequence 8, Appl
57	61	12.5	143	2	US-09-270-767-45872	Sequence 45872, A
58	61	12.5	281	2	US-09-270-767-61671	Sequence 61671, A
59	61	12.5	174	2	US-09-248-796A-19265	Sequence 19265, A
60	61	12.5	389	2	US-09-270-767-46116	Sequence 46116, A
61	61	12.5	1394	2	US-09-248-796A-19555	Sequence 19555, A
62	60.5	12.4	223	2	US-09-543-681A-5667	Sequence 5667, Ap
63	60.5	12.4	504	2	US-10-104-047-3467	Sequence 3467, Ap
64	60.5	12.4	525	2	US-09-540-236-2250	Sequence 2250, Ap
65	60.5	12.4	527	2	US-09-489-039A-10883	Sequence 10883, A
66	60	12.3	232	2	US-09-201-641-8	Sequence 8, Appl
67	60	12.3	232	2	US-09-323-998B-36	Sequence 36, Appl
68	60	12.3	421	2	US-09-489-039A-7512	Sequence 7512, Ap
69	60	12.3	734	2	US-10-008-355-5	Sequence 5, Appl
70	59.5	12.2	139	2	US-09-513-999C-4802	Sequence 4802, Ap
71	59.5	12.2	209	2	US-09-252-991A-20905	Sequence 20905, A
72	59.5	12.2	258	2	US-09-513-999C-4800	Sequence 4800, Ap
73	59.5	12.2	264	2	US-09-949-016-6012	Sequence 6012, Ap
74	59.5	12.2	276	2	US-09-949-016-11703	Sequence 11703, A
75	59.5	12.2	434	2	US-09-303-518D-334	Sequence 334, App

Query Match 91.2%; Score 445; DB 2; Length 107;
Best Local Similarity 89.0%; Pred. No. 3.5e-49;
Matches 81; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSRTTCTYLODAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 60
DB 17 MSRTTCTYLODAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 76

QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDK 91
DB 77 EHRKLEQEMVSLFPEGKDVHIEGYTPEDK 107

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRP
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 78.5%; Score 383; DB 2; Length 93;
Best Local Similarity 77.8%; Pred. No. 2.5e-41;
Matches 70; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSRTTCTYLODAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 60
DB 4 MSRTTCTYLODAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 63

QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDK 90
DB 64 EHRKLEQEMVSLFPEGKDVHIEGYTPEDK 93

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRP
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 46.7%; Score 228; DB 2; Length 122;
Best Local Similarity 52.3%; Pred. No. 2.4e-21;
Matches 46; Conservative 11; Mismatches 29; Indels 2; Gaps 2;

QY 1 MSRTTCTYLODAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 60

DB 33 MSRTTCTYLODAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 92

QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTP 87
DB 93 EHRKLEQEMVSLFPEGKDVHIEGYTP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRP
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 40.1%; Score 195.5; DB 2; Length 92;
Best Local Similarity 41.6%; Pred. No. 2.4e-17;
Matches 37; Conservative 15; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSRTTCTYLODAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 60
DB 4 MSRTTCTYLODAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 63

QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTP 88
DB 64 EHRKLEQEMVSLFPEGKDVHIEGYTP 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRP
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 26.6%; Score 130; DB 2; Length 110;
Best Local Similarity 34.9%; Pred. No. 7.4e-09;
Matches 29; Conservative 13; Mismatches 41; Indels 0; Gaps 0;

QY 5 IFCYTLQDAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 64
DB 25 IFCYTLQDAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 84

QY 65 IFCYTLQDAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 87
DB 85 IFCYTLQDAEGDGFQLYPGELGKRIYNEISKDAMAWOHQKOTMLINEKLMNNA 107

RESULT 6
US-09-167-299-3
; Sequence 3, Application US/09167299

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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 / Search time 56.9391 Seconds
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667.774 Million cell updates/sec

Title: US-09-955-502a-35

Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDARQDFQ.....SFLFGKDVHIGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
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- 4: /cgn2_6/prodata/1/pubppaa/US10a_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10b_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	100.0	91	US-09-955-502-14	Sequence 14, Appl
2	488	100.0	91	US-09-955-502-16	Sequence 16, Appl
3	488	100.0	91	US-09-955-502-17	Sequence 17, Appl
4	474	97.1	91	US-09-955-502-18	Sequence 18, Appl
5	472	96.7	88	US-09-955-502-15	Sequence 15, Appl
6	469	96.1	91	US-09-955-502-11	Sequence 11, Appl
7	469	96.1	91	US-09-955-502-12	Sequence 12, Appl
8	469	96.1	91	US-09-955-502-13	Sequence 13, Appl
9	393	80.5	90	US-09-955-502-20	Sequence 20, Appl
10	389	79.7	90	US-09-955-502-10	Sequence 10, Appl
11	386	79.1	78	US-09-955-502-19	Sequence 19, Appl
12	385	78.9	87	US-09-955-502-7	Sequence 7, Appl
13	383	78.5	91	US-09-955-502-5	Sequence 5, Appl
14	377	77.3	87	US-09-955-502-6	Sequence 6, Appl
15	371	76.0	87	US-09-955-502-8	Sequence 8, Appl
16	336	68.9	88	US-09-955-502-9	Sequence 9, Appl
17	259	53.1	76	US-09-955-502-21	Sequence 21, Appl
18	249	51.0	87	US-09-955-502-2	Sequence 2, Appl
19	249	51.0	87	US-09-955-502-3	Sequence 3, Appl
20	235	48.2	86	US-09-955-502-4	Sequence 4, Appl
21	232	47.5	89	US-09-955-502-22	Sequence 22, Appl
22	228	46.7	87	US-09-955-502-25	Sequence 25, Appl
23	222	45.5	90	US-09-955-502-23	Sequence 23, Appl
24	218	44.7	87	US-09-955-502-24	Sequence 24, Appl
25	218	44.7	88	US-09-955-502-33	Sequence 33, Appl
26	211	43.2	88	US-09-955-502-26	Sequence 26, Appl
27	211	43.2	88	US-09-955-502-27	Sequence 27, Appl

28	211	43.2	88	US-09-955-502-28	Sequence 28, Appl
29	206	42.2	87	US-09-955-502-29	Sequence 29, Appl
30	206	42.2	87	US-09-955-502-30	Sequence 30, Appl
31	197	40.4	87	US-09-955-502-31	Sequence 31, Appl
32	195	40.0	87	US-09-955-502-32	Sequence 32, Appl
33	177	15.8	1647	US-10-450-763-41109	Sequence 41109, A
34	72.5	14.9	786	US-10-732-923-4885	Sequence 4885, Ap
35	72	14.8	507	US-10-282-122A-68134	Sequence 68134, A
36	72	14.8	1261	US-10-437-963-189166	Sequence 189166,
37	71.5	14.7	184	US-10-393-840-52	Sequence 52, Appl
38	71	14.5	546	US-10-282-122A-66021	Sequence 66021, A
39	70.5	14.4	184	US-10-219-220-66	Sequence 66, Appl
40	70.5	14.4	184	US-10-393-840-118	Sequence 118, Ap
41	70.5	14.4	593	US-10-450-763-50306	Sequence 50306, A
42	69	14.1	503	US-10-450-763-46936	Sequence 46936, A
43	69	14.1	679	US-10-805-684-105	Sequence 105, Ap
44	68.5	14.0	449	US-10-424-559-278212	Sequence 278212,
45	68.5	14.0	608	US-10-032-585-7582	Sequence 7582, Ap
46	68.5	14.0	632	US-10-369-493-18744	Sequence 18744, A
47	68	13.9	280	US-09-323-998D-37	Sequence 37, Appl
48	68	13.9	280	US-10-389-566-2296	Sequence 2296, Ap
49	68	13.9	445	US-10-844-874-14	Sequence 14, Appl
50	68	13.9	445	US-10-713-970-13	Sequence 13, Appl
51	68	13.9	478	US-10-087-192-378	Sequence 378, Ap
52	68	13.9	689	US-10-369-493-17280	Sequence 17280, A
53	68	13.9	764	US-10-416-330-37	Sequence 37, Appl
54	68	13.9	764	US-10-491-467-15	Sequence 15, Appl
55	68	13.9	1206	US-10-085-198-144	Sequence 144, Ap
56	68	13.9	1214	US-10-717-665-24	Sequence 24, Appl
57	67.5	13.8	166	US-10-482-706-269	Sequence 269, Ap
58	67	13.7	119	US-10-437-963-158697	Sequence 158697,
59	67	13.7	167	US-10-389-566-1126	Sequence 1126, Ap
60	67	13.7	306	US-10-424-559-241560	Sequence 241560,
61	66.5	13.6	315	US-10-282-122A-57222	Sequence 57222, A
62	66.5	13.6	315	US-10-958-216-464	Sequence 464, Ap
63	66.5	13.6	315	US-10-958-216-466	Sequence 466, Ap
64	66.5	13.6	561	US-10-437-963-169643	Sequence 169643,
65	66.5	13.6	638	US-10-831-070-272	Sequence 272, Ap
66	66.5	13.6	2910	US-10-732-923-3342	Sequence 3342, Ap
67	66	13.5	120	US-10-388-566-1079	Sequence 1079, Ap
68	66	13.5	120	US-10-389-566-1125	Sequence 1125, Ap
69	66	13.5	459	US-10-087-192-375	Sequence 375, Ap
70	65.5	13.4	221	US-10-767-701-41912	Sequence 41912, A
71	65.5	13.4	481	US-10-732-923-982	Sequence 982, Ap
72	65.5	13.4	545	US-10-732-923-9369	Sequence 9369, Ap
73	65.5	13.4	546	US-09-874-923-2	Sequence 2, Appl
74	65.5	13.4	546	US-09-991-466-2	Sequence 2, Appl
75	65.5	13.4	546	US-10-098-732A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-09-955-502-14
Sequence 14, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
PRIOR FILING DATE: 2001-09-18
PRIORITY APPLICATION NUMBER: 60/234, 588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 14
LENGTH: 91
TYPE: PRT
ORGANISM: Salmonella paratyphi

US-09-955-502-14

Query Match 100.0%; Score 488; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 6,8e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTFTCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNA 60
DB 1 MSRTFTCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNA 60
QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 2

US-09-955-502-16

Sequence 16, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296,97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 91

TYPE: PR

ORGANISM: Salmonella dublin

US-09-955-502-16

Query Match 100.0%; Score 488; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 6,8e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTFTCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNA 60
DB 1 MSRTFTCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNA 60
QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 3

US-09-955-502-17

Sequence 17, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296,97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 91

TYPE: PR

ORGANISM: Salmonella typhi CT18

US-09-955-502-17

Query Match 100.0%; Score 488; DB 3; Length 91;

Best Local Similarity 100.0%; Pred. No. 6,8e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTFTCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNA 60
DB 1 MSRTFTCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNA 60
QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 4

US-09-955-502-18

Sequence 18, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296,97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18

LENGTH: 91

TYPE: PR

ORGANISM: Salmonella typhimurium

US-09-955-502-18

Query Match 97.1%; Score 474; DB 3; Length 91;
Best Local Similarity 97.8%; Pred. No. 2,9e-47;
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTFTCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNA 60
DB 1 MSRTFTCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHKQTMLINEKLLNMNA 60
QY 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91
DB 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 5

US-09-955-502-15

Sequence 15, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296,97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 88

TYPE: PR

ORGANISM: Salmonella enteritidis

US-09-955-502-15

Query Match 96.7%; Score 472; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 4,8e-47;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4,82187 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502a-35

Perfect score: 488
Sequence: 1 MSRTIFCTYLQDAEGQDFQ.....SFLPGKQVHLEGYPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep: *
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep: *
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep: *
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep: *
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB pep: *
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep: *
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep: *
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211	43.2	88	US-10-467-657-968	Sequence 968, App
2	68	13.9	478	US-10-821-234-915	Sequence 915, App
3	65	13.3	593	US-11-194-246-317	Sequence 317, App
4	64.5	13.2	177	US-10-467-657-1658	Sequence 1658, App
5	63.5	13.0	1432	US-10-510-386-218	Sequence 218, App
6	62	12.7	251	US-11-054-515-1496	Sequence 1496, App
7	62	12.7	604	US-10-942-072-4	Sequence 4, App11
8	62	12.7	1167	US-10-942-072-6	Sequence 6, App11
9	60.5	12.4	504	US-11-072-513-13467	Sequence 3467, App
10	59.5	12.2	264	US-10-821-234-1555	Sequence 1555, App
11	59.5	12.2	285	US-10-467-657-222	Sequence 222, App
12	59.5	12.2	285	US-10-467-657-8230	Sequence 8230, App
13	59.5	12.2	650	US-10-467-657-1948	Sequence 1948, App
14	59.5	12.2	834	US-10-453-372-658	Sequence 658, App
15	59.5	12.2	1995	US-11-069-834-60	Sequence 60, App1
16	59	12.1	257	US-11-054-515-1710	Sequence 1710, App
17	59	12.1	697	US-10-485-517-202	Sequence 202, App
18	59	12.1	1168	US-10-942-072-11	Sequence 11, App1
19	59	12.1	1450	US-10-485-517-152	Sequence 152, App
20	58.5	12.0	695	US-10-453-372-648	Sequence 648, App
21	58.5	12.0	700	US-10-995-561-922	Sequence 922, App
22	58.5	12.0	700	US-10-995-561-924	Sequence 924, App
23	58.5	12.0	749	US-11-098-686-10505	Sequence 10505, App
24	58.5	12.0	782	US-10-793-626-2352	Sequence 2352, App
25	58	11.9	448	US-10-618-320A-25	Sequence 25, App1

26	58	11.9	480	6	US-10-510-386-12	Sequence 12, App1
27	58	11.9	1501	7	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.8	242	7	US-11-022-562-220	Sequence 220, App
29	57.5	11.8	336	6	US-10-453-372-640	Sequence 640, App
30	57.5	11.8	577	7	US-11-072-175-187	Sequence 187, App
31	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
32	57.5	11.8	775	6	US-10-453-372-656	Sequence 656, App
33	57.5	11.8	793	6	US-10-995-561-925	Sequence 925, App
34	57.5	11.8	804	6	US-10-453-372-650	Sequence 650, App
35	57.5	11.8	847	6	US-10-453-372-654	Sequence 654, App
36	57.5	11.8	857	6	US-10-453-372-652	Sequence 652, App
37	57.5	11.8	905	6	US-10-453-372-658	Sequence 658, App
38	57.5	11.8	905	6	US-10-453-372-662	Sequence 662, App
39	57.5	11.8	905	6	US-10-453-372-664	Sequence 664, App
40	57.5	11.8	963	6	US-10-995-561-923	Sequence 923, App
41	57.5	11.8	963	6	US-10-453-372-660	Sequence 660, App
42	57.5	11.8	1012	6	US-10-453-372-646	Sequence 646, App
43	57.5	11.8	3803	6	US-10-995-561-773	Sequence 773, App
44	57.5	11.8	3960	6	US-10-995-561-771	Sequence 771, App
45	57.5	11.8	5335	6	US-10-995-561-777	Sequence 777, App
46	57.5	11.8	5406	6	US-10-995-561-774	Sequence 774, App
47	57.5	11.8	5415	6	US-10-995-561-779	Sequence 779, App
48	57.5	11.8	5464	6	US-10-995-561-775	Sequence 775, App
49	57.5	11.8	5935	6	US-10-995-561-776	Sequence 776, App
50	57	11.7	234	6	US-10-524-972-120	Sequence 120, App
51	57	11.7	234	6	US-10-524-972-108	Sequence 108, App
52	57	11.7	432	6	US-10-821-234-1463	Sequence 1463, App
53	57	11.7	440	7	US-11-072-512-3856	Sequence 3856, App
54	56.5	11.6	647	7	US-11-000-462-722	Sequence 722, App
55	56.5	11.6	1254	6	US-10-528-031-47	Sequence 47, App1
56	56.5	11.6	1897	6	US-10-821-234-1635	Sequence 1635, App
57	56.5	11.6	1907	7	US-11-000-463-260	Sequence 260, App
58	56.5	11.6	3433	6	US-10-714-781A-67	Sequence 67, App1
59	56	11.5	206	7	US-11-124-367A-116	Sequence 316, App
60	55.5	11.4	136	6	US-10-793-626-580	Sequence 580, App
61	55.5	11.4	279	7	US-11-098-686-10812	Sequence 10812, App
62	55.5	11.4	1188	7	US-11-115-639-42	Sequence 42, App1
63	55.5	11.4	1188	7	US-11-115-639-43	Sequence 43, App1
64	55	11.3	189	7	US-11-071-262-1	Sequence 1, App11
65	55	11.3	667	6	US-10-793-626-198	Sequence 198, App
66	55	11.3	783	7	US-11-038-284-33	Sequence 33, App1
67	55	11.3	793	7	US-11-037-243-67	Sequence 67, App1
68	55	11.3	873	7	US-11-038-284-35	Sequence 35, App1
69	55	11.3	889	7	US-11-038-284-15	Sequence 15, App1
70	55	11.3	1142	7	US-11-109-156-22	Sequence 22, App1
71	55	11.3	2668	7	US-11-124-368A-214	Sequence 214, App
72	55	11.2	317	6	US-11-124-368A-215	Sequence 215, App
73	54.5	11.2	450	6	US-10-523-503-74	Sequence 74, App1
74	54.5	11.2	450	6	US-10-618-320A-26	Sequence 26, App1
75	54.5	11.2	496	7	US-11-069-642-20	Sequence 20, App1

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACT Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

```
; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968
```

```
Query Match          43.2%; Score 211; DB 6; Length 88;
Best Local Similarity 43.8%; Pred. No. 3.2e-17;
Matches 39; Conservative 19; Mismatches 29; Indels 2; Gaps 2;
```

```
QY 1 MSRTICTYTLORDAEGODFOLYPGELGKRIYNEISKDAMAQOHQOTMLINEKKLMNNA 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MARWFCVYLNREAGCMKPPPLPNEIGKRIFFENVSQEMAAWTRHQTMLINEENRLSLADP 60
```

```
QY 61 EHRKLEQEMVSFLF-EGKDVIIEGYTP 88
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RAREVYLAQOMEQYFPFGDGADA-VQGVVPQ 88
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RESULT 2
US-10-821-234-915
; Sequence 915, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 915
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-915
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Query Match          13.9%; Score 68; DB 6; Length 478;
Best Local Similarity 25.5%; Pred. No. 3.4;
Matches 26; Conservative 20; Mismatches 26; Indels 28; Gaps 5;
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```
QY 8 TYLORDAEGODF--OLYPG-----ELGKRIYNEISKDAMAQOHQOTMLIN 51
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 380 SYLQRAYVDRDLFLARYGA.PQLQVEKVRTNDRKEGEVAVQYTGDRSFAFA-KALGVMD 438
```

```
QY 52 EKKLMNNAEHRKLEQEMVSFLFEGSKDVH-----EGYTP 87
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 439 DIKSGVPRAGYRGI-----VTFQFRGRVHLAPPTWEGYDP 475
```

```
RESULT 3
US-11-194-246-317
; Sequence 317, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Stefan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 317
; LENGTH: 593
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317
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Query Match          13.3%; Score 65; DB 7; Length 593;
Best Local Similarity 24.1%; Pred. No. 9.6;
Matches 20; Conservative 10; Mismatches 23; Indels 30; Gaps 2;
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```
QY 9 YLOR-DAEGODFOLYPGELGKRIYNE-----ISKDA 38
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 240 FLNRFPDNENTDFQKWRDEQRLQDTNLFERLRMAIWQTELTSMNLISAKSKOE 299
```

```
QY 39 WAQOHQOTMLINEKKLMNNAE 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 300 WRWYEAQODILKNTKLTALSK 322
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```
RESULT 4
US-10-467-657-1658
; Sequence 1658, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
```

```
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan9, version 1.04
; SEQ ID NO 1658
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1658
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Best Local Similarity 28.6%; Pred. No. 2.6;
Matches 20; Conservative 11; Mismatches 38; Indels 1; Gaps 1;
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   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 63 EYRRIIILYLSNEI-LIVRTKFSKNIFFSNEKKYKEIEKINKLYKMDWILFFNND 121
```

```
QY 80 VHIIEGYTPED 89
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 122 ITLDPYTGND 131
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```
RESULT 5
US-10-510-386-218
; Sequence 218, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
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; APPLICANT: Andersen, Jens Torne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 / Search time 73.9696 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502a-36

Perfect score: 486

Sequence: 1 MSRTIFCTPLQREAGODFO.....NFLPFGKEVHLEGYPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database:

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1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*
9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	91	5	ABB78158 Amino aci
2	486	100.0	91	5	ABB78157 Amino aci
3	486	100.0	91	5	ABB78156 Amino aci
4	469	96.5	91	5	ABB78161 Amino aci
5	469	96.5	91	5	ABB78159 Amino aci
6	469	96.5	91	5	ABB78162 Amino aci
7	455	93.6	91	5	ABB78163 Amino aci
8	453	93.2	88	5	ABB78160 Amino aci
9	450	92.6	107	7	ABO65445 Amino aci
10	402	82.7	90	5	ABB78155 Amino aci
11	396	81.5	90	5	ABB78155 Amino aci
12	395	81.3	78	5	ABB78164 Amino aci
13	389	80.0	93	7	ADPO5158 Amino aci
14	388	79.8	91	5	ABB78150 Amino aci
15	387	79.6	87	5	ABB78152 Amino aci
16	379	78.0	87	5	ABB78151 Amino aci
17	373	76.7	87	5	ABB78153 Amino aci
18	332	68.3	88	5	ABB78154 Amino aci
19	265	54.5	76	5	ABB78166 Amino aci
20	255	52.5	87	5	ABB78148 Amino aci
21	255	52.5	87	5	ABB78147 Amino aci
22	241	49.6	86	5	ABB78149 Amino aci
23	231.5	47.6	89	9	ABE41576 Amino aci
24	231.5	47.6	95	9	ABE38294 L. pneumo

25	231	47.5	87	5	ABB78170 Amino aci
26	231	47.5	122	7	ABO74609 Pseudomon
27	227	46.7	88	5	ABB78178 Amino aci
28	227	46.7	90	5	ABB78168 Amino aci
29	225	46.3	87	5	ABB78169 Amino aci
30	216.5	44.5	90	5	ABB78167 Amino aci
31	213	43.8	88	5	ABB78171 Amino aci
32	213	43.8	88	5	ABB78172 Amino aci
33	213	43.8	88	5	ABB78173 Amino aci
34	213	43.8	88	5	ABB77219 N. gonorr
35	206	42.4	87	5	ABB78175 Amino aci
36	200	41.2	87	5	ABB78177 Amino aci
37	200	41.2	87	5	ABB78174 Amino aci
38	200	41.2	87	5	ABB78176 Amino aci
39	199.5	41.0	92	6	ADA34169 Acinetoba
40	131	27.0	110	8	ADU05173 M. cattar
41	83	17.1	506	3	AAV74371 Neisseria
42	83	17.1	1647	4	ABG10750 Novel hum
43	81	16.7	507	6	ABU40210 Protein e
44	78	16.0	507	3	AAV74372 Neisseria
45	78	16.0	507	3	AAV74373 Neisseria
46	78	16.0	546	6	ABU38097 Protein e
47	76	15.6	548	4	AAE04737 Brugia ma
48	75	15.4	309	8	ADN46828 Thermococ
49	74.5	15.3	632	8	ADS29711 Bacterial
50	72	14.8	474	7	ABO75727 Pseudomon
51	71.5	14.7	679	9	ADZ85056 Partial F
52	71	14.6	311	7	ADM26256 Hyperther
53	70.5	14.5	285	4	ABP92683 Human pro
54	70.5	14.5	414	6	ABU11747 Human MDD
55	70.5	14.5	614	9	ADX06837 Cyclin-de
56	70.5	14.5	56	9	ADY16108 PRO polyP
57	70.5	14.5	764	5	ABB77432 Human tum
58	70.5	14.5	764	7	ADC99662 Human xrp
59	70.5	14.5	817	4	AAH38657 Human xrp
60	70.5	14.5	863	4	AAH38656 Human pol
61	70.5	14.5	1135	8	ADL10706 Human the
62	70.5	14.5	1181	8	ADL10708 Human the
63	70.5	14.5	1186	8	ADL10709 Human the
64	70.5	14.5	1188	8	ADH45460 Human mol
65	70.5	14.5	1206	5	ADH48860 NOVI61 pro
66	70.5	14.5	1214	7	ADK65785 Angiogene
67	69.5	14.3	374	4	AAH39682 Human pol
68	69.5	14.3	389	4	AAH41468 Human pol
69	69.5	14.3	481	5	AAU93169 Arabidops
70	69.5	14.3	481	7	ADD30148 Plant yle
71	69.5	14.3	481	7	ADD31497 Plant yle
72	69.5	14.3	481	8	ADL41933 Plant lat
73	69.5	14.3	485	5	ABB08477 Human lat
74	69.5	14.3	488	4	ABP94458 Human pro
75	69.5	14.3	488	4	AAH67252 Amino aci

ALIGNMENTS

RESULT 1	ABB78158 standard; protein; 91 AA.
ID	ABB78158;
AC	05-NOV-2002 (first entry)
DE	Amino acid sequence of a Yggx homologue.
KW	Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
OS	hydroxyl radical; DNA damage; Yggx homologue.
XX	Unidentified.
XX	US2002072118-A1.

PD 13-JUN-2002.
 XX 18-SEP-2001; 2001US-00955502.
 PF 22-SEP-2000; 2000US-0234588P.
 PR
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 PI Downs D, Gralnick JA;
 DR WPI, 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX
 SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3.1e-48;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLGRBAGDGFOLYPGELGKRIYNEISKEAWAOMHOKOTMLINEKLLMMNA 60
 DB 1 MSRTTCTFLGRBAGDGFOLYPGELGKRIYNEISKEAWAOMHOKOTMLINEKLLMMNA 60
 QY 61 EHRKLLBQEMVNFLEFGKEVHI EGYTPEDKX 91
 DB 61 EHRKLLBQEMVNFLEFGKEVHI EGYTPEDKX 91

RESULT 2
 ABB78157
 ID ABB78157 standard; protein; 91 AA.
 XX
 AC ABB78157;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgxB homologue.
 XX
 DE Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YgxB homologue.
 XX
 OS Unidentified.
 OS
 XX
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 PD
 PF 18-SEP-2001; 2001US-00955502.
 PF
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX

DR WPI, 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX

Sequence 91 AA;
 Query Match 100.0%; Score 486; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3.1e-48;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLGRBAGDGFOLYPGELGKRIYNEISKEAWAOMHOKOTMLINEKLLMMNA 60
 DB 1 MSRTTCTFLGRBAGDGFOLYPGELGKRIYNEISKEAWAOMHOKOTMLINEKLLMMNA 60
 QY 61 EHRKLLBQEMVNFLEFGKEVHI EGYTPEDKX 91
 DB 61 EHRKLLBQEMVNFLEFGKEVHI EGYTPEDKX 91

RESULT 3
 ABB78156
 ID ABB78156 standard; protein; 91 AA.
 XX
 AC ABB78156;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgxB homologue.
 XX
 DE Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YgxB homologue.
 XX
 OS *Escherichia coli*.
 OS
 XX
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 PD
 PF 18-SEP-2001; 2001US-00955502.
 PF
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI, 2002-589476/63.
 DR
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21, Search time 9.84893 Seconds
(without alignment)
889.003 Million cell updates/sec

Title: US-09-955-502A-36

Perfect score: 486
Sequence: 1 MSRTFTCTFLQREAGQDPQ.....NFLFRGKVEHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	91	A85954	hypothetical prote
2	486	100.0	91	A65082	hypothetical prote
3	486	100.0	91	F91108	hypothetical prote
4	469	96.5	91	AH0879	conserved hypotet
5	402	82.7	90	C82320	conserved hypotet
6	396	81.5	90	A10116	conserved hypotet
7	387	79.6	90	C64013	hypothetical prote
8	265	54.5	93	E84994	hypothetical prote
9	231	47.5	90	H83003	conserved hypotet
10	226	46.5	105	C82624	conserved hypotet
11	213	43.8	88	H81014	conserved hypotet
12	78	16.0	507	C81063	conserved hypotet
13	78	16.0	546	A81807	conserved hypotet
14	78	15.6	548	A54510	conserved hypotet
15	75.5	15.5	1638	D87749	conserved hypotet
16	75.5	15.5	2488	T42739	conserved hypotet
17	74.5	15.3	683	AC2256	conserved hypotet
18	72	14.8	265	T46013	hypothetical prote
19	72	14.8	447	T16527	hypothetical prote
20	72	14.8	507	A83105	hypothetical prote
21	72	14.8	511	A99574	hypothetical prote
22	69	14.2	258	A97991	hypothetical prote
23	69	14.2	258	B95121	hypothetical prote
24	69	14.2	548	A28209	hypothetical prote
25	69	14.2	1119	T15842	hypothetical prote
26	68	14.0	2672	A48126	hypothetical prote
27	67.5	13.9	209	T64172	hypothetical prote
28	67	13.8	235	G65212	hypothetical prote
29	67	13.8	324	T05429	hypothetical prote

30	67	13.8	433	2	A70465	probable GTP bindi
31	67	13.8	447	2	UC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2	T40058	probable chromatin
33	66.5	13.7	1260	2	T04440	hypothetical prote
34	66	13.6	593	2	C64097	probable soluble 1
35	66	13.6	689	2	P83902	beta-galactosidase
36	65.5	13.5	173	2	H86869	hypothetical prote
37	65.5	13.5	305	2	A75211	asparaginase (EC 3
38	65.5	13.5	323	2	A90536	lipoprotein (impor
39	65.5	13.5	365	2	B54128	Fe-binding protein
40	65.5	13.5	821	2	AT2417	hypothetical prote
41	65	13.4	251	2	B90428	hypothetical prote
42	65	13.4	330	2	S74456	regulatory protein
43	65	13.4	445	1	XDHMB	alpha-1,3-mannosyl
44	65	13.4	456	2	G71152	hypothetical prote
45	65	13.4	1008	2	H85055	probable transposo
46	65	13.4	1141	2	T29185	hypothetical prote
47	65	13.4	1230	2	S66850	SMC1 protein homol
48	64.5	13.3	245	2	AG2300	hypothetical prote
49	64.5	13.3	305	2	A71247	probable L-asparag
50	64.5	13.3	495	2	AH0985	probable zinc-prot
51	64.5	13.3	859	2	T29630	hypothetical prote
52	64	13.2	220	2	S62410	hypothetical prote
53	64	13.2	438	2	T37786	hypothetical prote
54	64	13.2	447	1	A38561	probable RNA-bindi
55	64	13.2	583	2	T48365	hypothetical prote
56	64	13.2	604	2	S66993	hypothetical prote
57	64	13.2	990	2	T43445	hypothetical prote
58	64	13.2	1051	2	S27002	hypothetical prote
59	64	13.2	1234	2	S52099	phospholipase C (B
60	64	13.2	1234	2	I38994	phospholipase C-be
61	63.5	13.1	243	2	H90521	hypothetical prote
62	63.5	13.1	243	2	T29635	hypothetical prote
63	63.5	13.1	460	2	T00639	hypothetical prote
64	63.5	13.1	591	1	POMMM	hypothetical prote
65	63	13.0	880	2	AE0179	gag polypeptin -
66	63	13.0	1251	2	AE6177	probable ATPase ch
67	63	13.0	1327	2	T14594	neuronal cell cycl
68	63	13.0	1611	1	WMTMPV	guanidine nucleoti
69	62.5	12.9	68	1	SVBSET	183K protein - pep
70	62.5	12.9	551	2	B84106	glutamate-tRNA lig
71	62.5	12.9	555	2	C96667	hypothetical prote
72	62.5	12.9	617	2	B71071	unknown protein, 7
73	62.5	12.9	964	1	T04325	probable prolyl en
74	62.5	12.9	1417	2	T00661	probable ATP-depen
75	62.	12.8	169	2	PM0560	hypothetical prote

ALIGNMENTS

RESULT 1
A85954
hypothetical protein yggx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
A:Accession: A85954
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobbeck, E.U.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yggx
C:Superfamily: fe(II) trafficking protein yggx
Query Match 100.0%; Score 486; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60
DB 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60

QY 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91
DB 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 2

hypotheetical protein b2962 - Escherichia coli (strain K-12)

C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9

A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(ii) trafficking protein Y9gx

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60
DB 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60

QY 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91
DB 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 3

hypotheetical protein Ecs3838 [imported] - Escherichia coli (strain O157:H7, substrain RI

C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C:Accession: F91108

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc

A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91108

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-91 <NAV>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAH37261.1;

A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:

A:Gene: Ecs3838
C:Superfamily: fe(ii) trafficking protein Y9gx

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60
DB 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60

QY 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91
DB 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 4

conserved hypotheetical protein STY3266 [imported] - Salmonella enterica subsp. enterica

C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C:Accession: AH0879

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
A:Authors: Farry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AH0879
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-91 <PAR>
A:Cross-references: UNIPARC:UPI00005444C; GB:AL513382; PIDN:CAD02936.1; PID:G16504189;

C:Genetics:
C:Superfamily: fe(ii) trafficking protein Y9gx

Query Match 96.5%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 7.9e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60
DB 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60

QY 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91
DB 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 5

conserved hypotheetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: C82320

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellera, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A62035; MUID:20406833; PMID:10952301
A:Accession: C82320

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-90 <HEI>
A:Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:

A:Experimental source: serogroup O1; strain N16961; biotype El tor
C:Genetics:

A:Gene: VC0451
A:Map position: 1
C:Superfamily: fe(ii) trafficking protein Y9gx

Query Match 82.7%; Score 402; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 3.6e-33;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60
DB 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEAQAQWQHKTMLINEKLLNMNNA 60

QY 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 90

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 66.1725 Seconds

(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-36

Perfect score: 486
Sequence: 1 MSRTTCTPLQREAEAGDFO.....NFLPFGKXVHTEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481	99.0	90	1	P048P4 escherichia
2	481	99.0	90	1	P048P3 escherichia
3	481	99.0	90	1	P048P5 shigella fl
4	477	98.1	90	1	O86f18 escherichia
5	464	95.5	90	1	O57K04 salmonella
6	464	95.5	90	1	O57K04 salmonella
7	464	95.5	90	1	P67618 salmonella
8	464	95.5	90	1	P67617 salmonella
9	411	84.6	90	1	O66m3 yersinia ps
10	404	83.1	90	1	O9kuz4 vibrio chol
11	402	82.7	90	1	O8dccc5 vibrio vuln
12	402	82.7	90	1	O7mhl4 vibrio vuln
13	399	82.1	90	1	O8bhe7 yersinia pe
14	396	81.5	90	1	O65vt7 mannheimia
15	389	80.0	90	1	P43048 haemophilus
16	387	79.6	90	1	O4qmd9 haemophilus
17	387	79.6	90	1	O61mk7 photobacter
18	382	78.6	90	1	O7a711 photobacter
19	381	78.4	90	1	O9c1b9 pasteurella
20	379	78.0	90	1	O7kdb6 haemophilus
21	373	76.7	90	1	O567t0 vibrio fusc
22	366	75.3	90	1	O567t0 vibrio fusc
23	366	75.3	90	1	O567t0 vibrio fusc
24	335	68.9	90	1	O567t0 vibrio fusc
25	332	68.3	92	1	O567t0 vibrio fusc
26	265	54.5	90	1	O567t0 vibrio fusc
27	255	52.5	90	1	O799q2 bordetella
28	255	52.5	90	1	O799q2 bordetella
29	255	52.5	90	1	O799q2 bordetella
30	247	50.8	90	1	O8d3cs wlglesworth
31	235	48.4	78	1	O8d3cs wlglesworth

32	231.5	47.6	89	1	PETP_LEGPA	O5x3x9 legionella
33	231.5	47.6	89	1	PETP_LEGPH	O5x3x9 legionella
34	231.5	47.6	90	1	PETP_PSEAB	O5x3x9 pseudomonas
35	231	47.5	91	1	PETP_XANAC	O5x3x9 pseudomonas
36	228.5	47.0	89	1	PETP_LEGPA	O5x3x9 pseudomonas
37	227	46.7	90	1	PETP_COXHU	O5x3x9 pseudomonas
38	227	46.7	90	1	PETP_PSEAB	O5x3x9 pseudomonas
39	227	46.7	90	2	O421P3 PSEBSY	O5x3x9 pseudomonas
40	226	46.5	90	1	PETP_XYLP	O5x3x9 pseudomonas
41	225	46.3	90	1	PETP_PSEBK	O5x3x9 pseudomonas
42	225	46.3	92	1	PETP_XANOR	O5x3x9 pseudomonas
43	223	45.9	90	2	O4228_AZCVI	O5x3x9 pseudomonas
44	222	45.7	90	1	PETP_XYLP	O5x3x9 pseudomonas
45	222	45.7	92	2	PETP_XANCP	O5x3x9 pseudomonas
46	222	45.7	90	1	O4UW14_XANCP	O5x3x9 pseudomonas
47	220	45.3	90	1	PETP_NITRU	O5x3x9 pseudomonas
48	215	44.2	87	1	O6T7F6_PSEFL	O5x3x9 pseudomonas
49	214	44.0	87	1	PETP_BUCBP	O5x3x9 pseudomonas
50	213	43.8	88	1	PETP_NEIGA	O5x3x9 pseudomonas
51	213	43.8	88	1	PETP_NEIMA	O5x3x9 pseudomonas
52	213	43.8	88	1	PETP_NEIMA	O5x3x9 pseudomonas
53	212	43.6	79	1	PETP_CANRP	O5x3x9 pseudomonas
54	212	43.6	90	2	O4K1Z_PSEPS	O5x3x9 pseudomonas
55	211	43.4	90	1	PETP_CHRYO	O5x3x9 pseudomonas
56	207	42.6	91	2	O4LS19_9BURK	O5x3x9 pseudomonas
57	206	42.4	91	1	PETP_BURPS	O5x3x9 pseudomonas
58	206	42.4	91	1	PETP_BURPS	O5x3x9 pseudomonas
59	206	42.4	91	1	PETP_RALSO	O5x3x9 pseudomonas
60	200	41.2	90	1	PETP_METCA	O5x3x9 pseudomonas
61	199	40.9	87	1	PETP_FRATY	O5x3x9 pseudomonas
62	194.5	40.0	90	1	PETP_AC1AD	O5x3x9 pseudomonas
63	144	29.6	96	2	O4FVJ7_9GAMM	O5x3x9 pseudomonas
64	142	29.2	92	2	O4NM04_9BELT	O5x3x9 pseudomonas
65	90.5	18.6	482	2	O5NM04_9BURK	O5x3x9 pseudomonas
66	85.5	17.6	514	2	O4I2P3_PSEBK	O5x3x9 pseudomonas
67	81	16.7	507	2	O4I2P3_PSEBK	O5x3x9 pseudomonas
68	81	16.7	508	2	O4I2P3_PSEBK	O5x3x9 pseudomonas
69	80	16.5	486	2	O4I2P3_PSEBK	O5x3x9 pseudomonas
70	78.5	16.2	760	2	O4VXR2_PLABE	O5x3x9 pseudomonas
71	78	16.0	507	2	O4I2P3_PSEBK	O5x3x9 pseudomonas
72	78	16.0	546	2	O4I2P3_PSEBK	O5x3x9 pseudomonas
73	78	16.0	2248	2	O4I2P3_PSEBK	O5x3x9 pseudomonas
74	77.5	15.9	337	2	O4I2P3_PSEBK	O5x3x9 pseudomonas
75	77.5	15.9	1123	2	O7R1J0_PLAYO	O5x3x9 pseudomonas

ALIGNMENTS

RESULT 1
ID PETP_ECO57 STANDARD; PRT; 90 AA.
AC P048P4; P52065; (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein. EC83838;
GN Name=y99x; OrderedLocNames=24307, EC83838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
CX NCBI_TaxID=83334;
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RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Rose D.N., Plunkett G., Burtand V., Mau B., Glaesner J.D.,
RA Rose D.N., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Heckert J., Klink S., Boutin A., Shao Y., Miller L.,
RA Gottlieb B.J., Davis N.W., Lim A., Dimalanta E.T., Potanowits K.,
RA Apodaca J., Anantharaman T.S., Iln J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

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RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC.
RX MEDLINE=21156231, PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Tida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Reg. 8:11-22(2001).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE005174; AAG58093.1; -; Genomic DNA.
CC EMBL; BA000007; BAB37261.1; -; Genomic DNA.
CC PIR; A85954; A85954.
CC PIR; F91108; F91108.
CC HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; Y9GX.
CC Pfam; PF04362; DUF495; 1.
CC DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
CC DR ProDom; PD029191; DUF495; 1.
CC KW Complete proteome; Iron.
CC FT INIT MET 0
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;
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Best Local Similarity 100.0%; Fred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTICTFLQREABGDFOLYVGEIGKRIYNEISKAWAQMOKOTMLINEKGLMMNAE 61
DB 1 SRTICTFLQREABGDFOLYVGEIGKRIYNEISKAWAQMOKOTMLINEKGLMMNAE 60
QY 62 HRKLLQEMVNFLEFGKEVHIGYTPEDKK 91
DB 61 HRKLLQEMVNFLEFGKEVHIGYTPEDKK 90
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AC POA8P3; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Probable Fe(2+) trafficking protein.
DB Name=Y9GX; OrderedLocustNames=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCB1_TaxId=562;
OK [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97443975; PubMed=9298646;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Berra N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Klinkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RT Science 277:1453-1474(1997).

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RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12."
RL Electrophoresis 18:1259-1313(1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=10493123;
RA Wastner V.C., Humphrey-Smith I.;
RT "Small genes/gene-products in Escherichia coli K-12."
RL FEMS Microbiol. Lett. 169:375-382(1998).
RN [4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/(SICI)1522-2663(19990801)20:11<2181::AID-ELPS2181>3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RT hydroxyapatite chromatography."
RL Electrophoresis 20:2181-2195(1999).
RN [5]
RP INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.J., Koutouloutsou A., Carrasco D., Demple B.;
RT "SoxRS-regulated expression and genetic analysis of the Y9GX gene of
RT Escherichia coli."
RL J. Bacteriol. 185:6624-6632(2003).
RN [6]
RP STRUCTURE BY NMR, AND FUNCTION.
RX PubMed=15883188; DOI=10.1110/PS.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;
RT "The solution structure of the oxidative stress-related protein Y9GX
RT from Escherichia coli."
RL Protein Sci. 14:1673-1678(2005).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes. Necessary to
CC maintain high levels of aconitase under oxidative stress.
CC -1- SUBUNIT: Monomer (Probable).
CC -1- INDUCTION: By oxidative stress and soxS.
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U28377; AAA69129.1; -; Genomic DNA.
CC EMBL; U00096; AAC75999.1; -; Genomic DNA.
CC PIR; A65082; A65082.
CC PDB; 1YHD; NMR; A=1-90.
CC SWISS-2DPAGE; POA8P3; COLI.
CC ECHOBASE; EB2809; -.
CC DR HAMAP; MF_00686; -; 1.
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; Y9GX.
CC Pfam; PF04362; DUF495; 1.
CC DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
CC DR ProDom; PD029191; DUF495; 1.
CC KW 3D-structure; Complete proteome; Direct protein sequencing; Iron.
CC FT INIT MET 0
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;
SQ
Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Fred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTICTFLQREABGDFOLYVGEIGKRIYNEISKAWAQMOKOTMLINEKGLMMNAE 61

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GenCore version 5.1.7
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411.985 Million cell updates/sec

Title: US-09-955-502a-36

Perfect score: 486

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/1aa/6-COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/7-COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/8-COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/9-COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	450	92.6	107	2	US-09-489-039A-11962
2	389	80.0	93	2	US-09-543-681A-5443
3	231	47.5	122	2	US-09-252-991A-23355
4	199.5	41.0	92	2	US-09-328-352-5456
5	131	27.0	110	2	US-09-540-236-2859
6	76	15.6	548	2	US-09-167-299-3
7	72	14.8	474	2	US-09-252-991A-24473
8	70.5	14.5	1214	2	US-10-164-595-24
9	67.5	13.9	184	2	US-09-325-932A-66
10	67.5	13.9	546	1	US-08-533-669A-2
11	67.5	13.9	546	2	US-09-183-861-2
12	67.5	13.9	546	2	US-09-022-765-2
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14	67.5	13.9	546	2	US-09-565-501A-2
15	67.5	13.9	546	2	US-09-639-206A-2
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17	67.5	13.9	546	2	US-08-798-841-2
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19	67.5	13.9	982	2	US-09-565-501A-95
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23	67.5	13.9	1427	2	US-09-565-501A-97
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28	67.5	13.9	1641	2	US-09-639-206A-96	Sequence 96, Appl
29	67.5	13.9	1641	2	US-09-874-923-96	Sequence 96, Appl
30	65.5	13.5	395	2	US-09-914-098-46	Sequence 46, Appl
31	65	13.4	292	2	US-09-328-352-5936	Sequence 5836, Ap
32	64.5	13.3	209	2	US-09-252-991A-20905	Sequence 20905, A
33	64	13.2	227	2	US-09-270-767-58283	Sequence 58283, A
34	64	13.2	280	2	US-09-323-998B-37	Sequence 37, Appl
35	64	13.2	448	2	US-09-270-767-42959	Sequence 42959, A
36	64	13.2	534	2	US-09-312-762A-5	Sequence 5, Appl
37	63.5	13.1	591	2	US-09-370-368-8	Sequence 8, Appl
38	63	13.0	525	2	US-09-540-236-2250	Sequence 2250, Ap
39	63	13.0	569	2	US-09-107-533A-6689	Sequence 6689, Ap
40	62.5	12.9	325	2	US-09-134-000C-3346	Sequence 4346, Ap
41	62.5	12.9	544	2	US-09-248-796A-18911	Sequence 18911, A
42	62.5	12.9	798	2	US-09-861-451A-12	Sequence 12, Appl
43	62	12.8	959	2	US-09-543-681A-6879	Sequence 6879, Ap
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45	62	12.8	1501	2	US-09-710-279-2850	Sequence 2850, Ap
46	62	12.8	1529	2	US-09-134-001C-3945	Sequence 3945, Ap
47	61.5	12.7	57	2	US-09-562-737-124	Sequence 125, App
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49	61.5	12.7	311	2	US-09-248-796A-26397	Sequence 7295, Ap
50	61.5	12.7	419	2	US-09-543-681A-7295	Sequence 4, Appl
51	61.5	12.7	680	2	US-09-298-924-4	Sequence 1, Appl
52	61.5	12.7	720	1	US-08-840-236-1	Sequence 1004, Ap
53	61.5	12.7	720	1	US-08-505-448A-1	Sequence 16, Appl
54	61	12.6	308	2	US-09-198-452A-1004	Sequence 934, App
55	61	12.6	444	2	US-09-861-451A-16	Sequence 4802, Ap
56	61	12.6	480	2	US-09-438-185A-934	Sequence 6012, Ap
57	60.5	12.4	139	2	US-09-513-999C-4802	Sequence 11703, A
58	60.5	12.4	258	2	US-09-513-999C-4800	Sequence 48, Appl
59	60.5	12.4	264	2	US-09-949-016-6012	Sequence 2, Appl
60	60.5	12.4	276	2	US-09-949-016-11703	Sequence 7, Appl
61	60.5	12.4	404	2	US-09-914-098-48	Sequence 41085, A
62	60.5	12.4	640	2	US-09-873-404-2	Sequence 56301, A
63	60.5	12.4	640	2	US-10-243-733-2	Sequence 61671, A
64	60.5	12.4	1076	2	US-09-171-991-7	Sequence 19265, A
65	60	12.3	98	2	US-09-270-767-41085	Sequence 221, App
66	60	12.3	98	2	US-09-270-767-56301	Sequence 205, App
67	60	12.3	184	2	US-09-270-767-61671	Sequence 6400, Ap
68	60	12.3	271	2	US-09-248-796A-19265	Sequence 41746, A
69	60	12.3	279	2	US-09-198-452A-221	Sequence 46116, A
70	60	12.3	279	2	US-09-438-185A-205	Sequence 8705, Ap
71	60	12.3	331	2	US-09-328-352-6400	Sequence 32, Appl
72	60	12.3	337	2	US-09-270-767-41746	
73	60	12.3	389	2	US-09-270-767-46116	
74	60	12.3	410	2	US-09-949-016-8705	
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ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 2004001
CURRENT FILING DATE: 2000-01-27
PRIORITY FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity 91.2%; Pred. No. 1e-46; Indels 0; Gaps 0;
Matches 83; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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DB 61 EHRKLLQEMVNFLEPGKEVHIEGYTPEDK 91
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US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
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; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Best Local Similarity 80.0%; Pred. No. 3.8e-41; Indels 0; Gaps 0;
Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREABGQDFOLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNA 60
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DB 61 EHRKLLQEMVNFLEPGKEVHIEGYTPEDK 90
64 DRRKLLQEMVRFLEPGHVDHIDGYTPPEK 93

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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DB 33 MSRTTCTFLQREABGQDFOLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNA 92
QY 61 EHRKLLQEMVNFLEPGKEVHIEGYTP 87
DB 93 EDRKFLQEMDKFLSGEDYAKADGYVP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-035A
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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DB 61 EHRKLLQEMVNFLEPGKEVHIEGYTP 88
64 EAKKFLQEMVRFLEPGHVDHIDGYTPPEK 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

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DB 65 LLEQEMVNFLEPGKEVHIEGYTP 87
85 YLNEQREKFLDNGDYERKAGYTP 107

RESULT 6
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OM protein - protein search, using sw model

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Title: US-09-955-502a-36

Perfect score: 486

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database: Published Applications AA.Main:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	91	3	US-09-955-502-11
2	486	100.0	91	3	US-09-955-502-12
3	486	100.0	91	3	US-09-955-502-13
4	469	96.5	91	3	US-09-955-502-14
5	469	96.5	91	3	US-09-955-502-16
6	469	96.5	91	3	US-09-955-502-17
7	455	93.6	91	3	US-09-955-502-18
8	453	93.2	88	3	US-09-955-502-15
9	402	82.7	90	3	US-09-955-502-10
10	396	81.5	90	3	US-09-955-502-20
11	395	81.3	78	3	US-09-955-502-19
12	388	79.8	91	3	US-09-955-502-5
13	387	79.6	87	3	US-09-955-502-7
14	379	78.0	87	3	US-09-955-502-8
15	373	76.7	87	3	US-09-955-502-6
16	332	68.3	88	3	US-09-955-502-9
17	265	54.5	76	3	US-09-955-502-21
18	255	52.5	87	3	US-09-955-502-2
19	255	52.5	87	3	US-09-955-502-3
20	241	49.6	86	3	US-09-955-502-4
21	231	47.5	87	3	US-09-955-502-25
22	227	46.7	88	3	US-09-955-502-33
23	226	46.5	90	3	US-09-955-502-23
24	225	46.3	89	3	US-09-955-502-22
25	213	43.8	87	3	US-09-955-502-24
26	213	43.8	88	3	US-09-955-502-26
27	213	43.8	88	3	US-09-955-502-27

ALIGNMENTS

RESULT 1
US-09-955-502-11
Sequence 11, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 91
TYPE: PRT
ORGANISM: Escherichia coli K-12 MG1655

US-09-955-502-11

Query Match 100.0%; Score 486; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.2e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLORAEAGDGFOLYPGELGKRIYNEISKMAWQOHKOTMLINEKCLNMNNA 60
DB 1 MSRTTCTFLORAEAGDGFOLYPGELGKRIYNEISKMAWQOHKOTMLINEKCLNMNNA 60
QY 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 2

US-09-955-502-12
Sequence 12, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 91
TYPE: PRT
ORGANISM: Escherichia coli O157:H7EDL933
US-09-955-502-12

Query Match 100.0%; Score 486; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 7.2e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLORAEAGDGFOLYPGELGKRIYNEISKMAWQOHKOTMLINEKCLNMNNA 60
DB 1 MSRTTCTFLORAEAGDGFOLYPGELGKRIYNEISKMAWQOHKOTMLINEKCLNMNNA 60
QY 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 3

US-09-955-502-13
Sequence 13, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 91
TYPE: PRT
ORGANISM: Escherichia coli O157:H7
US-09-955-502-13

Query Match 100.0%; Score 486; DB 3; Length 91;

Best Local Similarity 100.0%; Pred. No. 7.2e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLORAEAGDGFOLYPGELGKRIYNEISKMAWQOHKOTMLINEKCLNMNNA 60
DB 1 MSRTTCTFLORAEAGDGFOLYPGELGKRIYNEISKMAWQOHKOTMLINEKCLNMNNA 60
QY 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 4

US-09-955-502-14
Sequence 14, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 91
TYPE: PRT
ORGANISM: Salmonella paratyphi
US-09-955-502-14

Query Match 96.5%; Score 469; DB 3; Length 91;
Best Local Similarity 94.5%; Pred. No. 5.9e-45;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLORAEAGDGFOLYPGELGKRIYNEISKMAWQOHKOTMLINEKCLNMNNA 60
DB 1 MSRTTCTFLORAEAGDGFOLYPGELGKRIYNEISKMAWQOHKOTMLINEKCLNMNNA 60
QY 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPEDKK 91
DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 5

US-09-955-502-16
Sequence 16, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 91
TYPE: PRT
ORGANISM: Salmonella dublin
US-09-955-502-16

Query Match 96.5%; Score 469; DB 3; Length 91;
Best Local Similarity 94.5%; Pred. No. 5.9e-45;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4,82187 Seconds
(without alignments)
280,957 Million cell updates/sec

Title: US-09-955-502a-36

Perfect score: 486
Sequence: 1 MSRTFCTFLQREAGQDFQ.....NFLPFGKVLHGTYPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New.*
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
6: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	43.8	88	6	US-10-467-657-968
2	66	13.6	593	7	US-11-194-246-317
3	65.5	13.5	395	7	US-11-009-658-46
4	65	13.4	478	6	US-10-821-234-915
5	62	12.8	1501	6	US-10-793-626-2850
6	61.5	12.7	179	6	US-10-467-657-6542
7	60.5	12.4	264	6	US-10-821-234-1555
8	60.5	12.4	404	7	US-11-009-658-48
9	60.5	12.4	834	6	US-10-453-372-658
10	60	12.3	448	6	US-10-618-320A-25
11	60	12.3	480	6	US-10-510-386-12
12	60	12.3	667	6	US-10-793-626-198
13	59.5	12.2	177	6	US-10-467-657-1658
14	59	12.1	266	5	US-09-995-493-6
15	59	12.1	604	6	US-10-942-072-4
16	59	12.1	1142	7	US-11-109-156-22
17	59	12.1	1167	6	US-10-942-072-6
18	58.5	12.0	336	6	US-10-453-372-640
19	58.5	12.0	349	6	US-10-821-234-1387
20	58.5	12.0	577	7	US-11-072-175-187
21	58.5	12.0	695	6	US-10-453-372-648
22	58.5	12.0	700	6	US-10-995-561-922
23	58.5	12.0	700	6	US-10-995-561-924
24	58.5	12.0	775	6	US-10-453-372-656
25	58.5	12.0	793	6	US-10-995-561-925

26	58.5	12.0	804	6	US-10-453-372-650	Sequence 650, App
27	58.5	12.0	847	6	US-10-453-372-652	Sequence 654, App
28	58.5	12.0	857	6	US-10-453-372-652	Sequence 654, App
29	58.5	12.0	905	6	US-10-453-372-652	Sequence 658, App
30	58.5	12.0	905	6	US-10-453-372-652	Sequence 662, App
31	58.5	12.0	905	6	US-10-453-372-652	Sequence 664, App
32	58.5	12.0	963	6	US-10-995-561-923	Sequence 923, App
33	58.5	12.0	963	6	US-10-453-372-660	Sequence 660, App
34	58.5	12.0	1012	6	US-10-453-372-646	Sequence 646, App
35	58.5	12.0	1299	6	US-10-821-234-1145	Sequence 1145, App
36	58.5	12.0	3803	6	US-10-995-561-773	Sequence 773, App
37	58.5	12.0	3960	6	US-10-995-561-771	Sequence 771, App
38	58.5	12.0	5335	6	US-10-995-561-777	Sequence 777, App
39	58.5	12.0	5406	6	US-10-995-561-774	Sequence 774, App
40	58.5	12.0	5415	6	US-10-995-561-779	Sequence 779, App
41	58.5	12.0	5464	6	US-10-995-561-775	Sequence 775, App
42	58.5	12.0	5935	6	US-10-995-561-776	Sequence 776, App
43	58	11.9	251	7	US-11-054-515-1496	Sequence 1496, App
44	58	11.9	1995	7	US-11-069-834-60	Sequence 60, App
45	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
46	57	11.7	194	7	US-11-072-512-2906	Sequence 2906, App
47	57	11.7	279	7	US-11-098-686-10812	Sequence 10812, App
48	57	11.7	504	7	US-11-072-512-3467	Sequence 3467, App
49	56	11.5	296	7	US-11-087-227-10	Sequence 10, App
50	56	11.5	372	7	US-11-143-986-5	Sequence 5, App
51	56	11.5	372	7	US-11-143-986-6	Sequence 6, App
52	56	11.5	386	7	US-11-143-986-2	Sequence 2, App
53	56	11.5	386	7	US-11-143-986-3	Sequence 3, App
54	56	11.5	397	7	US-11-022-562-223	Sequence 223, App
55	56	11.5	426	7	US-11-098-686-10340	Sequence 10340, App
56	56	11.5	427	7	US-11-186-284-91	Sequence 91, App
57	56	11.5	481	6	US-10-793-626-28	Sequence 28, App
58	56	11.5	697	6	US-10-485-517-202	Sequence 202, App
59	56	11.5	752	6	US-10-793-626-1036	Sequence 1036, App
60	56	11.5	1168	6	US-10-942-072-11	Sequence 11, App
61	56	11.5	1188	7	US-11-115-639-42	Sequence 42, App
62	56	11.5	1188	7	US-11-115-639-43	Sequence 43, App
63	56	11.5	1404	6	US-10-878-556A-169	Sequence 169, App
64	55.5	11.4	207	7	US-11-124-367A-438	Sequence 437, App
65	55.5	11.4	317	7	US-11-124-367A-437	Sequence 436, App
66	55.5	11.4	328	7	US-11-124-367A-436	Sequence 3856, App
67	55.5	11.4	440	7	US-11-072-512-3856	Sequence 2547, App
68	55.5	11.4	623	7	US-11-072-512-2547	Sequence 23, App
69	55.5	11.4	2101	6	US-10-857-780-23	Sequence 61, App
70	55	11.3	257	6	US-10-667-295-61	Sequence 1710, App
71	55	11.3	257	7	US-11-084-515-1710	Sequence 60, App
72	55	11.3	286	6	US-10-667-295-60	Sequence 59, App
73	55	11.3	327	6	US-10-667-295-59	Sequence 8, App
74	55	11.3	359	7	US-11-087-227-8	Sequence 6, App
75	55	11.3	359	7	US-11-192-450-6	

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwinn9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match
Best Local Similarity 43.8%; Score 213; DB 6; Length 88;
Matches 39; Conservative 16; Mismatches 33; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDPOLYPGELGRIYNEISKEAMAOHQKQTMLINEKLMNNA 60
DB 1 MARWFCVCLNKEAEAGMKPEPLPNEIGKRIFFENVSQEAAMATRHQTMLINEKRLSLADP 60

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPE 88
DB 61 RAREYLAQQMEQYFPDGDADAVQGYVPO 88

RESULT 2
US-11-194-246-317
Sequence 317, Application US/11194246
Publication No. US20050272089A1
GENERAL INFORMATION:
APPLICANT: Mott, John
APPLICANT: Treppod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET

FILE REFERENCE: 00592.US1 (Mar 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: Patentin version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match
Best Local Similarity 44.4%; Score 66; DB 7; Length 593;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 35 SKEAMAOHQKQTMLINEKLMNNAE 61
DB 296 SKQWRMYEAKQDILKTKLTLSKE 322

RESULT 3
US-11-009-658-46
Sequence 46, Application US/11009658
Publication No. US20060003430A1
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: lysophosphatidic Acid Acetyltransferases
FILE REFERENCE: BB1332
CURRENT APPLICATION NUMBER: US/11/009,658
CURRENT FILING DATE: 2004-12-10
PRIOR APPLICATION NUMBER: US/09/914,098
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/121,119
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Microsoft Office 97
SEQ ID NO 46
LENGTH: 395
TYPE: PRT
ORGANISM: Zea mays

US-11-009-658-46

Query Match
Best Local Similarity 13.5%; Score 65.5; DB 7; Length 395;
Matches 28; Conservative 19; Mismatches 36; Indels 45; Gaps 4;

QY 1 MSRTIFCTFLQREAGQDPOLYPGELGRIYNEISKEAMAOHQKQTMLINEKLMNNA 52
DB 224 ISKLGICIFVQRESKTPDFKGVSGAVSERIH-----RAHQQKNA PMMLPFGGTTNGDY 278

QY 53 -----KLN-----MNAEHRKLEQEMVNFLEPGKEVHIE 83
DB 279 LLPFTGALAKAPQVILRYPYKRFMAWDSGARGHVLILCOFVNYL---EVALP 335

QY 84 GYTPEDKX 91
DB 336 VYPSBQS 343

RESULT 4
US-10-821-234-915
Sequence 915, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andermani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia

FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PC_SEQ_genes Version 1.0
SEQ ID NO 915
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-915

Query Match
Best Local Similarity 13.4%; Score 65; DB 6; Length 478;
Matches 27; Conservative 18; Mismatches 26; Indels 34; Gaps 5;

QY 8 TFLQREAGQDP--QLYP-----GELGRIYNEISKEAMAOHQKQTM 48
DB 380 SYLQREAYDRDFLARVYGAPQLQVEKVRTNDRKEIGEVAVQYTGDSPKAFAP---KALG 435

QY 49 LINEKLMNNAEHRKLEQEMVNFLEPGKEVHI-----EGYTP 87
DB 436 VMDLKSQVPRAGYRGI-----VTFQFRGRVHLAPPTWGYDP 475

RESULT 5
US-10-793-626-2850
Sequence 2850, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY WILLIAM JOHN
TITLE OF INVENTION: STRAPHLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2850
LENGTH: 1501
TYPE: PRT
ORGANISM: Artificial Sequence

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 73.1567 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-37

Perfect score: 473
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Scoring table: BLOSUM62
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Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

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2: Geneseq19908:.*
3: Geneseq20008:.*
4: Geneseq20018:.*
5: Geneseq20028:.*
6: Geneseq20038:.*
7: Geneseq20048:.*
8: Geneseq20058:.*
9: Geneseq20068:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	473	100.0	90	5	ABB78165 Amino aci
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3	396	83.7	91	5	ABB78158 Amino aci
4	396	83.7	91	5	ABB78157 Amino aci
5	396	83.7	91	5	ABB78156 Amino aci
6	393	83.1	91	5	ABB78161 Amino aci
7	393	83.1	91	5	ABB78159 Amino aci
8	393	83.1	91	5	ABB78162 Amino aci
9	389	82.2	93	7	ADFO5158 Bacteriat
10	389	82.2	93	7	ADFO5158 Bacteriat
11	379	80.1	91	5	ABB78163 Amino aci
12	366	77.4	90	5	ABB78155 Amino aci
13	363	76.7	87	5	ABB78152 Amino aci
14	357	75.5	91	5	ABB78150 Amino aci
15	351	74.2	87	5	ABB78153 Amino aci
16	346	72.2	87	5	ABB78151 Amino aci
17	342	72.3	78	5	ABB78164 Amino aci
18	308	65.1	76	5	ABB78154 Amino aci
19	256	54.1	76	5	ABB78166 Amino aci
20	233	49.3	88	5	ABB78178 Amino aci
21	226	47.8	87	5	ABB78148 Amino aci
22	226	47.8	87	5	ABB78147 Amino aci
23	221	46.7	122	7	ABO74609 Pseudomon
24	218.5	46.2	89	9	ABE41576 L. pneumo

25	218.5	46.2	95	9	ABB38294 L. pneumo
26	212	44.8	86	5	ABB78149 Amino aci
27	210	44.4	87	5	ABB78170 Amino aci
28	206	43.6	90	5	ABB78168 Amino aci
29	199	42.1	87	5	ABB78175 Amino aci
30	198	41.9	88	5	ABB78171 Amino aci
31	198	41.9	88	5	ABB78172 Amino aci
32	198	41.9	88	5	ABB78173 Amino aci
33	198	41.9	88	5	ABB78174 Amino aci
34	194.5	41.1	90	5	ABB78167 Amino aci
35	193	40.8	87	5	ABB78174 Amino aci
36	188	39.7	87	5	ABB78169 Amino aci
37	186	39.3	87	5	ABB78177 Amino aci
38	186	39.3	87	5	ABB78176 Amino aci
39	176.5	37.3	92	6	ADA34169 Acinetoba
40	175.5	37.3	92	6	ADA34169 Acinetoba
41	143	30.2	110	8	ADL05173 M. catarr
42	81	17.1	102	5	ABP31411 Human ORF
43	81	17.1	2000	6	ABP31411 Human ORF
44	81	17.1	2000	7	ADK62602 Disease t
45	74	15.6	397	4	ABB11207 Human PI-
46	74	15.6	403	6	ABM71645 Staphyloc
47	74	15.6	506	5	AAU79180 Human par
48	74	15.6	576	4	ABG19914 Novel hum
49	74	15.6	589	5	ABM47871 ISGP-1.
50	74	15.6	1116	4	AA667293 Amino aci
51	74	15.6	1116	5	AAU79181 Human pro
52	73.5	15.5	641	6	ADM87230 Human pro
53	73	15.4	397	8	ADM67978 Photorhab
54	70.5	14.9	635	4	ADM87687 Human EST
55	70	14.8	869	3	ADM69129 Drosophili
56	70	14.8	869	3	ADM69129 Drosophili
57	69.5	14.7	867	6	ADM64441 Thermosta
58	69.5	14.7	870	7	ADFO4483 Protein e
59	68.5	14.7	1589	4	ABG08898 Novel hum
60	68.5	14.7	1589	4	ABG22603 Novel hum
61	68.5	14.7	1589	4	ABG30099 Novel hum
62	69.5	14.7	1589	4	ABG28504 Novel hum
63	69.5	14.7	1589	4	ABG04197 Novel hum
64	69	14.6	209	7	ABO72159 Pseudomon
65	68	14.4	256	6	ABU25179 Protein e
66	68	14.4	344	7	ABO23534 Borrella
67	68	14.4	506	3	AAV74371 Neisseria
68	67.5	14.3	617	5	AAW49439 Pyrococcu
69	67.5	14.3	701	7	ABO74542 Pseudomon
70	67	14.2	415	2	AAW22982 Canine he
71	67	14.2	415	2	AAW72649 Canine he
72	67	14.2	415	2	AAW72649 Canine he
73	67	14.2	415	2	AAW72649 Canine he
74	66.5	14.1	184	4	AAE39123 CHV PCG5
75	66.5	14.1	758	8	ABO04791 Novel hum
					ABE21214 Bacteriat

ALIGNMENTS

RESULT 1	ABB78165	standard, protein, 90 AA.
ID	ABB78165	standard, protein, 90 AA.
AC	ABB78165	
XX		
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KM	hydroxyl radical; DNA damage; YggX homologue.	
XX		
OS	Unidentified.	
XX		
PN	US2002072118-A1.	

PD 13-JUN-2002.
 XX
 XX 18-SEP-2001; 2001US-00955502.
 XX
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 XX
 XX WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 XX The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 XX Sequence 90 AA;
 SQ

Query Match 100.0%; Score 473; DB 5; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.3e-48;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTFCFTFLKKDAERDQPOLYPGEIGKRIYNEISKAMSGWITKQTMLINEKLSMMNI 60
 DB 1 MSRTTFCFTFLKKDAERDQPOLYPGEIGKRIYNEISKAMSGWITKQTMLINEKLSMMNI 60
 QY 61 EDRKLLBOEMVNFLEFGQDVHIAGYTPPSK 90
 DB 61 EDRKLLBOEMVNFLEFGQDVHIAGYTPPSK 90

RESULT 2
 ABO65445
 ID ABO65445 standard; protein; 107 AA.
 XX
 XX ABO65445;
 AC
 XX 29-JUL-2004 (first entry)
 DT
 XX Klebsiella pneumoniae polypeptide seqid 11962.
 DE
 XX Recombinant expression vector; transcription regulatory element;
 XX Klebsiella pneumoniae protein; antibacterial; Vaccine.
 KM
 XX Klebsiella pneumoniae.
 OS
 XX US6610836-B1.
 PN
 XX 26-AUG-2003.
 PD
 XX 27-JAN-2000; 2000US-00489039.
 PF
 XX 29-JAN-1999; 99US-0117747P.
 PR
 XX (GENO-) GENOME THERAPEUTICS CORP.
 PA
 XX Breton GL, Osborne M;
 PI
 XX WPI; 2003-895346/82.
 DR

DR N-PSDB; ACH98996.
 XX
 XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 PT
 XX
 XX Disclosure; SEQ ID NO 11962; 932pp; English.
 XX

The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention

Query Match 84.6%; Score 400; DB 7; Length 107;
 Best Local Similarity 83.3%; Pred. No. 1.5e-39;
 Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTTFCFTFLKKDAERDQPOLYPGEIGKRIYNEISKAMSGWITKQTMLINEKLSMMNI 60
 DB 17 MSRTTFCFTFLKKDAERDQPOLYPGEIGKRIYNEISKAMSGWITKQTMLINEKLSMMNI 76
 QY 61 EDRKLLBOEMVNFLEFGQDVHIAGYTPPSK 90
 DB 77 EHRKLLBOEMVNFLEFGQDVHIAGYTPPSK 106

RESULT 3
 ABB78158
 ID ABB78158 standard; protein; 91 AA.
 XX
 XX ABB78158;
 AC
 XX 05-NOV-2002 (first entry)
 DT
 XX Amino acid sequence of a YggX homologue.
 DE
 XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.
 KW
 XX Unidentified.
 OS
 XX US2002072118-A1.
 PN
 XX 13-JUN-2002.
 PD
 XX 18-SEP-2001; 2001US-00955502.
 PF
 XX 22-SEP-2000; 2000US-0234588P.
 PR
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 PI
 XX WPI; 2002-589476/63.
 DR

Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 XX The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from *Salmonella enterica* serovar Typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.7407 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-37

Perfect score: 473

Sequence: 1 MSRTFCTELKKDAERQDFQ.....VNFLPEGQDVHAGYTPPSK 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	100.0	90	2	A10116 conserved hypothe
2	396	83.7	91	2	A85954 hypothetical prote
3	396	83.7	91	2	A65082 hypothetical prote
4	396	83.7	91	2	P91108 hypothetical prote
5	393	83.1	91	2	AH0879 conserved hypothe
6	374	79.1	90	2	C64013 conserved hypothe
7	366	77.4	90	2	C64320 conserved hypothe
8	256	54.1	93	2	B84994 conserved hypothe
9	221	46.7	90	2	H83003 conserved hypothe
10	203	42.9	105	2	C82624 conserved hypothe
11	198	41.9	88	2	H81014 conserved hypothe
12	81	17.1	2672	2	A48126 translation activa
13	76.5	16.2	511	2	A39574 ABC transporter at
14	74	15.6	403	2	B89808 conserved hypothe
15	71.5	15.1	1008	2	H72310 conserved hypothe
16	70	14.8	265	2	T46013 conserved hypothe
17	70	14.8	1119	2	T18491 conserved hypothe
18	69.5	14.7	996	2	A71080 conserved hypothe
19	69	14.6	1386	2	RMLVLC2 DNA-directed RNA p
20	68.5	14.5	165	2	A81382 shikimate kinase (
21	68	14.4	344	2	D70126 conserved hypothe
22	68	14.4	583	2	T48365 conserved hypothe
23	68	14.4	820	2	G88996 conserved hypothe
24	67.5	14.3	160	2	E70416 conserved hypothe
25	67.5	14.3	336	2	C64468 conserved hypothe
26	67.5	14.3	617	2	B71071 conserved hypothe
27	67.5	14.3	629	2	B83107 conserved hypothe
28	67	14.2	394	2	B70206 conserved hypothe
29	66.5	14.1	139	2	B97709 conserved hypothe

30	66.5	14.1	420	2	A25876 vitellogenin III p
31	66.5	14.1	648	2	A71647 glycine-tRNA ligase
32	66	14.0	705	2	T47949 hypothetical prote
33	66	14.0	799	2	T02656 probable salt-indu
34	65.5	13.8	91	2	H90521 hypothetical prote
35	65.5	13.8	688	2	S57131 hypothetical prote
36	65	13.7	118	2	G64302 hypothetical prote
37	65	13.7	411	2	A48946 aspartate kinase (
38	65	13.7	738	2	B69863 two-component sens
39	65	13.7	2101	2	A42184 nuclear mitotic ap
40	64.5	13.6	245	2	AG2300 hypothetical prote
41	64	13.5	158	2	A59102 hypothetical prote
42	64	13.5	235	2	AD1735 hypothetical prote
43	64	13.5	346	2	P97871 uroporphyrinogen d
44	64	13.5	1611	1	WMTMPV 183K protein - pep
45	63.5	13.4	548	2	A54510 60K filarial antiq
46	63.5	13.4	548	2	A28209 Mutator-like trans
47	63.5	13.4	715	2	D84480 DNA-directed RNA p
48	63.5	13.4	884	1	RNBP3 hypothetical prote
49	63.5	13.4	1010	2	F75134 hypothetical prote
50	63.5	13.4	1119	2	T15842 hypothetical prote
51	63	13.3	254	2	A64437 hypothetical prote
52	63	13.3	264	2	G89808 hypothetical prote
53	63	13.3	269	2	A81286 hypothetical prote
54	63	13.3	507	2	C81063 fumarate hydratase
55	62.5	13.3	546	2	A81807 fumarate hydratase
56	63	13.3	821	1	A39616 protein kinase RAD
57	63	13.3	974	2	A40580 lodestar maternal-
58	63	13.3	1027	2	T27970 hypothetical prote
59	62.5	13.2	173	2	H86869 lysophospholipase
60	62.5	13.2	259	2	D69998 leukotoxin secreti
61	62.5	13.2	477	2	B61378 glycine-tRNA ligase
62	62.5	13.2	674	2	D97864 repeat organellar
63	62.5	13.2	869	2	T12422 hypothetical prote
64	62.5	13.2	1939	2	T18372 conserved hypothe
65	62	13.1	143	2	B83688 conserved hypothe
66	62	13.1	212	2	B71853 probable biotin ac
67	62	13.1	224	2	C64240 mobilization prote
68	62	13.1	353	1	ROMVGR gag polypeptide -
69	62	13.1	375	2	A26898 maipin - human
70	62	13.1	498	2	C90413 dihydroperoxide sy
71	62	13.1	593	2	C64097 probable soluble 1
72	62	13.1	1030	2	T37868 probable helicase
73	61.5	13.0	222	2	S62001 MEIS protein - Yea
74	61.5	13.0	287	2	P82265 conserved hypothe
75	61.5	13.0	339	2	A90395 conserved hypothe

ALIGNMENTS

RESULT 1
A10116 conserved hypothetical protein YP00953 [Imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: A10116
R:Parkhill, J., Wren, B.W., Thomson, N.R., Tibball, R.W., Holden, M.T.G., Prentice, M.B.,
deno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.M., Dougan, G.,
11, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S., Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A10116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <KUR>
A:Cross-references: UNIPARC:UP100000DCC4; GB:AL590842; PIRN:CAC89796.1; PIR:G15979022;
C:Genetics:
A:Gene: YP00953
C:Superfamily: fe(II) trafficking protein Y9GX
Query Match 100.0%; Score 473; DB 2; Length 90;

Best Local Similarity 100.0%; Pred. NO. 1.2e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTICTFLKDAERQDFQLYGEIGKRIYNEISKEAQSMTIQTMLNEKKLSMNI 600

DB 1 MSRTICTFLKDAERQDFQLYGEIGKRIYNEISKEAQSMTIQTMLNEKKLSMNI 600

QY	61	EDRLLEQEMVNFLEFGQDVHIAGITPPSK	90
Db	61	EDRLLEQEMVNFLEFGQDVHIAGITPPSK	90

RESULT 2

hypothetical protein ysgX [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
Cispecies: Escherichia coli

Riperna, N.T., Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001

A,Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Residues: 1-91 <S>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:ig12517511; P
A:Experimental source: strain O157:H7, substrain EDL933

A:Gene: Y9gX
C:Superfamily: Fe(II) trafficking protein Y9gX

Query Match	83.7%	Score 396	DB 2	Length 91
Best Local Similarity	82.2%	Pred. NO. 9.4e-34		
Matches 74; Conservative	8; Mismatches	8; Indels	0; Gaps	0

```

1 MSRTIFCTPLQREAGDDPOLYPBELGKRIYNEISKAAVQWQHKGITMLINEKLNMMNA 66

```

Db 61 EHRKLEQEMVNFLEFGKGVHIEGYTPEDK 90

RESULT 3

hypothetical protein b2962 - *Escherichia coli* (strain K-12)
C1Species: *Escherichia coli*

R. Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997.

A1Title: The complete genome sequence of *Escherichia coli* K-12.

A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065, UNIPARC:UPI0000163A04, GB:AEO00378, GB:U00096, NID:2
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein YggX

Query Match	83.7%	Score 396;	DB 2;	Length 91;
Best Local Similarity	82.2%	Pred. No. 9.4e-34;		
Matches 74; Conservative	8;	Mismatches 8;	Indels 0;	Gaps 0

QY 61 EDRLLEQEMVNFLEFGQDVHIAGYPSK 90
| | | | | | | | | | : | | | | |
Db 61 EHRKLEQEMVNFLEFGKEVHIIEGYPSDK 90

RESULT 4

hypothetical protein Ec33838 [imported] - Escherichia coli (strain O157:H7, substrain RH C) [Species: Escherichia coli
C:Date: 18-Jul-2001 #genome revision 18-Jul-2001 #rev change 05-Oct-2004
C:Date: 18-Jul-2001 #genome revision 18-Jul-2001 #rev change 05-Oct-2004

Gasaavara, N.; Yasunaga, T.; Kubara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A>Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno-
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession number:

A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PDB:3AB37261.1;
B:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC9383
A:Gene: EC9383
A:Gene: EC9383

Query Match	83.7%	Score 396	DB 2	Length 91
Best Local Similarity	82.2%	Pred. No.	9.4e-34	
Matches 74	Conservative 8	Mismatches 8	Indels 0	Gaps 0

Db

1 MSRTTCTFLQREABGQDFPOLYPGELGRIRYNEISLEAWAQWQHQTMLINEKKLNNMNA 600

Db 61 EHRKLEQEMVNFLEFGKSVHIEGYTPEDK 90

RESULT 5

conserved hypothetical protein STY326 [imported] - *Salmonella enterica* subsp. *enterica* C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhi

th, T.; Comercon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A1:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A: Molecule type: DNA
A: Residues: 1-91 <PAR>
A: Cross-references: UNIPARC:UPI000005A44C; GB:HL513382; PIDN:CAD02936.1; PID:g16504189;
C: Genets:

Query Match	Score	DB	Length
Best Local Similarity	83.1%	2	91
	81.1%		
	Pred. No. 1.9e-33		

[illegible]

	61	EDRLLEQEWVFLFEGDVHIAGYTPPSK	90
Qy		:	
	61	EHRLLLEGWVSFLFEGKDVIHISGYTPEDK	90
Dd			

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 65.4453 Seconds

(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502a-37

Perfect score: 473
Sequence: 1 MSRTFTCTFLKXDAERQDFQ.....VNFLEGGDVHLAGYTPPSK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	100.0	90	1	FERP_YERPE
2	466	98.5	90	1	FERP_YERPE
3	412	87.1	90	1	FERP_EBOWT
4	391	82.7	90	1	FERP_EBOWT
5	391	82.7	90	1	FERP_EBOWT
6	391	82.7	90	1	FERP_EBOWT
7	388	82.0	90	1	FERP_SALCH
8	388	82.0	90	1	FERP_SALCH
9	388	82.0	90	1	FERP_SALCH
10	388	82.0	90	1	FERP_SALCH
11	387	81.8	90	1	FERP_SALCH
12	379	80.1	90	1	FERP_PHOLL
13	374	79.1	90	1	FERP_PHOPR
14	374	79.1	90	1	FERP_HABIN
15	374	79.1	90	2	Q4QMD9_HABIS
16	366	77.4	90	1	FERP_VIBCH
17	362	76.5	90	1	FERP_VIBCH
18	357	75.5	90	1	FERP_VIBPA
19	357	75.5	90	1	FERP_VIBVY
20	355	75.1	90	1	FERP_VIBVY
21	354	74.8	91	1	FERP_PASNU
22	351	74.2	94	1	FERP_HABDU
23	330	69.8	90	1	FERP_VIBFL
24	308	65.1	92	1	FERP_SHEON
25	305	64.5	90	1	FERP_IDILO
26	256	54.1	77	1	FERP_BUCAL
27	240	50.7	78	1	FERP_WIGGR
28	237	50.1	90	1	FERP_BORBR
29	237	50.1	90	1	FERP_BORBR
30	237	50.1	90	1	FERP_BORBR
31	234	49.5	78	1	FERP_BUCAP

32	233	49.3	90	1	FERP_COXBU
33	228	48.2	90	1	FERP_NITREU
34	222.5	47.0	89	1	FERP_LEGPL
35	221	46.7	90	1	FERP_PSEAB
36	220	46.5	91	1	FERP_XANAC
37	218.5	46.2	89	1	FERP_LEGPA
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39	216	45.7	87	1	FERP_BUCBP
40	216	45.7	92	1	FERP_XANOR
41	213	45.0	90	1	FERP_CHARVO
42	210	44.4	92	2	FERP_XANCP
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44	208	44.0	90	2	Q4U228_AZCVI
45	208	44.0	91	1	FERP_BURMA
46	208	44.0	91	1	FERP_BURPS
47	207	43.8	90	1	FERP_XYLPT
48	206	43.6	90	1	FERP_PSEBM
49	206	43.6	90	2	Q6T7F6_PSEFL
50	206	43.6	90	2	Q4ZLP3_PSESY
51	206	43.6	91	2	Q4LS19_9BURK
52	203	42.9	90	1	FERP_XYLPA
53	203	42.9	91	1	FERP_RALSO
54	199	42.1	79	1	FERP_CANRP
55	198	41.9	88	1	FERP_NEIGL
56	198	41.9	88	1	FERP_NEIMA
57	198	41.9	88	1	FERP_NIRMB
58	197	41.6	90	1	FERP_PSEBK
59	193	40.8	90	1	FERP_MERCA
60	188	39.7	90	2	QAKUT2_PSEBS
61	184	38.9	87	1	FERP_FRATV
62	167.5	35.4	90	1	FERP_ACIDM
63	148	31.3	96	2	Q4FVU7_9GAMM
64	138	29.2	92	2	Q4NWD4_9DEL7
65	82	17.3	1555	2	Q5UW02_PIAF7
66	81	17.1	2672	1	GCN1_YEAST
67	78.5	16.6	502	2	Q4T616_TETNG
68	77.5	16.4	452	2	Q6F6U1_LEPIN
69	77.5	16.4	464	2	Q7ZP14_LEPIC
70	77	16.3	2248	2	Q4UB40_THEAN
71	76.5	16.2	511	2	Q98Q71_MYCPV
72	76	16.1	2249	2	Q4MYU4_THEPA
73	75	15.9	1032	2	Q4XVW2_PLACH
74	74	15.6	330	2	Q6XKS4_CLOPR
75	74	15.6	403	2	Q5H1P0_STYAC

ALIGNMENTS

RESULT 1	
ID_FERP_YERPE	STANDARD; PRT; 90 AA.
AC Q8ZHE7;	
DT 10-OCT-2003 (Rel. 42, Created)	
DT 10-OCT-2003 (Rel. 42, Last sequence update)	
DT 13-SEP-2005 (Rel. 48, Last annotation update)	
DE Probable Fe(2+) trafficking protein.	
GN OrderedLocusNames=YPO0953, Y3340, YP3488;	
OS Yersinia pestis.	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Yersinia.	
OX NCBI_Taxid=632;	
RN [1]	
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC STRAIN=CO-92 / Biovar Orientalis;	
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;	
RA Parthali J., Wren B.W., Thomson N.R., Titchall R.W., Holden M.T.G.,	
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,	
RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,	
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,	
RA Fellwell T., Hamlin N., Holtroyd S., Jagsis K., Karlyshev A.V.,	
RA Leather S., Moute S., Oyston P.C.F., Quail M.A., Rutherford K.M.,	
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrrell B.G.;	

RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burdland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 RN [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=91001 / Biovar Mediaevalis;
 RX PubMed=15368893;
 RX Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
 RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
 RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
 RA Yang H., Wang J., Huang P., Yang R.;
 RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
 avirulent to humans.";
 RL DNA Res. 11:179-197(2004).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 acquisition and iron-regulating processes, such as synthesis and/or
 repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL: AJ14145; CAC89796.1; -; Genomic DNA.
 DR EMBL: AB013935; AAM68890.1; -; Genomic DNA.
 DR EMBL: AE017140; AAS63643.1; -; Genomic DNA.
 DR SMR: Q8ZHE7; 1-90.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; Y9GX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 DR Prodom: PD029191; DUF495; 1.
 KW Complete proteome; Iron.
 KM COMPLETE PROTEOME; IRON.
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 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MSRTFTCTFLKDAERODPOLYPGEIGRIYNEISKEAMSQWITKQTLINKEKLSMNNI 60
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 DB 61 EDRKLLBEMVNFLEFGQDVHIAGYTPPSK 90
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 AC Q666M3;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 GN OrderedLocNames=YPTB3225;
 OS Yersinia pseudotuberculosis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OC NCBI_TaxID=633;
 RN [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=IP32953 / Serotype I;
 RX PubMed=1558858; DOI=10.1073/pnas.0404012101;
 RX Chain P.S.G., Carmiel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
 RA Brubaker R.R., Fowler J., Hinebusch J., Marceau M., Medigue C.,
 RA Simonet M., Chenaï-Franckque V., Souza B., Decheux D., Elliott J.M.,
 RA Desbise A., Hauser L.U., Garcia B.;
 RT "Insights into the evolution of Yersinia pestis through whole-genome
 comparison with Yersinia pseudotuberculosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 acquisition and iron-regulating processes, such as synthesis and/or
 repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
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 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL: BX936398; CAH22463.1; -; Genomic DNA.
 DR SMR: Q666M3; 1-90.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; Y9GX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 DR Prodom: PD029191; DUF495; 1.
 KW Complete proteome; Iron.
 KM COMPLETE PROTEOME; IRON.
 SQ SEQUENCE 90 AA; 10608 MW; C7375E7954752E64 CRC64;
 Query Match 98.5%; Score 466; DB 1; Length 90;
 Best Local Similarity 98.9%; Pred. No. 3.4e-40;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 DB 1 MSRTFTCTFLKDAERODPOLYPGEIGRIYNEISKEAMSQWITKQTLINKEKLSMNNI 60
 QY 61 EDRKLLBEMVNFLEFGQDVHIAGYTPPSK 90
 DB 61 EDRKLLBEMVNFLEFGQDVHIAGYTPPSK 90
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 AC Q6D8J9;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 GN OrderedLocNames=ECA0975;
 OS Yersinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OK NCBI_TaxID=29471;
 RN [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sepahnia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holava M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 RA Axtell R., Baeson N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Frazer A., Hance Z., Hauser K., Jagels K., Moulé S., Norbertczak H.,
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 18.0609 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502a-37

Perfect score: 473
Sequence: 1 MSRTFCTFLKKDAERODFO.....VNFLEGQDVHAGYPPSK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents, AA:*
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3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/BCTUS-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400	84.6	107	US-09-489-039A-11962	Sequence 11962, A
2	389	82.2	93	US-09-543-681A-5443	Sequence 5443, Ap
3	221	46.7	122	US-09-252-991A-23355	Sequence 23355, A
4	176.5	37.3	92	US-09-328-352-5456	Sequence 2356, Ap
5	143	30.2	110	US-09-540-236-2859	Sequence 2859, Ap
6	69.5	14.7	870	US-09-543-681A-4768	Sequence 4768, Ap
7	69	14.6	209	US-09-252-991A-20905	Sequence 20905, A
8	67.5	14.3	701	US-09-252-991A-23288	Sequence 23288, A
9	67	14.2	415	US-08-602-010A-10	Sequence 10, Appl
10	67	14.2	415	US-08-680-726A-10	Sequence 10, Appl
11	67	14.2	415	US-09-092-409-10	Sequence 2, Appl
12	65	13.7	411	US-07-684-135A-2	Sequence 10190, A
13	65	13.7	1559	US-09-949-016-10190	Sequence 4, Appl
14	65	13.7	2101	US-08-466-390-4	Sequence 4, Appl
15	65	13.7	2101	US-08-470-950-4	Sequence 4, Appl
16	65	13.7	2101	US-08-467-781-4	Sequence 4, Appl
17	65	13.7	2101	US-08-195-487-4	Sequence 4, Appl
18	65	13.7	2101	US-08-483-924-4	Sequence 4, Appl
19	65	13.7	2101	US-09-452-294-1	Sequence 1, Appl
20	65	13.7	2101	US-09-296-662-32	Sequence 32, Appl
21	65	13.7	2107	US-09-949-016-7646	Sequence 7646, Ap
22	65	13.7	2107	US-09-949-016-7647	Sequence 7647, Ap
23	65	13.7	2115	US-09-296-662-33	Sequence 33, Appl
24	64.5	13.6	242	US-08-908-332-1	Sequence 1, Appl
25	64	13.5	184	US-09-328-352A-66	Sequence 66, Appl
26	64	13.5	534	US-09-312-762A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity 83.3%; Pred. No. 1.4e-44;
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DB 17 MSRTTCTFLKDAERODPOLYPGEIGKRIYNEISKEAMSQWITKQTMLINEKLSMMNI 76

QY 61 EDRKLEQEMVNFLEFGQDVHIAGYTPPSK 90
DB 77 EHRKLEQEMVNFLEFGQDVHIAGYTPPSK 106

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 82.2%; Score 389; DB 2; Length 93;
Best Local Similarity 80.0%; Pred. No. 3.3e-43;
Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

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QY 61 EDRKLEQEMVNFLEFGQDVHIAGYTPPSK 90
DB 64 DDKLEQEMVNFLEFGQDVHIAGYTPPSK 93

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Best Local Similarity 51.1%; Pred. No. 4.8e-21;
Matches 46; Conservative 13; Mismatches 29; Indels 2; Gaps 2;

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DB 33 MSRTTCTFLKDAERODPOLYPGEIGKRIYNEISKEAMSQWITKQTMLINEKLSMMNI 92

QY 61 EDRKLEQEMVNFLEFGQDVHIA-GYTPPS 89
DB 93 EDRKLEQEMVNFLEFGQDVHIA-GYTPPS 121

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 37.3%; Score 176.5; DB 2; Length 92;
Best Local Similarity 36.6%; Pred. No. 2.2e-15;
Matches 34; Conservative 18; Mismatches 35; Indels 1; Gaps 1;

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DB 4 MSRTTCTFLKDAERODPOLYPGEIGKRIYNEISKEAMSQWITKQTMLINEKLSMMNI 63

QY 61 EDRKLEQEMVNFLEFGQDVHIA-GYTP 87
DB 64 EAKKLEQEMVNFLEFGQDVHIA-GYTP 91

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

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Best Local Similarity 36.1%; Pred. No. 6.9e-11;
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QY 5 ICFCTFLKDAERODPOLYPGEIGKRIYNEISKEAMSQWITKQTMLINEKLSMMNI 64
DB 25 VFCRTYQDLPFLPFPNAKQGEIOTISAKANWALEIOTMLINEKLSMIDPOAKK 84

QY 65 ILEQEMVNFLEFGQDVHIAGYTP 87
DB 85 YLNEQREKFLNDGDXKPGYKP 107

RESULT 6
US-09-543-681A-4768
; Sequence 4768, Application US/09543681A

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:34:35 ; Search time 56.3134 Seconds
(without alignments)
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Title: US-09-955-502A-37
Perfect score: 473
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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	473	100.0	90	US-09-955-502-20	Sequence 20, Appl
2	396	83.7	91	US-09-955-502-11	Sequence 11, Appl
3	396	83.7	91	US-09-955-502-12	Sequence 12, Appl
4	396	83.7	91	US-09-955-502-13	Sequence 13, Appl
5	393	83.1	91	US-09-955-502-14	Sequence 14, Appl
6	393	83.1	91	US-09-955-502-16	Sequence 16, Appl
7	393	83.1	91	US-09-955-502-17	Sequence 17, Appl
8	389	82.2	88	US-09-955-502-15	Sequence 15, Appl
9	379	80.1	91	US-09-955-502-18	Sequence 18, Appl
10	366	77.4	90	US-09-955-502-10	Sequence 10, Appl
11	363	76.7	87	US-09-955-502-7	Sequence 7, Appl
12	357	75.5	87	US-09-955-502-5	Sequence 5, Appl
13	351	74.2	87	US-09-955-502-8	Sequence 8, Appl
14	346	73.2	87	US-09-955-502-6	Sequence 6, Appl
15	342	72.3	78	US-09-955-502-19	Sequence 19, Appl
16	308	65.1	88	US-09-955-502-9	Sequence 9, Appl
17	256	54.1	76	US-09-955-502-21	Sequence 21, Appl
18	233	49.3	88	US-09-955-502-33	Sequence 33, Appl
19	226	47.8	87	US-09-955-502-2	Sequence 2, Appl
20	226	47.8	87	US-09-955-502-3	Sequence 3, Appl
21	212	44.8	86	US-09-955-502-4	Sequence 4, Appl
22	210	44.4	90	US-09-955-502-25	Sequence 25, Appl
23	206	43.6	90	US-09-955-502-23	Sequence 23, Appl
24	203	42.9	89	US-09-955-502-22	Sequence 22, Appl
25	199	42.1	87	US-09-955-502-29	Sequence 29, Appl
26	199	42.1	87	US-09-955-502-30	Sequence 30, Appl
27	198	41.9	88	US-09-955-502-26	Sequence 26, Appl

28	198	41.9	88	US-09-955-502-27	Sequence 27, Appl
29	198	41.9	88	US-09-955-502-28	Sequence 28, Appl
30	188	39.7	87	US-09-955-502-24	Sequence 24, Appl
31	186	39.3	87	US-09-955-502-31	Sequence 31, Appl
32	186	39.3	87	US-09-955-502-32	Sequence 32, Appl
33	81	17.1	102	US-09-864-408A-768	Sequence 768, App
34	74	15.6	397	US-10-276-774-1577	Sequence 1577, Ap
35	74	15.6	506	US-10-343-663A-26	Sequence 26, Appl
36	74	15.6	576	US-10-450-763-50273	Sequence 50273, A
37	74	15.6	589	US-10-297-880-1	Sequence 1, Appl
38	74	15.6	770	US-10-343-663A-68	Sequence 68, Appl
39	74	15.6	1116	US-09-790-318-2	Sequence 32, Appl
40	74	15.6	1116	US-10-112-944-323	Sequence 32, App
41	74	15.6	1116	US-10-343-663A-27	Sequence 27, Appl
42	73	15.4	635	US-10-112-944-780	Sequence 780, App
43	70.5	14.9	635	US-11-097-143-34179	Sequence 34179, A
44	70	14.8	184	US-10-392-840-52	Sequence 52, Appl
45	69.5	14.7	600	US-10-437-963-104086	Sequence 104086,
46	69.5	14.7	867	US-10-282-122A-69006	Sequence 69006, A
47	69.5	14.7	1589	US-10-450-763-34556	Sequence 34556, A
48	69.5	14.7	1589	US-10-450-763-39257	Sequence 39257, A
49	69.5	14.7	1589	US-10-450-763-52962	Sequence 52962, A
50	69.5	14.7	1589	US-10-450-763-58863	Sequence 58863, A
51	69.5	14.7	1589	US-10-450-763-60458	Sequence 60458, A
52	68	14.4	256	US-10-282-122A-53103	Sequence 53103, A
53	68	14.4	344	US-09-820-843A-35	Sequence 10, Appl
54	67	14.2	415	US-10-156-275-10	Sequence 189166,
55	67	14.2	1261	US-10-437-963-189166	Sequence 35150, A
56	66.5	14.1	184	US-10-450-763-35150	Sequence 10247, A
57	66.5	14.1	758	US-10-369-493-10247	Sequence 12814, A
58	66.5	14.1	1317	US-10-732-923-12814	Sequence 239277,
59	66	14.0	268	US-10-424-599-239277	Sequence 30849, A
60	66	14.0	582	US-10-450-763-30849	Sequence 14933, A
61	66	14.0	1006	US-10-437-963-147933	Sequence 7224, Ap
62	65	13.7	842	US-10-032-585-7224	Sequence 1548, Ap
63	65	13.7	1575	US-10-741-600-1548	Sequence 1548, Ap
64	65	13.7	1575	US-10-741-600-1549	Sequence 1550, Ap
65	65	13.7	2140	US-10-741-600-1550	Sequence 32, Appl
66	65	13.7	1601	US-10-977-955-32	Sequence 18, Appl
67	65	13.7	2101	US-10-723-681-18	Sequence 33, Appl
68	65	13.7	2115	US-10-977-955-33	Sequence 5050, Ap
69	64.5	13.6	553	US-10-756-149-5050	Sequence 189628,
70	64.5	13.6	553	US-10-437-963-189628	Sequence 118, App
71	64	13.5	184	US-10-219-220-66	Sequence 5, Appl
72	64	13.5	184	US-10-393-840-118	Sequence 43781, A
73	64	13.5	534	US-09-312-762A-5	Sequence 22170, A
74	64	13.5	681	US-10-767-701-43781	
75	63	13.3	470	US-11-097-143-22170	

ALIGNMENTS

RESULT 1
US-09-955-502-20
Sequence 20, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 20
LENGTH: 90
TYPE: PRT
ORGANISM: Yersinia pestis

US-09-955-502-20

Query Match	100.0%;	Score 473;	DB 3;	Length 90;
Best Local Similarity	100.0%;	Pred. No. 4.5e-47;		
Matches 90; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 MSRTIPCTFLKDAERODPOLYGEIGRIYNESKAANSOWITQTMLINEKLSMNI   60
        |||||
Db       1 MSRTIFCTFLKDAERODPOLYGEIGRIYNESKAANSOWITQTMLINEKLSMNI   60
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Qy 61 EDRKLLLEQEMVNFLEFGQDVHVIAGYTPPSK 90
|||
Db 61 EDRKLLLEQEMVNFLEFGQDVHVIAGYTPPSK 90

RESULT 2

US-09-955-502-11
 : Sequence 11, Application US/09955502
 : Patent No. US20020072118A1
 : GENERAL INFORMATION:
 : APPLICANT: Downs, Diana M.
 : APPLICANT: Grainick, Jeff A.
 : TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
 : TITLE OF INVENTION: Oxygen-Labile Proteins
 : FILE REFERENCE: 960296.97559
 : CURRENT APPLICATION NUMBER: US/09/955,502
 : CURRENT FILING DATE: 2001-09-18
 : PRIOR APPLICATION NUMBER: 60/234,588
 : PRIOR FILING DATE: 2000-09-22
 : NUMBER OF SEQ ID NOS: 33
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 11
 : LENGTH: 91
 : TYPE: PRT
 : ORGANISM: Escherichia coli K-12 MG1655
 US-09-955-502-11

Query Match	83.7%	Score 396,	DB 3,	Length 91,
Best Local Similarity	82.2%	Pred. No. 4.1e-38,		
Matches 74; Conservative	8;	Mismatches 8;	Indels 0;	Gaps 0.

QY 1 MSRTIFCTFLKDAERDQFLYPERIGRIYNEISKEAWSQWITKQTMLINEKLSMNNI 60

Db 1 MSRTIFCTFLQRAEGDQFLYPGELGRIYNEISKEAWAOWHKQTMLINEKLSMNNNA 60

Qy	61	EDRKLLQEMVNFLEFGQDVHIAGYTPSPK	90
		:	
Dp	61	EHRKLLQEMVNFLEFGKEVHIEGYTPEDK	90

RESULT 3

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US-09-955-502-12
; Sequence 12, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 91
; TYPE: PRS
; ORGANISM: Escherichia coli O157:H7EDL933
US-09-955-502-12
Query Match      83.7%; Score 396; DB 3; Length 91;

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Best Local Similarity 82.2%; Pred. No. 4.1e-38;
Matches 74; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

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QY      1 MSRTTCTPLPKDAERQDFOLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60
        |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::||
Db      1 MSRTTCTPLPORAEGODFOLYPGEIGKRIYNEISKEAQAQWQKQTMLINEKLSMNA 60

```

QY 61 EDRKLLIQEMVNFLEFGQDVHIAGYTPPSK 90
| | | | | | | | | | : | | | | |
Db 61 EHRKLLIQEMVNFLEFGKEVHIEGYTPEDK 90

RESULT 4

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US-09-955-502-13
; Sequence 13, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Grainick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296, 97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/34,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ. ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 91
; TYPE: PR1
; ORGANISM: Escherichia coli O157:H7
US-09-955-502-13

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Query Match	83.7%	Score 396	DB 3	Length 91
Best Local Similarity	82.2%	Pred. No. 4.1e-38		
Matches 74	Conservative	8	Mismatches 8	Indels 0
			Gaps	0

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Db      1 MSRTICTFLREAGODFOLYPGELGRIYNEISKEANAOWOHQTMLINEKKLSMNA 60
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QY 61 EDRKLLQEMVNFLEFGQDVHIAGYTPPSK 90
| | | | | | | | | | : | | | | | | |
Db 61 EHRKLLQEMVNFLEFGKEVHIIEGYTPPSK 90

RESULT 5

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US-09-955-502-14
Sequence 14, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method For Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960256, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
/
/
LENGTH: 91
/
/
TYPE: PRT
/
/
ORGANISM: Salmonella paratyphi
/
US-09-955-502-14

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Query Match	83.1%;	Score 393;	DB 3;	Length 91;
Best Local Similarity	81.1%;	Pred. No. 9.2e-38;		
Matches 73; Conservative	9;	Mismatches 8;	Indels 0;	Gaps 0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 73.8041 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502a-23

Perfect score: 485
Sequence: 1 MTRIVWCRKRYKEELPGLERA.....DKFLSGEYVAQAGYVPEK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*
- 9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485	100.0	90	5	ABB78168 Amino aci
2	432	89.1	87	5	ABB78169 Amino aci
3	415	85.6	122	7	ABO74609 Pseudomon
4	408	84.1	92	5	ABB78170 Amino aci
5	253.5	52.3	92	6	ADA34169 Acinetoba
6	239	49.3	91	5	ABB78150 Amino aci
7	234	48.2	89	9	ABB41576 Amino aci
8	234	48.2	95	9	ABB38294 L. pneumo
9	230	47.4	87	5	ABB78152 Amino aci
10	228	47.0	88	5	ABB78154 Amino aci
11	228	47.0	90	5	ABB78155 Amino aci
12	228	47.0	93	7	ADP05158 Bacterial
13	228	47.0	107	7	ABO65445 Klebsiell
14	227	46.8	91	5	ABB78158 Amino aci
15	227	46.8	91	5	ABB78157 Amino aci
16	227	46.8	91	5	ABB78156 Amino aci
17	226	46.6	87	5	ABB78177 Amino aci
18	224	46.2	87	5	ABB78151 Amino aci
19	222	45.8	91	5	ABB78161 Amino aci
20	222	45.8	91	5	ABB78159 Amino aci
21	222	45.8	91	5	ABB78162 Amino aci
22	221	45.6	87	5	ABB78153 Amino aci
23	219	45.2	87	5	ABB78176 Amino aci
24	218	44.9	87	5	ABB78148 Amino aci

25	218	44.9	87	5	ABB78147	Abb78147 Amino aci
26	216	44.5	88	5	ABB78160	Abb78160 Amino aci
27	215	44.3	88	5	ABB78178	Abb78178 Amino aci
28	212	43.7	91	5	ABB78163	Abb78163 Amino aci
29	208	42.9	87	5	ABB78175	Abb78175 Amino aci
30	207	42.7	110	8	ADL05173	Adl05173 M. catarr
31	206	42.5	90	5	ABB78165	Abb78165 Amino aci
32	202	41.6	87	5	ABB78174	Abb78174 Amino aci
33	200.5	41.3	86	5	ABB78149	Abb78149 Amino aci
34	198	40.8	88	5	ABB78171	Abb78171 Amino aci
35	198	40.8	88	5	ABB78172	Abb78172 Amino aci
36	198	40.8	88	5	ABB78173	Abb78173 Amino aci
37	198	40.8	88	6	ABP77219	Abp77219 N. gonorr
38	195	40.2	78	5	ABB78164	Abb78164 Amino aci
39	190.5	39.3	90	5	ABB78167	Abb78167 Amino aci
40	165	34.0	76	5	ABB78166	Abb78166 Amino aci
41	72	14.8	97	5	ABG70345	Abg70345 Novel hum
42	70.5	14.5	1091	5	ABB48258	Abb48258 Listeria
43	69	14.2	468	2	AAV41734	AAV41734 Human PRO
44	69	14.2	468	3	AAV33436	AAV33436 Human PRO
45	69	14.2	468	3	AAV44290	AAV44290 Human PRO
46	69	14.2	468	3	AAV24418	AAV24418 Human PRO
47	69	14.2	468	3	AAV23628	AAV23628 Human PRO
48	69	14.2	468	4	AAV80398	AAV80398 Secreted
49	69	14.2	468	4	AAV64998	AAV64998 Human PRO
50	69	14.2	468	5	ABBA4866	ABBA4866 Human PRO
51	69	14.2	468	5	ABG65287	ABG65287 Human PRO
52	69	14.2	468	5	ABP65092	ABP65092 Hypoxia-1
53	69	14.2	468	5	ABP95472	ABP95472 Human ang
54	69	14.2	468	6	ABO25236	ABO25236 Novel hum
55	69	14.2	468	6	ABU72242	ABU72242 Novel hum
56	69	14.2	468	6	ABU84922	ABU84922 Novel hum
57	69	14.2	468	6	ABU61120	ABU61120 Human PRO
58	69	14.2	468	6	ABU80389	ABU80389 Human PRO
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62	69	14.2	468	6	ABO19582	ABO19582 Novel hum
63	69	14.2	468	6	ABB73843	ABB73843 Human PRO
64	69	14.2	468	7	ADB76559	ADB76559 Human PRO
65	69	14.2	468	7	ADC43985	ADC43985 Human PRO
66	69	14.2	468	7	ADC61745	ADC61745 Human PRO
67	69	14.2	468	7	ADC63709	ADC63709 Human PRO
68	69	14.2	468	7	ADC66809	ADC66809 Human PRO
69	69	14.2	468	7	ADC68933	ADC68933 Human PRO
70	69	14.2	468	7	ADC62933	ADC62933 Human PRO
71	69	14.2	468	7	ADC68058	ADC68058 Human PRO
72	69	14.2	468	7	ADC41378	ADC41378 Human PRO
73	69	14.2	468	7	ADC67433	ADC67433 Human PRO
74	69	14.2	468	7	ADC62369	ADC62369 Human PRO
75	69	14.2	468	7	ADC62369	ADC62369 Human PRO

ALIGNMENTS

RESULT 1
ID ABB78168 standard; protein; 90 AA.
XX ABB78168;
AC 05-NOV-2002 (first entry)
DE Amino acid sequence of a YggX homologue.
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
OS Pseudomonas syringae.
XX US2002072118-A1.
XX

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.84055 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-23

Perfect score: 485

Sequence: 1 MTRWTMCRKRYKEELFGLRRA.....DKFLSGERYAQAEGVVPPEK 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	415	85.6	90	2	H83003 conserved hypotet
2	237	48.9	90	2	C64013 hypothetical prote
3	228	47.0	90	2	C82320 conserved hypotet
4	227	46.8	91	2	A85954 hypothetical prote
5	227	46.8	91	2	A65082 hypothetical prote
6	227	46.8	91	2	F91108 hypothetical prote
7	222	45.8	91	2	AH0879 conserved hypotet
8	206	42.5	90	2	AI0116 conserved hypotet
9	200	41.2	105	2	C82624 conserved hypotet
10	198	40.8	88	2	H81014 conserved hypotet
11	165	34.0	93	2	B84994 hypothetical prote
12	70.5	14.5	1091	2	AF1380 glycosidase homolo
13	69.5	14.3	1090	2	glycosidase homolo
14	67.5	13.9	297	2	T47857 myb protein-like -
15	67.5	13.9	421	2	A85039 conserved hypotet
16	67.5	13.9	508	2	S74848 neopullulanase - S
17	67	13.8	670	2	T29898 kinesin protein OS
18	66.5	13.7	1123	1	S53048 alpha-mannosidase
19	66.5	13.7	1121	2	T31558 phosphoprotein pho
20	65.5	13.5	767	2	T31558 hypothetical prote
21	65.5	13.5	879	2	PC1225 protein-tyrosine k
22	65.5	13.4	1308	2	T05178 hypothetical prote
23	65	13.3	165	2	C75419 hypothetical prote
24	64.5	13.3	181	2	B97341 rubrerythrin [limo
25	64.5	13.3	181	2	P97341 rubrerythrin [limo
26	64.5	13.3	2131	2	S01446 hypothetical prote
27	64	13.2	205	2	D71440 GTP-binding protei
28	64	13.2	559	2	A82202 hypothetical prote
29	64	13.2	909	2	AC2365 hypothetical prote

30	64	13.2	3430	1	GNVWV genome polypotein
31	64	13.2	4717	2	T41581 hypothetical coile
32	63.5	13.1	284	2	D82486 transformi lipase ac
33	63.5	13.1	388	1	Q0TV maltose/maltodextr
34	63.5	13.1	419	2	AE1340 maltose/maltodextr
35	63.5	13.1	419	2	AC1711 hypothetical prote
36	63.5	13.0	959	2	H69344 hypothetical prote
37	63	13.0	435	2	D82905 hypothetical prote
38	63	13.0	643	2	S55610 polypotein - equi
39	63	13.0	995	2	A84014 SNF helicase BH29
40	62.5	12.9	458	2	F84275 hypothetical prote
41	62.5	12.9	559	2	H82532 conserved hypotet
42	62.5	12.9	585	1	F64159 hypothetical prote
43	62.5	12.9	887	2	B96598 hypothetical prote
44	62.5	12.9	985	2	S15965 hypothetical prote
45	62	12.8	1104	2	T01811 hypothetical prote
46	61.5	12.7	382	2	UC5531 c-Jun amino-termin
47	61.5	12.7	465	2	T41830 LRF-4 orf90 - Bomb
48	61.5	12.7	470	2	D84614 hypothetical prote
49	61.5	12.7	505	2	I37206 protein-tyrosine k
50	61.5	12.7	773	2	G66856 hypothetical prote
51	61	12.6	150	2	F90212 hypothetical prote
52	61	12.6	211	2	S71559 GTP-binding protei
53	61	12.6	297	2	AE0400 probable membrane
54	61	12.6	298	2	B98066 primosome componen
55	61	12.6	774	2	T14555 DNA polymerase hom
56	61	12.6	796	1	JY0107 glucose dehydrogen
57	61	12.6	796	2	H85495 glucose dehydrogen
58	61	12.6	796	2	H90644 glucose dehydrogen
59	61	12.6	1486	2	B85618 hypothetical prote
60	61	12.6	1486	2	G90754 kinesin-like cell
61	61	12.6	1486	2	C64832 cell division prot
62	61	12.6	4540	2	T30838 cytoplasmic dynein
63	60.5	12.5	288	2	T45715 hypothetical prote
64	60.5	12.5	339	2	AG2041 queuine tRNA-ribos
65	60.5	12.5	713	2	B84583 hypothetical prote
66	60.5	12.5	985	2	T10339 DNA-directed DNA p
67	60.5	12.5	1047	2	T16203 hypothetical prote
68	60.5	12.5	1128	1	Q08B47 DNA-binding protei
69	60	12.4	133	2	A72229 hypothetical prote
70	60	12.4	177	2	D70862 hypothetical prote
71	60	12.4	245	2	S49045 luxP protein - Vib
72	60	12.4	276	2	H81931 probable bis(5'-nu
73	60	12.4	295	2	G64407 heterodisulfide re
74	60	12.4	437	2	C96840 hypothetical prote
75	60	12.4	651	2	A13294 cell division prot

ALIGNMENTS

RESULT 1
H83003 conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: H83003
R:Stover, C.K.; Pham, X.Q.; Brwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapidig, K.; Iam,
. J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen
A:Reference number: AB2950, MUID:20437337, PMID:10984043
A:Accession: H83003
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: UNIPARC:UP1000000CSP26; GB:AB004927; GB:AB004091; NID:g9951437; PIDN:
A:Experimental source: strain PA01
C:Gene: PA5148
C:Superfamily: fe(II) trafficking protein YggX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 66.4237 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502a-23
Perfect score: 485
Sequence: 1 MTRVTMCRKYEKELPGLERA.....DKFLSGERYQAAGYVPEK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485	100.0	90	1	FERP_PSESM
2	485	100.0	90	2	Q4ZLF3_PSESM
3	439	90.5	90	1	FERP_PSESM
4	425	87.6	90	2	Q4KJ72_PSESM
5	419	86.4	90	2	Q6T7F6_PSESM
6	415	85.6	90	1	FERP_PSESM
7	410	84.5	90	2	Q4J228_AZOV
8	264	54.4	90	1	FERP_IDIOL
9	253.5	52.3	90	1	FERP_ACIAD
10	244	50.3	90	1	FERP_PHOPR
11	237	48.9	90	1	FERP_HABIN
12	237	48.9	90	1	FERP_VIBPA
13	237	48.9	90	2	Q4QMD9_HABIS
14	236	48.7	90	1	FERP_VIBVU
15	236	48.7	90	1	FERP_VIBVY
16	235	48.5	90	1	FERP_PHOUL
17	234	48.2	89	1	FERP_LEGPA
18	234	48.2	89	1	FERP_LEGPH
19	233	48.0	89	1	FERP_LEGPH
20	233	48.0	90	1	FERP_METCA
21	233	48.0	91	1	FERP_MANSN
22	231	47.6	90	1	FERP_PASNU
23	229	47.2	90	1	FERP_NITBU
24	228	47.0	90	1	FERP_VIBCH
25	228	47.0	90	1	FERP_VIBF1
26	228	47.0	92	1	FERP_SHEON
27	228	47.0	96	2	Q4FVJ7_9GAMM
28	225	46.4	90	1	FERP_BORRA
29	225	46.4	90	1	FERP_BORPA
30	225	46.4	90	1	FERP_BORPE
31	224	46.2	90	1	FERP_ERWCT

32	222	45.8	90	1	FERP_ECO57	P0a8p4 escherichia
33	222	45.8	90	1	FERP_ECOLI	P0a8p3 escherichia
34	222	45.8	90	1	FERP_SHIFL	P0a8p5 shigella fi
35	222	45.8	91	1	FERP_RALSO	O8y010 raietonia b
36	221	45.6	94	1	FERP_HABDU	O7vxb6 haemophilus
37	218	44.9	90	1	FERP_ECOL6	O8fe19 escherichia
38	217	44.7	90	1	FERP_SALCH	O57K04 salmonella
39	217	44.7	90	1	FERP_SALPA	O5pmm1 salmonella
40	217	44.7	90	1	FERP_SALTI	P67618 salmonella
41	217	44.7	90	1	FERP_SALTY	P67617 salmonella
42	215	44.3	90	1	FERP_COXBU	O83d06 coxiella bu
43	215	44.3	91	1	FERP_BURMA	O621u9 burkholderi
44	215	44.3	91	1	FERP_BURPA	O63sj4 burkholderi
45	214	44.1	90	1	FERP_YERS	O66m3 yersinia ps
46	214	43.5	92	1	FERP_YANOR	O5gy22 xanthomonas
47	209	43.1	91	2	Q4LST9_9BURK	O41819 burkholderi
48	206	42.5	90	1	FERP_YERE	O82he7 yersinia pe
49	204	42.1	90	1	FERP_XYLPT	O87d06 xyliella fas
50	202	41.6	91	1	FERP_XANAC	O63j17 xanthomonas
51	200	41.2	90	1	FERP_XYLPA	O9pc73 xyliella fas
52	198	40.8	88	1	FERP_NEIG1	O5f553 neisseria g
53	198	40.8	88	1	FERP_NEIMA	O5f553 neisseria m
54	198	40.8	88	1	FERP_NEIMB	P67616 neisseria m
55	198	40.8	92	1	FERP_XANCP	O8p829 xanthomonas
56	198	40.8	92	2	Q4UW14_XANCP	O4UW14 xanthomonas
57	195	40.2	90	1	FERP_CHRYO	O7nsr4 chromobacte
58	189	39.0	78	1	FERP_MIGBR	O8d3c5 aspergillus
59	189	39.0	87	1	FERP_FRATT	O5mjh8 francisella
60	179	36.9	79	1	FERP_CANBP	O7vrg9 candidatus
61	175	36.1	78	1	FERP_BUCAP	O8K925 buchnera ap
62	170	35.1	87	1	FERP_BUCBP	O89a44 buchnera ap
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64	165	34.0	92	2	Q4NWD4_9DELT	O4nwg4 anaeromyxob
65	165	34.0	92	2	Q5B5X5_EMENT	O5b5x5 aspergillus
66	165	34.0	92	2	Q6PWS_ORYSA	O6pws5 oryza sativ
67	165	34.0	92	2	Q93D60_ECOLI	O93d60 escherichia
68	165	34.0	92	2	Q415C8_GIBZE	O415c8 gibberella
69	165	34.0	92	2	Q4WPT2_ASPFU	O4wpt2 aspergillus
70	165	34.0	92	2	Q81DY9_PLAUF	O81dy9 plasmodium
71	165	34.0	92	2	Q5SGT4_DICDI	O5sgt4 dictyosteli
72	165	34.0	92	2	Q6BU74_DESHA	O6bu74 debariomyce
73	165	34.0	92	2	Q8K127_RHLET	O8k127 rhizobium
74	165	34.0	92	2	Q54X22_DICDI	O54x22 dictyosteli
75	165	34.0	92	2	Q5AUL5_EMENT	O5aul5 aspergillus

ALIGNMENTS

RESULT 1	FERP_PSESM	STANDARD	PRT	90 AA.
ID	FERP_PSESM			
AC	Q87UF5			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	OrderedLocusNames=PSPT05343;			
OC	Pseudomonas syringae (pv. tomato).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;			
OC	Pseudomonadaceae; Pseudomonas.			
OX	NCBI_TaxID=323;			
RM	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=DC3000;			
RX	MEDLINE=2834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;			
RA	Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,			
RA	Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonin I.T.,			
RA	Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,			
RA	Nelson W.C., Davidson T.W., Zafar N., Zhou L., Liu Y., Yuan Q.,			
RA	Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,			
RA	Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,			
RA	Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,			

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RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collmer A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB016853; AA058769.1; -; Genomic_DNA.
DR SMR; Q87UF5; 1-79.
DR TIGR; PSP05343; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10621 MW; 108628BD6532973 CRC64;

Query Match 100.0%; Score 485; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRTWCRKYEELPGLERAPYPGAKGEDI FNHVSQKAWDMQKHQTLLINERRLMNNA 60
DB 1 MRRTWCRKYEELPGLERAPYPGAKGEDI FNHVSQKAWDMQKHQTLLINERRLMNNA 60

QY 61 EDRKFLQTEMDFLGSGEYFAQAGYVPEK 90
DB 61 EDRKFLQTEMDFLGSGEYFAQAGYVPEK 90

RESULT 2
Q4ZLP3 PSESY PRELIMINARY; PRT; 90 AA.
ID Q4ZLP3.
AC Q4ZLP3.
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
DE Hypothetical protein.
GN ORFNames=Payr_4902;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Laitner F., DiBartolo G., Copeland A., Lykidis A., Truong S.,
RA Nolan M., Goldsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,
RA Land M., Richardson P.M., Kyriades N.C., Ivanova N.;
RT "Comparison of two complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000."
RT Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG Loper J.;
RA Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Feil H., Feil W.S., Lindow S.E.;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; CP000075; AAY39929.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 90 AA; 10621 MW; 108628BD6532973 CRC64;

Query Match 100.0%; Score 485; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRTWCRKYEELPGLERAPYPGAKGEDI FNHVSQKAWDMQKHQTLLINERRLMNNA 60
DB 1 MRRTWCRKYEELPGLERAPYPGAKGEDI FNHVSQKAWDMQKHQTLLINERRLMNNA 60

QY 61 EDRKFLQTEMDFLGSGEYFAQAGYVPEK 90
DB 61 EDRKFLQTEMDFLGSGEYFAQAGYVPEK 90

RESULT 3
FETP PSEPK STANDARD; PRT; 90 AA.
ID FETP PSEPK
AC Q88R49.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=PP0285;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22423060; PubMed=12534463;
DOI=10.1046/j.1462-2920.2002.00356.x;
RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beaman M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moralez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber U., Stjepandic D., Honeisel J., Straetz M., Heim S.,
RA Kiewitz C., Bisen J.A., Timmis K.N., Duesterhoeft A., Tnemmler B.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB016775; AAN65916.1; -; Genomic_DNA.
DR SMR; Q88R49; 1-79.
DR TIGR; PP0285; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10596 MW; 0C802FD7163B75A2 CRC64;

Query Match 90.5%; Score 439; DB 1; Length 90;
Best Local Similarity 88.6%; Pred. No. 1.3e-39;
Matches 78; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MRRTWCRKYEELPGLERAPYPGAKGEDI FNHVSQKAWDMQKHQTLLINERRLMNNA 60

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 18.246 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-23
Perfect score: 485
Sequence: 1 MTRVWCKRYKXRLPGLERA.....DKFLSGEYQAQAGVPPPK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	415	85.6	122	US-09-252-991A-23355	Sequence 23355, A
2	253.5	52.3	92	US-09-328-352-5456	Sequence 5456, Ap
3	228	47.0	93	US-09-543-681A-5443	Sequence 5443, Ap
4	228	47.0	107	US-09-489-039A-11962	Sequence 11962, A
5	207	42.7	110	US-09-540-236-2859	Sequence 2859, Ap
6	69	14.2	468	US-09-976-559-462	Sequence 462, App
7	69	14.2	468	US-09-999-833A-337	Sequence 337, App
8	69	14.2	468	US-10-020-445A-337	Sequence 337, App
9	69	14.2	588	US-09-902-540-13586	Sequence 13586, A
10	67.5	13.9	502	US-09-252-991A-26986	Sequence 26986, A
11	66.5	13.7	1122	US-10-146-704-2	Sequence 2
12	66	13.6	148	US-09-673-395A-389	Sequence 389, App
13	66	13.6	381	US-10-104-047-3313	Sequence 3313, App
14	66	13.6	401	US-09-489-847-202	Sequence 202, App
15	66	13.6	401	US-10-012-231A-100	Sequence 100, App
16	66	13.6	401	US-10-015-389A-100	Sequence 100, App
17	66	13.6	401	US-10-006-768A-100	Sequence 100, App
18	66	13.6	401	US-10-015-671A-100	Sequence 100, App
19	66	13.6	401	US-10-015-393A-100	Sequence 100, App
20	66	13.6	401	US-10-011-833A-100	Sequence 100, App
21	66	13.6	401	US-10-006-041A-100	Sequence 100, App
22	66	13.6	401	US-10-012-064A-100	Sequence 100, App
23	66	13.6	401	US-10-030-269A-8	Sequence 8, Appli
24	66	13.6	422	US-09-489-847-357	Sequence 357, App
25	65	13.4	451	US-09-543-681A-7401	Sequence 7401, Ap
26	65	13.4	582	US-09-902-540-11161	Sequence 11161, A
27	64.5	13.3	600	US-10-104-047-3845	Sequence 3845, Ap

28	64	13.2	314	2	US-09-716-865-4	Sequence 4, Appli
29	64	13.2	443	2	US-09-248-796A-16816	Sequence 16816, A
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31	63	13.0	551	2	US-09-138-172-2	Sequence 2, Appli
32	62.5	12.9	284	2	US-09-934-899-14	Sequence 14, Appl
33	62.5	12.9	284	2	US-09-934-868-34	Sequence 34, Appl
34	62.5	12.9	284	2	US-10-701-200-34	Sequence 34, Appl
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38	62	12.8	1042	2	US-09-792-024-106	Sequence 106, App
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40	61.5	12.7	454	2	US-09-771-161A-95	Sequence 95, Appl
41	61.5	12.7	469	2	US-09-131-750-29	Sequence 29, Appl
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51	61	12.6	553	2	US-09-134-000C-4071	Sequence 4071, Ap
52	61	12.6	671	2	US-09-248-796A-17595	Sequence 17595, A
53	60.5	12.5	464	2	US-09-724-864-40	Sequence 40, Appl
54	60.5	12.5	464	2	US-09-823-038A-47	Sequence 47, Appl
55	60.5	12.5	536	2	US-09-594-506-32	Sequence 32, Appl
56	60	12.4	163	2	US-09-270-767-33714	Sequence 33714, A
57	60	12.4	217	2	US-09-543-681A-7862	Sequence 7862, Ap
58	60	12.4	342	2	US-10-227-327-1	Sequence 1, Appli
59	60	12.4	499	2	US-09-561-763-2	Sequence 2, Appli
60	60	12.4	499	2	US-09-431-367B-2	Sequence 2, Appli
61	60	12.4	1244	2	US-09-543-681A-6274	Sequence 6274, Ap
62	59.5	12.3	247	2	US-09-489-039A-13121	Sequence 13121, A
63	59	12.2	212	1	US-08-531-525-18	Sequence 18, Appl
64	59	12.2	212	1	US-08-718-270A-18	Sequence 18, Appl
65	59	12.2	212	2	US-09-399-913-67	Sequence 67, Appl
66	59	12.2	212	2	US-09-350-614-67	Sequence 67, Appl
67	59	12.2	216	2	US-09-949-016-10750	Sequence 10750, A
68	59	12.2	317	2	US-09-107-532A-4653	Sequence 4653, Ap
69	59	12.2	1487	2	US-09-489-039A-12113	Sequence 12113, A
70	58.5	12.1	257	2	US-09-949-002-491	Sequence 491, App
71	58.5	12.1	282	2	US-10-000-489-28	Sequence 28, Appl
72	58.5	12.1	312	1	US-08-525-505A-4	Sequence 4, Appli
73	58.5	12.1	312	2	US-09-976-594-1009	Sequence 1009, Ap
74	58.5	12.1	312	2	US-09-949-002-367	Sequence 367, App
75	58.5	12.1	382	2	US-09-025-580-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; SEQ ID NO OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 56.7882 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502a-23
Perfect score: 485
Sequence: 1 MTRITWCRKRYKEELFGLERRA.....DKFLSGRYAQAEGYVPEK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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3	408	84.1	87 3 US-09-955-502-25
4	239	49.3	91 3 US-09-955-502-5
5	230	47.4	87 3 US-09-955-502-7
6	228	47.0	88 3 US-09-955-502-9
7	228	47.0	90 3 US-09-955-502-10
8	227	46.8	91 3 US-09-955-502-11
9	227	46.8	91 3 US-09-955-502-12
10	226	46.6	87 3 US-09-955-502-13
11	226	46.6	87 3 US-09-955-502-32
12	224	46.2	87 3 US-09-955-502-6
13	222	45.8	91 3 US-09-955-502-14
14	222	45.8	91 3 US-09-955-502-16
15	222	45.8	91 3 US-09-955-502-17
16	221	45.6	87 3 US-09-955-502-8
17	219	45.2	87 3 US-09-955-502-31
18	218	44.9	87 3 US-09-955-502-2
19	218	44.9	87 3 US-09-955-502-3
20	216	44.5	88 3 US-09-955-502-15
21	215	44.3	88 3 US-09-955-502-33
22	212	43.7	91 3 US-09-955-502-18
23	208	42.9	87 3 US-09-955-502-29
24	208	42.9	87 3 US-09-955-502-30
25	206	42.5	90 3 US-09-955-502-20
26	200.5	41.3	86 3 US-09-955-502-4
27	200	41.2	89 3 US-09-955-502-22

28	198	40.8	88 3 US-09-955-502-26	Sequence 26, Appl
29	198	40.8	88 3 US-09-955-502-27	Sequence 27, Appl
30	198	40.8	88 3 US-09-955-502-28	Sequence 28, Appl
31	195	40.2	78 3 US-09-955-502-19	Sequence 19, Appl
32	165	34.0	76 3 US-09-955-502-21	Sequence 21, Appl
33	74.5	15.4	596 4 US-10-437-963-150475	Sequence 130475,
34	72	14.3	902 4 US-10-437-963-156143	Sequence 45, Appl
35	69.5	14.3	902 4 US-09-726-643-51	Sequence 156143,
36	69	14.2	468 3 US-09-978-292A-337	Sequence 51, Appl
37	69	14.2	468 3 US-09-978-697-337	Sequence 337, Appl
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52	69	14.2	468 3 US-09-978-832A-337	Sequence 337, Appl
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63	69	14.2	468 3 US-09-978-832A-337	Sequence 337, Appl
64	69	14.2	468 3 US-09-978-832A-337	Sequence 337, Appl
65	69	14.2	468 3 US-09-978-832A-337	Sequence 337, Appl
66	69	14.2	468 3 US-09-978-832A-337	Sequence 337, Appl
67	69	14.2	468 3 US-09-978-832A-337	Sequence 337, Appl
68	69	14.2	468 3 US-09-978-832A-337	Sequence 337, Appl
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ALIGNMENTS

RESULT 1
US-09-955-502-23
Sequence 23, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 23
LENGTH: 90
TYPE: PRT
ORGANISM: Pseudomonas syringae

US-09-955-502-23

Query Match	100.0%;	Score 485;	DB 3;	Length 90;
Best Local Similarity	100.0%;	Pred. No. 7.4e-51;		
Matches 90;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db 1 MTRTWCRKRYKKEELPGLERAPYPGAKGEDI FNHVSQKAWADWQKQOTLLINERRLLNMNA 60

QY 61 EDRKFLQTEMDFKLSGEEYAGAEGVPPPK 90
DB 61 EDRKFLQTEMDFKLSGEEYAGAEGVPPPK 90

RESULT 2
US-09-95

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US-09-955-502-24
: Sequence 24, Application US/09955502
: Patent No. US20020072118A1
: GENERAL INFORMATION:
: APPLICANT: Downs, Diana M.
: APPLICANT: Gralnick, Jeff A.
: TITLE OR INVENTION: Method for Preventing Superoxide Damage to Cells and
: TITLE OR INVENTION: Oxygen-Labile Proteins
: FILE REFERENCE: 960296.97559
: CURRENT APPLICATION NUMBER: US/09/955,502
: PRIORITY FILING DATE: 2001-09-18
: PRIOR APPLICATION NUMBER: 60/234,588
: PRIOR FILING DATE: 2000-09-22
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 24
:
: LENGTH: 87
: TYPE: PRT
: ORGANISM: Pseudomonas putida
US-09-955-502-24

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Query Match	89.14;	Score 432;	DB 3;	Length 87;
Best Local Similarity	88.54;	Pred. No. 1.9e-44;		
Matches 77;	Conservative	6;	Mismatches 4;	Indels 0;
			Gaps	0

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Db      1 MTRITVMSCKRYQGEELPGLERAPYPYPAKGQDLFEHISQKAMADWQKHQTMLINERRLNNMNA 60
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OY 61 EDRKFLQTEMDFLSGEEYAQAEGVYP 87
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RESULT 3
US-09-95

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/ Sequence 25: Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ TITLE OF INVENTION: Oxygen-Labile Proteins
/ FILE REFERENCE: 960296, 97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ PRIOR FILING DATE: 2000-09-22
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 87
/ TYPE: prt
/ ORGANISM: Pseudomonas aeruginosa
US-09-955-502-25

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Best Local Similarity 83.9%; Pred. No. 1.6e-41;
Matches 73; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

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RESULT 4
US-09-95

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: Sequence 5 Application US/09955502
: Patent No. US20020072118A1
: GENERAL INFORMATION:
: APPLICANT: Downs, Diana M.
: APPLICANT: Gralnick, Jeff A.
: TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
: TITLE OF INVENTION: Oxygen-Labile Proteins
: FILE REFERENCE: 960296, 97559
: CURRENT APPLICATION NUMBER: US/09/955,502
: CURRENT FILING DATE: 2001-09-18
: PRIOR APPLICATION NUMBER: 60/334,588
: PRIOR FILING DATE: 2000-09-22
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 5
: LENGTH: 91
: TYPE: prt
: ORGANISM: Actinobacillus actinomycetemcomitans
US-09-955-502-5

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Best Local Similarity	49.4%;	Pred. No. 5.8e-21;		
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Db 1 MARWVFERLRKQEAEGLDLPQLYSGELGRI FDSISKQAWGEWMKKQTMLVNEKKLNMMNA 6

QY 61 EDRKFLQTENDKFLSGEEYAQAGVPRPE 89
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Db 61 EHRKLLGEQEMVNFLLFEGKDVIHIEGYPRPE 89

RESULT
US-09-95

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/ Sequence 7 Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ TITLE OF INVENTION: Oxygen-Labile Proteins
/ FILE REFERENCE: 960236.97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234, 588
/ PRIOR FILING DATE: 2000-09-22
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 87
/ TYPE: PRT
/ ORGANISM: Haemophilus influenzae
US-09-955-502-7

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Query Match	47.4%	Score 230;	DB 3;	Length 87;
Best Local Similarity	51.7%;	Pred. No. 6.8e-20;		
Matches 45; conservative	13;	Mismatches 29;	Indels 0;	Gaps 0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.92027 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502a-23

Perfect score: 485

Sequence: 1 MTRVTCRKYKBEPLGRLERA.....DKFLSGEYVQAQEGYVPEK 90

Scoring table:

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Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	66	13.6	381	7	US-11-072-512-3113
3	66	13.6	401	6	US-10-131-826A-486
4	66	13.6	1560	7	US-11-059-982-1
5	65.5	13.3	879	6	US-10-770-726-78
6	64.5	13.3	600	7	US-11-072-512-3845
7	63.5	13.1	746	7	US-11-072-175-169
8	63	13.0	844	6	US-10-453-372-852
9	63	13.0	844	6	US-10-453-372-856
10	61	12.6	3433	6	US-10-714-781A-67
11	58.5	12.1	313	7	US-11-156-084-335
12	58.5	12.1	1308	6	US-10-912-971-12
13	58.5	12.1	1308	6	US-11-113-202-16
14	58	12.0	415	6	US-10-763-712A-25
15	58	12.0	436	6	US-10-763-712A-5
16	57.5	11.9	689	7	US-11-121-438-2
17	57.5	11.9	844	7	US-11-097-463-4
18	57.5	11.9	1386	7	US-11-091-643-6
19	57	11.8	166	7	US-11-176-830-954
20	56	11.5	307	6	US-10-454-437-268
21	56	11.5	370	6	US-10-873-528-160
22	56	11.5	805	6	US-10-485-517-198
23	56	11.5	928	7	US-11-130-594-8
24	55.5	11.4	691	7	US-11-098-686-11189
25	55	11.3	426	6	US-10-858-730-81

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Sequence 3113, App
Sequence 486, App
Sequence 1, App1
Sequence 78, App1
Sequence 3845, App
Sequence 169, App
Sequence 852, App
Sequence 856, App
Sequence 67, App1
Sequence 331, App
Sequence 12, App1
Sequence 16, App1
Sequence 25, App1
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Sequence 5, App1
Sequence 4, App1
Sequence 6, App1
Sequence 954, App
Sequence 268, App
Sequence 160, App
Sequence 199, App
Sequence 8, App1
Sequence 1189, App
Sequence 81, App1

26	54.5	11.2	312	6	US-10-986-501-124	Sequence 124, App
27	54.5	11.2	320	7	US-10-467-657-3354	Sequence 3254, App
28	54.5	11.2	423	6	US-11-070-080-16	Sequence 16, App1
29	54.5	11.2	2335	6	US-10-821-223-1510	Sequence 1610, App
30	54	11.1	504	7	US-11-055-822-136	Sequence 136, App
31	54	11.1	623	7	US-11-072-512-2547	Sequence 2547, App
32	54	11.1	1102	7	US-11-098-686-10951	Sequence 10951, App
33	53.5	11.0	293	7	US-11-072-512-2088	Sequence 2088, App
34	53.5	11.0	408	7	US-11-135-855-39	Sequence 39, App1
35	53.5	11.0	434	7	US-11-135-855-40	Sequence 40, App1
36	53.5	11.0	441	7	US-11-174-150-48	Sequence 48, App1
37	53.5	11.0	526	7	US-11-055-822-124	Sequence 124, App
38	53.5	11.0	856	6	US-10-510-947-8	Sequence 8, App1
39	53.5	11.0	856	7	US-11-042-988-13	Sequence 13, App1
40	53.5	11.0	856	7	US-11-135-235-1	Sequence 1, App1
41	53.5	11.0	1122	6	US-10-995-561-705	Sequence 705, App
42	53.5	11.0	1129	6	US-10-995-561-706	Sequence 706, App
43	53.5	11.0	1432	6	US-10-510-386-218	Sequence 218, App
44	53.5	11.0	1704	7	US-11-075-046-40	Sequence 40, App1
45	53	10.9	289	7	US-11-093-118-39	Sequence 39, App1
46	53	10.9	327	7	US-11-093-118-37	Sequence 37, App1
47	53	10.9	479	7	US-11-024-251-33	Sequence 33, App1
48	53	10.9	502	7	US-11-182-016-30	Sequence 30, App1
49	53	10.9	627	6	US-10-493-909-47	Sequence 47, App1
50	53	10.9	677	6	US-10-982-545-12	Sequence 12, App1
51	53	10.9	833	6	US-10-667-295-102	Sequence 102, App
52	53	10.9	839	6	US-10-667-295-101	Sequence 101, App
53	53	10.9	856	6	US-10-467-657-8534	Sequence 8534, App
54	53	10.9	876	7	US-11-242-730-5	Sequence 5, App1
55	53	10.9	1196	6	US-10-667-295-100	Sequence 100, App
56	52.5	10.8	130	7	US-10-793-957-110	Sequence 1310, App
57	52.5	10.8	189	7	US-11-103-957-87	Sequence 87, App1
58	52.5	10.8	181	6	US-10-467-657-1918	Sequence 1918, App
59	52.5	10.8	166	7	US-11-017-512-2218	Sequence 2218, App
60	52	10.7	362	7	US-11-098-686-11138	Sequence 11138, App
61	52	10.7	418	7	US-11-072-512-3417	Sequence 3417, App
62	52	10.7	426	6	US-10-858-730-80	Sequence 80, App1
63	52	10.7	488	7	US-11-055-822-850	Sequence 850, App1
64	52	10.7	645	6	US-10-510-386-32	Sequence 32, App1
65	52	10.7	913	7	US-11-018-868-164	Sequence 164, App
66	52	10.7	1450	6	US-10-485-517-152	Sequence 152, App
67	52	10.7	279	7	US-10-055-877-197	Sequence 197, App
68	51.5	10.6	377	7	US-11-072-512-3433	Sequence 3433, App
69	51.5	10.6	520	7	US-11-072-512-2424	Sequence 2424, App
70	51.5	10.6	520	7	US-11-072-512-2730	Sequence 2730, App
71	51.5	10.6	552	6	US-10-131-826A-196	Sequence 196, App
72	51.5	10.6	552	6	US-11-072-512-4405	Sequence 4405, App
73	51.5	10.6	690	6	US-10-467-657-4758	Sequence 4758, App
74	51.5	10.6	1449	7	US-11-052-554A-237	Sequence 237, App
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ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-968

Query Match 40.8%; Score 198; DB 6; Length 88;
Best Local Similarity 41.4%; Pred. No. 2.5e-16;
Matches 36; Conservative 19; Mismatches 32; Indels 0; Gaps 0;

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DB 1 MARWVFCVRLNKEAGKMPPLPNELGKRIENVSQKAMAAWTRQVTLINENRLSLADP 60

QY 61 EDRKFLQTBMDKFLSGEYVAQNEGYVP 87
DB 61 RAREYLAQOMEQYFPGDGADNAVQGYVP 87

RESULT 2
US-11-072-512-3313
Sequence 3313, Application US/11072512
Publication No. US2006029945A1
GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOHYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 064335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3313
LENGTH: 381
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3313

Query Match 13.6%; Score 66; DB 7; Length 381;
Best Local Similarity 33.3%; Pred. No. 3.3;
Matches 13; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 26 KGEDIFNHSQKAMADWQKHQTLLINERLNNMNAEDRK 64
DB 326 RGEDYNNMDENEBASETDXQAALAGNDRNIDVFNVEDQK 364

RESULT 3
US-10-131-826A-486
Sequence 486, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gunney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 486
LENGTH: 401
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-486

Query Match 13.6%; Score 66; DB 6; Length 401;
Best Local Similarity 33.3%; Pred. No. 3.5;
Matches 13; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

QY 26 KGEDIFNHSQKAMADWQKHQTLLINERLNNMNAEDRK 64
DB 346 RGEDYNNMDENEBASETDXQAALAGNDRNIDVFNVEDQK 384

RESULT 4
US-11-059-982-1
Sequence 1, Application US/11059982
Publication No. US20050255507A1
GENERAL INFORMATION:
APPLICANT: Jenkins, Robert B.
APPLICANT: Yang, Ping
APPLICANT: Thibodeau, Steve
APPLICANT: Wang, Liang
APPLICANT: Scheid, Daniel
TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND
FILE REFERENCE: 07039-505001
CURRENT APPLICATION NUMBER: US/11/059,982
CURRENT FILING DATE: 2005-02-17

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502a-24

Perfect score: 472

Sequence: 1 MRRTWCKRYQBELPGLERP.....AEWDKFPAGEBYAAGGYVP 87

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

A_Geneseq_21:.*
1: geneseq19808:.*
2: geneseq19908:.*
3: geneseq20008:.*
4: geneseq20018:.*
5: geneseq20028:.*
6: geneseq20038:.*
7: geneseq20048:.*
8: geneseq20058:.*
9: geneseq20068:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472	100.0	87	5	ABB78169 Amino aci
2	432	91.5	90	5	ABB78168 Amino aci
3	400	84.7	87	5	ABB78170 Amino aci
4	400	84.7	122	7	ABO74609 Pseudomon
5	265.5	56.2	92	6	ADA34169 Actinobac
6	239	50.6	87	5	ABB78177 Amino aci
7	237	50.2	87	5	ABB78176 Amino aci
8	237	50.2	88	5	ABB78154 Amino aci
9	232	49.2	89	9	ABB41576 L. pneumo
10	232	49.2	95	9	ABB38294 L. pneumo
11	229	48.5	87	5	ABB78175 Amino aci
12	229	48.5	87	5	ABB78152 Amino aci
13	228	48.3	90	5	ABB78155 Amino aci
14	228	48.3	91	5	ABB78150 Amino aci
15	225	47.7	87	5	ABB78151 Amino aci
16	225	47.7	91	5	ABB78158 Amino aci
17	225	47.7	91	5	ABB78157 Amino aci
18	225	47.7	91	5	ABB78156 Amino aci
19	224	47.5	110	8	ADL05173 M. catarr
20	223	47.2	87	5	ABB78174 Amino aci
21	222	47.0	87	5	ABB78148 Amino aci
22	222	47.0	87	5	ABB78147 Amino aci
23	219	46.4	87	5	ABB78153 Amino aci
24	219	46.4	88	5	ABB78171 Amino aci

25	219	46.4	88	5	ABB78172 Amino aci
26	219	46.4	88	5	ABB78173 Amino aci
27	219	46.4	88	6	ABP77219 N. gonorr
28	218	46.2	88	5	ABB78160 Amino aci
29	218	46.2	91	5	ABB78161 Amino aci
30	218	46.2	91	5	ABB78159 Amino aci
31	218	46.2	91	5	ABB78162 Amino aci
32	213	45.1	107	7	ABO65445 Klebsiell
33	211	44.7	91	5	ABB78163 Amino aci
34	209	44.3	93	7	ADP05158 Bacteri
35	204.5	43.3	86	5	ABB78149 Amino aci
36	204	43.2	88	5	ABB78178 Amino aci
37	197.5	41.8	78	5	ABB78164 Amino aci
38	188.5	39.9	90	5	ABB78167 Amino aci
39	188	39.8	90	5	ABB78165 Amino aci
40	159	33.7	76	5	ABB78166 Amino aci
41	73	15.5	451	7	ADP07116 Bacteri
42	72	15.3	259	3	AAQ43535 Arabidops
43	72	15.3	307	3	AAQ43534 Arabidops
44	72	15.3	795	4	ABG07025 Novel hum
45	72	15.3	844	8	ADH71956 Human pro
46	72	15.3	844	8	ADH71956 Human pro
47	72	15.3	847	8	ADH71956 Human pro
48	72	15.3	901	8	ADT49817 Murine IO
49	70	14.8	670	8	ADN23314 Bacteri
50	69.5	14.7	1091	5	ABB48258 Listeria
51	69	14.6	247	6	ABU33468 Protein e
52	69	14.6	251	4	AAW3928 Human pol
53	69	14.6	251	4	ADL32064 Human pro
54	67.5	14.3	689	5	ABB49714 Listeria
55	67.5	14.3	689	5	ABU33095 Protein e
56	67	14.2	559	8	ADN21954 Bacteri
57	67	14.2	567	8	ADN24711 Bacteri
58	66	14.0	140	5	ABB47381 Listeria
59	66	14.0	250	8	ADN47605 Thermococ
60	66	14.0	967	6	ADE52670 Human pro
61	66	14.0	1490	6	ABP98817 Human str
62	66	14.0	1651	4	ABG14648 Novel hum
63	66	14.0	2142	6	ABP98818 Human str
64	66	14.0	2202	5	ABG37482 Human NOV
65	65.5	13.9	484	9	ABB37045 L. pneumo
66	65.5	13.9	484	9	ABB40396 L. pneumo
67	65.5	13.9	926	8	ADN24302 Bacteri
68	65	13.8	36946	9	ADV97835 Murine pr
69	64.5	13.7	309	4	ABG15321 Novel hum
70	64.5	13.7	323	2	AAV05836 Banana ri
71	64.5	13.7	350	4	ABB64322 Drosophi
72	64.5	13.7	1518	6	ABJ18375 Breast sp
73	64.5	13.7	1641	2	AAV05846 Banana ri
74	64	13.6	317	7	ADC95026 E. faeciu
75	64	13.6	1042	4	AAU15096 Protein e

ALIGNMENTS

RESULT 1
ABB78169
ID ABB78169 standard; protein; 87 AA.
XX ABB78169;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX Pseudomonas putida.
XX
XX OS
XX PN US2002072118-A1.

PD 13-JUN-2002.
 XX
 XX 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 CC
 SQ Sequence 87 AA;

Query Match 100.0%; Score 472; DB 5; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.8e-51;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRTWCRKYOEBLPGIERPPYPGAKGODIFEHISOKAMADQKHOTMLINERLNMNNA 60
 DB 1 MTRTWCRKYOEBLPGIERPPYPGAKGODIFEHISOKAMADQKHOTMLINERLNMNNA 60
 QY 61 EDRKFLQAEEMDKFPAGEEYVAQAEGYVP 87
 DB 61 EDRKFLQAEEMDKFPAGEEYVAQAEGYVP 87

RESULT 2
 ABB78168
 ID ABB78168 standard; protein; 90 AA.
 XX
 AC ABB78168;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.
 XX
 DE Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.
 KM
 OS *Pseudomonas syringae*.
 OS
 PN US2002072118-A1.
 PN
 PD 13-JUN-2002.
 PD
 PF 18-SEP-2001; 2001US-00955502.
 PF
 PR 22-SEP-2000; 2000US-0234588P.
 PR
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 CC
 SQ Sequence 90 AA;

Query Match 91.5%; Score 432; DB 5; Length 90;
 Best Local Similarity 88.5%; Pred. No. 2.2e-46;
 Matches 77; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRTWCRKYOEBLPGIERPPYPGAKGODIFEHISOKAMADQKHOTMLINERLNMNNA 60
 DB 1 MTRTWCRKYOEBLPGIERPPYPGAKGODIFEHISOKAMADQKHOTMLINERLNMNNA 60
 QY 61 EDRKFLQAEEMDKFPAGEEYVAQAEGYVP 87
 DB 61 EDRKFLQAEEMDKFPAGEEYVAQAEGYVP 87

RESULT 3
 ABB78170
 ID ABB78170 standard; protein; 87 AA.
 XX
 AC ABB78170;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.
 XX
 DE Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.
 KM
 OS unidentified.
 OS
 PN US2002072118-A1.
 PN
 PD 13-JUN-2002.
 PD
 PF 18-SEP-2001; 2001US-00955502.
 PF
 PR 22-SEP-2000; 2000US-0234588P.
 PR
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 DR
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-24

Perfect score: 472

Sequence: 1 MFTWVCRKQOEELPGLERP.....AEMDKFPAGEHYAQAEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	400	84.7	90	2 H83003	conserved hypotet
2	228	48.5	90	2 C64013	hypothetical prote
3	228	48.3	90	2 C82320	conserved hypotet
4	225	47.7	91	2 A85954	hypothetical prote
5	225	47.7	91	2 A65082	hypothetical prote
6	225	47.7	91	2 P91108	hypothetical prote
7	219	46.4	88	2 H81014	conserved hypotet
8	218	46.2	91	2 AH0879	conserved hypotet
9	198	41.9	105	2 C82624	conserved hypotet
10	188	39.8	90	2 A10116	conserved hypotet
11	159	33.7	93	2 B84994	hypothetical prote
12	70	14.8	670	2 T29898	kinasin protein OS
13	69.5	14.7	1091	2 AP1380	glycosidase homolo
14	69	14.6	155	2 C75419	hypothetical prote
15	68.5	14.5	1090	2 AG1749	transferring homolo
16	68	14.4	388	1 QOYV	transcription anti
17	67.5	14.3	689	2 AC1408	transcription anti
18	66.5	14.1	1134	2 T30340	adenosine de
19	66	14.0	140	2 AB1428	transcription regu
20	66	14.0	1553	2 S67483	adenosinetriphosph
21	65.5	13.9	926	2 T24923	hypothetical prote
22	65.5	13.9	959	2 H69344	hypothetical prote
23	65	13.8	528	2 T24730	hypothetical prote
24	64.5	13.7	767	2 T31558	hypothetical prote
25	64	13.6	140	2 A11801	transcription regu
26	64	13.6	732	2 S23001	transcription regu
27	63.5	13.5	288	2 T45715	hypothetical prote
28	63.5	13.5	397	2 C87470	hypothetical prote
29	63.5	13.5	689	2 AC1784	transcription anti

30	63	13.3	150	2 F90212	hypothetical prote
31	63	13.3	555	2 C87515	ABC transporter. A
32	63	13.3	559	2 T12680	peroxisomal target
33	63	13.3	561	2 T06628	hypothetical prote
34	63	13.3	568	2 G84455	hypothetical prote
35	62.5	13.2	352	2 F84799	hypothetical prote
36	62.5	13.2	677	2 G69895	formate dehydrogen
37	62.5	13.2	985	2 S15965	hypothetical prote
38	62	13.1	242	2 S67270	COAR-binding fact
39	62	13.1	1175	2 D35815	myosin heavy chain
40	62	13.1	1175	2 C35815	myosin heavy chain
41	62	13.1	1201	2 A35815	myosin heavy chain
42	62	13.1	1201	2 B35815	myosin heavy chain
43	62	13.1	2385	2 A32491	myosin heavy chain
44	62	13.1	2411	2 B32491	myosin heavy chain
45	61.5	13.0	284	2 D82486	probable lipase ac
46	61.5	13.0	339	2 AG2041	queine tRNA-ribos
47	61.5	13.0	430	2 I48755	mSAPIA - mouse
48	61.5	13.0	470	2 D84614	hypothetical prote
49	61.5	13.0	709	2 D86907	elongation factor
50	61.5	13.0	863	2 JC7537	beta-N-acetylgluco
51	61	12.9	213	2 B27898	beta-crystallin B3
52	61	12.9	245	2 S49045	luxp protein - Vib
53	61	12.9	310	2 A25027	arabinose operon r
54	61	12.9	389	2 T14751	hypothetical prote
55	61	12.9	410	1 O4886M	cytochrome P450 10
56	61	12.9	474	2 S16250	phytoene dehydroge
57	61	12.9	604	2 S36493	Et protein - human
58	61	12.9	1212	2 B82809	exodeoxyribonuclea
59	60.5	12.8	88	2 A13122	IS3 family transpo
60	60.5	12.8	88	2 F98164	insertion element
61	60.5	12.8	142	2 F81296	hypothetical prote
62	60.5	12.8	323	2 B83215	conserved hypotet
63	60.5	12.8	335	2 T33483	hypothetical prote
64	60.5	12.8	458	2 F84275	hypothetical prote
65	60.5	12.8	508	2 S74848	neopullulanase - S
66	60.5	12.8	843	2 A47132	major vault protei
67	60.5	12.8	1083	1 S53048	alpha-mannosidase
68	60	12.7	177	2 D70862	hypothetical prote
69	60	12.7	282	2 D97138	DNA replication pr
70	60	12.7	290	2 JN0504	H+/K+-exchanging A
71	60	12.7	310	2 AB0275	arabinose operon r
72	60	12.7	326	2 G96812	protein F3P.6 [im
73	60	12.7	352	2 F89884	phe-tRNA synthetas
74	60	12.7	373	2 A96927	probable N6-adenin
75	60	12.7	426	2 D87153	serine hydroxymeth

ALIGNMENTS

RESULT 1
H83003 conserved hypothetical protein PA5148 [Imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C/Accession: H83003
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bro
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Llim,
..; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A/Reference number: AB2950, MIMD:20457337, PMID:10984043
A/Accession: H83003
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <STO>
A/Cross-references: UNIPARC:UPI000000C5F26; GB:AE004927; GB:AE004091; NID:99951437; PIDN:
A/Experimental source: strain PA01
C/Genes:
A/Gene: PA5148
C/Superfamily: Fe(II) trafficking protein YggX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-24
Perfect score: 472
Sequence: 1 MTRVMCRKQBELPGLERP.....AEMDKFPAGEYVAQAEQYVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472	100.0	90	1	FETP_PSEPK
2	439	93.0	90	2	O4KJ22_PSEFS
3	432	91.5	90	1	FETP_PSESM
4	432	91.5	90	2	O4ZLF3_PSESY
5	411	87.1	90	2	O6T7P6_PSEFL
6	400	84.7	90	1	FETP_PSEAE
7	393	83.3	90	2	O4J228_AZOV1
8	261.5	55.4	90	1	FETP_ACTAD
9	250	53.0	90	1	FETP_IDTLO
10	244	51.7	96	2	O4FV07_PGAMM
11	239	50.6	90	1	FETP_METCA
12	237	50.2	92	1	FETP_SHSON
13	234	49.6	91	1	FETP_MANSM
14	233	49.4	91	1	FETP_RALSO
15	232	49.2	89	1	FETP_LBQPA
16	232	49.2	89	1	FETP_LBQPH
17	232	49.2	90	1	FETP_NITEU
18	231	48.9	89	1	FETP_LBQPL
19	229	48.5	90	1	FETP_HARIN
20	229	48.5	90	1	FETP_PHOPR
21	229	48.5	90	2	O4OMD9_HAR18
22	229	48.5	91	1	FETP_BURMA
23	229	48.5	91	1	FETP_BURPS
24	228	48.3	90	1	FETP_VIBCH
25	226	47.9	90	1	FETP_VIBVU
26	226	47.9	90	1	FETP_VIBVY
27	225	47.7	90	1	FETP_PASMU
28	225	47.7	90	1	FETP_VIBPA
29	223	47.2	91	2	O4LS19_9BURK
30	222	47.0	90	1	FETP_BORBR
31	222	47.0	90	1	FETP_BORPA

32	222	47.0	90	1	FETP_BORBE	O7WVC4 bordetella
33	220	46.6	90	1	FETP_ECO57	PA894 escherichia
34	220	46.6	90	1	FETP_BCOLI	PA893 escherichia
35	220	46.6	90	1	FETP_PHOLL	O7N711 photorhabdu
36	220	46.6	90	1	FETP_SHIFL	PA895 shigella fl
37	219	46.4	88	1	FETP_NEIG1	O5I553 neisseria g
38	219	46.4	88	1	FETP_NEIMA	PE7615 neisseria m
39	219	46.4	88	1	FETP_NEIMB	PE7616 neisseria m
40	219	46.4	90	1	FETP_ERMCT	O6D819 ewingia car
41	219	46.4	90	1	FETP_VIBP1	O6E760 vibrio fusc
42	219	46.4	94	1	FETP_HARDU	O7VX06 haemophilus
43	216	45.8	90	1	FETP_BCOL6	O8E199 escherichia
44	213	45.1	90	1	FETP_SALCH	O57K04 salmonella
45	213	45.1	90	1	FETP_SALPA	O5PMU1 salmonella
46	213	45.1	90	1	FETP_SALTI	PE7618 salmonella
47	213	45.1	90	1	FETP_SALTY	PE7617 salmonella
48	207	43.9	90	1	FETP_CHRVO	O7N874 chromobacte
49	206	43.6	91	1	FETP_XANAC	O6D117 xanthomonas
50	206	43.6	92	1	FETP_XANOR	O5GY22 xanthomonas
51	204	43.2	90	1	FETP_COXBU	O83D06 coxiella bu
52	199	42.2	92	2	FETP_XANCP	O8B829 xanthomonas
53	199	42.2	92	2	O4UW14_XANCP	O4UW14 xanthomonas
54	198	41.9	90	1	FETP_XYUFA	O9PC73 xylella fas
55	196	41.5	90	1	FETP_YERPS	O666M3 yersinia ps
56	194	41.1	90	1	FETP_XYLFT	O87D06 xylella fas
57	193	40.9	78	1	FETP_WIGBR	O8D365 wigleswort
58	188	39.8	90	1	FETP_YERPE	O8ZHE7 yersinia pe
59	185	39.2	87	1	FETP_FRATT	O5N118 francisella
60	180	38.1	79	1	FETP_CANBF	O7V939 candidatus
61	177	37.5	78	1	FETP_BUCAP	O8K925 buchiera ap
62	172	36.4	92	2	O4NMQ4_9DEBLT	O4NMQ4 anaeroxob
63	159	33.7	77	1	FETP_BUCAI	PE7614 buchiera ap
64	157	33.3	87	1	FETP_BUCBP	O89A44 buchiera ap
65	84	17.8	703	2	O4WPT2_ASPTU	O4WPT2 aspergillus
66	79.5	16.8	280	2	O81BR9_BACCR	O81BR9 bacillus ce
67	78.5	16.6	603	2	O6BPW5_ORYSA	O6BPW5 oryza sativ
68	74	15.7	220	2	O5WAP4_BACSK	O5WAP4 bacillus cl
69	74	15.7	1141	2	O5B318_EMENI	O5B318 emenii
70	72	15.3	307	2	O9FJ06_ARATH	O9FJ06 arabidopsis
71	72	15.3	844	1	PRIC2_HUMAN	O7Z356 homo sapien
72	72	15.3	845	1	PRIC2_MOUSE	O80Y04 mus musculu
73	71	15.0	437	2	O60BH0_ORYSA	O60BH0 oryza sativ
74	70.5	14.9	259	2	O52J13_BRARE	O52J13 brachydanio
75	70.5	14.9	353	2	O6NN67_DROME	O6NN67 drosophila

ALIGNMENTS

RESULT 1
FETP_PSEPK STANDARD; PRT; 90 AA.
ID FETP_PSEPK
AC O8BR49;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DR Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=PP0285;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160486;
RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22423060; PubMed=12534463;
DOI=10.1046/j.1462-2920.2002.00366.x;
RA Neilson K.E., Weinel C., Paulsen I.T., Gill S.R., Pod M., Holmes M.,
Martins dos Santos V.A.P., Fouts D.E., Dodson R.J., Hilbert H.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzapple B.K., Scanlan D., Tran K.,
RA Moazzaz A., Utecherack T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hohetsel J., Straetz M., Heim S.,

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RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Frazer C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC
CC EMBL; AEO16775; AAN65916.1; -; Genomic_DNA.
DR SMR; Q88R49; 1-79.
DR TIGR; PP0285; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10596 MW; 0C802FD7163B75A2 CRC64;

Query Match 100.0%; Score 472; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 9, 6e-44;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRTWCKRYQSELPGLERPPYPGAKGQDIFEHISQKAWADWQKHQTMLINERKLNMMNA 60
DB 1 MTRTWCKRYQSELPGLERPPYPGAKGQDIFEHISQKAWADWQKHQTMLINERKLNMMNA 60
QY 61 EDRKFLQAEWDKFPAGEBYAQAEGYVP 87
DB 61 EDRKFLQAEWDKFPAGEBYAQAEGYVP 87

RESULT 2
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ID QAKT2_PSEFS PRELIMINARY; PRT; 90 AA.
AC QAKT2;
DT 13-SEP-2005 (TREMURE1.31, Created)
DT 13-SEP-2005 (TREMURE1.31, Last sequence update)
DT 13-SEP-2005 (TREMURE1.31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PFL_0357;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
ON NCBI_TaxID=220664;
RX NUCLEOTIDE SEQUENCE.
RP STRAIN=PF-5;
RC PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodidi D., Deboy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Guim M.L., Zhou L., Nelson W.C., Weidman J., Mackinnon K., Tran K.,
RA Khouri H.M., Pierson B., Pierson J., Thomasow L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AA95766.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 90 AA; 10483 MW; 816D3C74C2B7C12 CRC64;

Query Match 93.0%; Score 439; DB 2; Length 90;
Best Local Similarity 88.5%; Pred. No. 3, 9e-40;
Matches 77; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MTRTWCKRYQSELPGLERPPYPGAKGQDIFEHISQKAWADWQKHQTMLINERKLNMMNA 60
DB 1 MTRTWCKRYQSELPGLERPPYPGAKGQDIFEHISQKAWADWQKHQTMLINERKLNMMNA 60
QY 61 EDRKFLQAEWDKFPAGEBYAQAEGYVP 87
DB 61 EDRKFLQAEWDKFPAGEBYAQAEGYVP 87

RESULT 3
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ID FETP_PSESM STANDARD; PRT; 90 AA.
AC Q87U5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderdLocuNames=PSPO5343;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
ON NCBI_TaxID=323;
RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=DC3000;
RC MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Guim M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beaman M.J., Haft D.H.,
RA Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Uterback T.R., Van Aken S.B., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Frazer C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC removed.
CC -----
CC
CC EMBL; AEO16853; AAO58769.1; -; Genomic_DNA.
DR SMR; Q87U5; 1-79.
DR TIGR; PSPT05343; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10621 MW; 1086288DF6532973 CRC64;

Query Match 91.5%; Score 432; DB 1; Length 90;
Best Local Similarity 88.5%; Pred. No. 2, 3e-39;
Matches 77; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-24

Perfect score: 472
Sequence: 1 MRRTWCKRYOEELPGLRRP.....AEWDKFEAGEYQAQGVYP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5/COMB.pep:*
2: /cgn2_6/prodata/1/1aa/6/COMB.pep:*
3: /cgn2_6/prodata/1/1aa/H/COMB.pep:*
4: /cgn2_6/prodata/1/1aa/PCTUS/COMB.pep:*
5: /cgn2_6/prodata/1/1aa/RE/COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	400	84.7	122	2	US-09-252-991A-23355
2	265.5	56.2	92	2	US-09-328-352-5456
3	224	47.5	110	2	US-09-540-236-2859
4	213	44.1	107	2	US-09-489-039A-11962
5	209	44.3	93	2	US-09-543-681A-5443
6	73	15.5	451	2	US-09-543-681A-7401
7	69	14.6	443	2	US-09-248-796A-16816
8	64.5	13.7	163	2	US-09-248-796A-16816
9	64	13.6	317	2	US-09-107-532A-4653
10	64	13.6	420	2	US-09-248-796A-15323
11	64	13.6	1042	2	US-09-792-024-106
12	63	13.3	314	2	US-09-716-865-4
13	62.5	13.2	284	2	US-09-934-899-14
14	62.5	13.2	284	2	US-09-934-868-34
15	62.5	13.2	284	2	US-10-701-200-34
16	62	13.1	242	2	US-09-538-092-763
17	62	13.1	448	2	US-09-107-532A-4482
18	62	13.1	1156	2	US-08-996-083-1
19	62	13.1	1156	2	US-09-429-516-1
20	62	13.1	1156	2	US-09-429-516-3
21	61.5	13.0	689	2	US-10-200-012-2
22	61	12.9	342	2	US-10-227-327-1
23	61	12.9	381	2	US-09-949-016-9788
24	61	12.9	381	2	US-09-964-899-13
25	60.5	12.8	205	2	US-09-919-039-258
26	60	12.7	352	1	US-08-785-052-2
27	60	12.7	352	1	US-08-913-581-2

28	60	12.7	569	2	US-09-252-991A-32290	Sequence 32290, A
29	60	12.7	689	2	US-09-489-039A-7677	Sequence 7677, Ap
30	59.5	12.6	468	2	US-09-976-594-462	Sequence 462, App
31	59.5	12.6	468	2	US-09-999-833A-337	Sequence 337, App
32	59.5	12.6	468	2	US-10-020-445A-337	Sequence 337, App
33	59	12.5	184	2	US-09-040-229B-9	Sequence 9, App1
34	59	12.5	212	1	US-08-531-525-18	Sequence 18, App1
35	59	12.5	212	1	US-08-718-270A-18	Sequence 18, App1
36	59	12.5	212	2	US-09-399-913-67	Sequence 67, App1
37	59	12.5	212	2	US-09-350-614-67	Sequence 67, App1
38	59	12.5	216	2	US-09-949-016-10750	Sequence 10750, A
39	59	12.5	278	2	US-09-328-352-7544	Sequence 7544, Ap
40	59	12.5	298	2	US-09-543-681A-8107	Sequence 8107, Ap
41	59	12.5	454	2	US-09-771-161A-95	Sequence 95, App1
42	59	12.5	477	2	US-09-949-016-10716	Sequence 10716, A
43	59	12.5	504	2	US-09-538-092-1170	Sequence 1170, Ap
44	59	12.5	505	2	US-09-949-016-6117	Sequence 6117, Ap
45	59	12.5	505	2	US-09-771-161A-186	Sequence 186, App
46	59	12.5	513	2	US-09-949-016-11517	Sequence 11517, A
47	59	12.5	1242	2	US-09-583-110-5051	Sequence 5051, Ap
48	59	12.5	1243	2	US-09-107-433-3942	Sequence 3942, Ap
49	58.5	12.4	205	2	US-09-216-393B-124	Sequence 124, App
50	58.5	12.4	361	2	US-09-270-767-37733	Sequence 37733, A
51	58.5	12.4	783	2	US-09-902-540-11823	Sequence 11823, A
52	58.5	12.4	913	2	US-09-623-624-2	Sequence 2, App1
53	58.5	12.4	913	2	US-10-270-595-2	Sequence 2, App1
54	58.5	12.4	1122	2	US-10-146-704-2	Sequence 2, App1
55	58	12.3	129	2	US-09-489-039A-11601	Sequence 11601, A
56	58	12.3	140	2	US-09-248-796A-15755	Sequence 15755, A
57	58	12.3	292	2	US-09-328-352-5836	Sequence 5836, Ap
58	58	12.3	444	2	US-09-861-451A-16	Sequence 16, App1
59	58	12.3	582	2	US-09-902-540-11161	Sequence 11161, A
60	58	12.3	861	2	US-09-826-312A-10	Sequence 10, App1
61	58	12.3	861	2	US-09-542-497A-10	Sequence 10, App1
62	58	12.3	861	2	US-10-108-767-10	Sequence 10, App1
63	58	12.3	903	1	US-08-220-151-8	Sequence 8, App1
64	58	12.3	903	1	US-08-413-118-8	Sequence 8, App1
65	58	12.3	903	2	US-08-804-439A-22	Sequence 22, App1
66	58	12.3	903	2	US-08-473-446-8	Sequence 8, App1
67	58	12.3	903	2	US-08-720-229-22	Sequence 22, App1
68	58	12.3	904	2	US-08-632-537-1	Sequence 22, App1
69	58	12.3	904	4	PCT-US96-05316-1	Sequence 1, App1
70	58	12.3	904	6	5244792-4	Sequence 1, App1
71	57.5	12.2	324	2	US-09-252-991A-26001	Sequence 26001, A
72	57.5	12.2	324	2	US-09-252-991A-24826	Sequence 24826, A
73	57.5	12.2	337	2	US-09-489-039A-14173	Sequence 14173, A
74	57.5	12.2	368	2	US-09-252-991A-19658	Sequence 19658, A
75	57.5	12.2	502	2	US-09-252-991A-26986	Sequence 26986, A

ALIGNMENTS

RESULT 1
US-09-252-991A-23355
Sequence 23355, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23355
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23355

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Best Local Similarity	79.3%	Pred. No. 5.3e-46		
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[illegible]

RESULT 2
US-09-328-352-5456
; Sequence 5456, Application US/09328352

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1  APPLICANT: Gary L. Breton et al.
2  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
3  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
4  FILE REFERENCE: GTC99-03PA
5  CURRENT APPLICATION NUMBER: US/09/328,352
6  CURRENT FILING DATE: 1999-06-04
7  NUMBER OF SEQ ID NOS: 8252
8  SEQ ID NO 5456
9  LENGTH: 92
10 TYPE: PRT
11 ORGANISM: Acinetobacter baumannii
12 OS-09-328-352-5456

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Query Match	56.2%	Score 265.5	DB 2	Length 92
Best Local Similarity	53.4%	Pred. No. 5.1e-28		
Matches 47; Conservative	20;	Mismatches 20;	Indels 1;	Gaps 1;

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Db 4 MSROYFRCKTQKKEHGDIFAPFGAKQOEPEFNNSKOMQEMLOHOTTILNKRLLNVEP 63
QY 61 EDRKFTLAEMDKFPGAGEYVAQ-AGEYVP 87
QY 64 EAKKPLEORKEFPNNDESVEKAGWGP 91

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RESULT 3
US-09-540-236-2859
: Sequence 2859, Application US/09540236
: Patent No. 6673910
: GENERAL INFORMATION:
: APPLICANT: Gary L. Breton et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATALANICA
: TITLE OF INVENTION: PCR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2709.2005-001
: CURRENT APPLICATION NUMBER: US/09/540,236
: CURRENT FILING DATE: 2000-04-04
: NUMBER OF SEQ ID NOS: 3840
: SEQ ID NO 2859
: LENGTH: 110
: TYPE: PRT
: ORGANISM: M.cattarrhalis
: US-09-540-236-2859

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Query Match	47.5%	Score 224	DB 2	Length 110
Best Local Similarly	49.4%	Pred. No. 2.6e-22		
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0y      5 VMCRRQEBELPGLERPPYGAQCGDIFEHISQKAMADWQKHQTMLINEKRLNMNNAEDRK 64
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Db      25 VFCRRQQNPLKLPNPFPPNAKGQBIQDITISAKANMAMLEIQTMLINEKHSIMIDPAKK 84

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65 FLQAE~~MDK~~FFAGEEYAQAE~~GY~~P 87

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Db      85 YLNEQREKFLDNGDYEKPAGYKP 107
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RESULT 4
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Query Match	45.1%	Score 213	DB 2	length 107
Best Local Similarity	50.0%	Pred. No.	7.6e-21	
Matches 44		Conservative	29	Indels 2
				Gaps 2

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QY      MTRTVMRKAYOEELPGLERPRYPGAGGODI FPHISOKAMWDQXKOTMLINERGLMNNNA 6
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      17 MSKRIFCTPLQREADGDDPGLYFPGELSKRIYINISKEANAQWQHKOTMLINERGLSLMNP 76
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      61 EDRKFTLQAEWDKF-FAGEEYTAQAEIVTP 87
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      77 EHRKLTLEQEWQPLFEGKD-VHIEGYTP 103
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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RESULT 5
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Query Match	44.3%	Score 209	DB 2	Length 93
Best Local Similarly	47.7%	Pred. No. 2.2e-20		
Matches 42	Conservative 13	Mismatches 31	Indels 2	Gaps 2

[illegible]

RESULT 6
US-09-543-681A-7401
; Sequence 7401, Application US/09543681A

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 54.8952 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502a-24
Perfect score: 472
Sequence: 1 MTRTWCKRYQBELPGLRRP.....AEMDKFPAGEYQAEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472	100.0	87	3	US-09-955-502-24
2	432	91.5	90	3	US-09-955-502-23
3	400	84.7	87	3	US-09-955-502-25
4	239	50.6	87	3	US-09-955-502-32
5	237	50.2	87	3	US-09-955-502-31
6	237	50.2	88	3	US-09-955-502-9
7	229	48.5	87	3	US-09-955-502-7
8	229	48.5	87	3	US-09-955-502-29
9	229	48.5	87	3	US-09-955-502-30
10	228	48.3	90	3	US-09-955-502-10
11	228	48.3	91	3	US-09-955-502-5
12	225	47.7	87	3	US-09-955-502-6
13	225	47.7	91	3	US-09-955-502-11
14	225	47.7	91	3	US-09-955-502-12
15	225	47.7	91	3	US-09-955-502-13
16	222	47.0	87	3	US-09-955-502-2
17	222	47.0	87	3	US-09-955-502-3
18	219	46.4	87	3	US-09-955-502-8
19	219	46.4	88	3	US-09-955-502-26
20	219	46.4	88	3	US-09-955-502-27
21	219	46.4	88	3	US-09-955-502-28
22	218	46.2	88	3	US-09-955-502-15
23	218	46.2	91	3	US-09-955-502-14
24	218	46.2	91	3	US-09-955-502-16
25	218	46.2	91	3	US-09-955-502-17
26	211	44.7	91	3	US-09-955-502-18
27	204.5	43.3	86	3	US-09-955-502-4

28	204	43.2	88	3	US-09-955-502-33	Sequence 33, Appl1
29	198	41.9	89	3	US-09-955-502-22	Sequence 22, Appl1
30	197.5	41.8	78	3	US-09-955-502-19	Sequence 19, Appl1
31	188	39.8	90	3	US-09-955-502-20	Sequence 20, Appl1
32	159	33.7	76	3	US-09-955-502-21	Sequence 21, Appl1
33	78.5	16.6	596	4	US-10-437-963-130475	Sequence 130475, Appl1
34	73	15.5	766	4	US-10-437-963-146099	Sequence 146099, A
35	72	15.3	795	5	US-10-450-763-37384	Sequence 37384, A
36	71	15.0	313	4	US-10-437-963-173240	Sequence 173240, A
37	70	14.8	451	4	US-10-437-963-137284	Sequence 137284, A
38	70	14.8	670	4	US-10-369-493-5967	Sequence 5967, Ap
39	69.5	14.7	186	4	US-10-425-115-271944	Sequence 271944, A
40	69.5	14.7	902	4	US-10-437-963-156143	Sequence 156143, A
41	69	14.6	247	4	US-10-282-122A-61392	Sequence 61392, A
42	69	14.6	897	4	US-10-437-963-165505	Sequence 165505, A
43	69	14.6	981	4	US-10-437-963-165498	Sequence 165498, A
44	68.5	14.5	526	4	US-10-437-963-156176	Sequence 156176, A
45	68	14.4	794	4	US-10-437-963-156176	Sequence 156176, A
46	68	14.4	900	4	US-10-437-963-173233	Sequence 173233, A
47	67.5	14.3	689	4	US-10-437-963-126879	Sequence 126879, A
48	67.5	14.3	818	4	US-10-437-963-156121	Sequence 156121, A
49	67.5	14.3	890	4	US-10-437-963-156221	Sequence 156221, A
50	67	14.2	365	4	US-10-437-963-107715	Sequence 107715, A
51	67	14.2	559	4	US-10-369-493-4607	Sequence 4607, Ap
52	67	14.2	560	5	US-10-732-923-13914	Sequence 13914, A
53	67	14.2	561	5	US-10-732-923-13915	Sequence 13915, A
54	67	14.2	567	4	US-10-369-493-7364	Sequence 7364, Ap
55	67	14.2	576	4	US-10-424-599-243409	Sequence 243409, A
56	67	14.2	867	4	US-10-437-963-146098	Sequence 146098, A
57	66	14.0	659	4	US-10-437-963-107737	Sequence 107737, A
58	66	14.0	764	4	US-10-437-963-161225	Sequence 161225, A
59	66	14.0	830	4	US-10-437-963-161221	Sequence 161221, A
60	66	14.0	876	4	US-10-437-963-173236	Sequence 173236, A
61	66	14.0	1152	4	US-10-437-963-173239	Sequence 173239, A
62	66	14.0	1501	5	US-10-732-923-22706	Sequence 22706, A
63	66	14.0	1553	5	US-10-732-923-22705	Sequence 22705, A
64	66	14.0	1555	5	US-10-732-923-22584	Sequence 22584, A
65	66	14.0	1651	5	US-10-450-763-45007	Sequence 45007, A
66	66	14.0	2202	4	US-10-094-466-12	Sequence 12, Appl1
67	65.5	13.9	202	4	US-10-767-701-34267	Sequence 34267, A
68	65.5	13.9	284	4	US-10-437-963-156187	Sequence 156187, A
69	65.5	13.9	534	5	US-10-732-923-13918	Sequence 13918, A
70	65.5	13.9	571	5	US-10-732-923-13917	Sequence 13917, A
71	65.5	13.9	639	4	US-10-437-963-177051	Sequence 177051, A
72	65.5	13.9	682	4	US-10-437-963-177042	Sequence 177042, A
73	65.5	13.9	926	4	US-10-369-493-6965	Sequence 6965, Ap
74	65	13.8	391	5	US-10-732-923-13919	Sequence 13919, A
75	65	13.8	1011	4	US-10-437-963-173228	Sequence 173228, A

ALIGNMENTS

RESULT 1
US-09-955-502-24
; Sequence 24, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downe, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296, 97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pseudomonas putida

US-09-955-502-24

Query Match	100.0%;	Score 472;	DB 3;	Length 87;
Best Local Similarity	100.0%;	Pred. No. 6.4e-49;		
Matches	87;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Qy 1 MTRITWCRKYOEBELPGIERPPYVGAAGDIFEHISOKAMADWQKQTMLINEKRLNMNA 600
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Db 1 MTRITWCRKYOEBELPGIERPPYVGAAGDIFEHISOKAMADWQKQTMLINEKRLNMNA 600

QY 61 EDRKFLQAE~~MDKFF~~AGGE~~YYAQA~~EGYVP 87
Db 61 EDRKFLQAE~~MDKFF~~AGGE~~YYAQA~~EGYVP 87

RESULT 2

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US-09-955-502-23
/ Sequence 23, Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ FILE REFERENCE: 960296.97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ PRIOR FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 90
/ TYPE: PRT
/ ORGANISM: Pseudomonas syringae
/ US-09-955-502-23

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Query Match	91.5%	Score 432;	DB 3;	Length 90;
Best Local Similarity	88.5%	Pred. No. 4	4e-44;	
Matches 77;	Conservative	6;	Mismatches 4;	Indels 0;
			Gaps	0

Oy 1 MTRTWNCRKRYOEELPGLEBPYPYGAKGODI FEHISQKAWADWOKHOTMLINERRLNMNA 600
||||| : ||||| : ||||| : ||||| : |||||
Db 1 MTRTWNCRKRYEELPGLEBAPYGAKEGDI FNNHSQKAWADWOKHOTLLINERRLLMNA 600

Qy 61 EDRKFLQAEIMDKFFPAGEEYIAQAEGLVP 87
||| : |||
Db 61 EDRKFLQTEIMDKFLSGEETIAQAEGLVP 87

RESULT 3

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US-09-955-502-25
/ Sequence 25, Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ FILE REFERENCE: 960296,97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ PRIOR APPLICATION NUMBER: 2001-09-18
/ PRIOR FILING DATE: 2000-09-22
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 25
/ LENGTH: 87
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-09-955-502-25

```

Query Match 84.7%; Score 400; DB 3; Length 87;

Best Local Similarity 79.3%; Pred. No. 3.1e-40;
Matches 69; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

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QY      1 MTRITWCRKIQEELPGIERPPYPGAKODIFEHISQKAWADMQKHQTMLINERKLMMNA    600
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB      1 MSRTWCRKHEELPGIDRPPYPGAKABDIYNNVSRKAMDWMQKHQTMLINERLMMNA    600
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QY 61 EDRKFLQAEEMDKFFAGBEEYAQAEGVYP 87
 Db 61 EDRKFLQAEEMDKFLSGEDYAKADGVYP 87

RESULT 4

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US-09-955-502-32
/ Sequence 32, Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OR INVENTION: Method for Preventing Superoxide Damage to Cells and
/ TITLE OR INVENTION: Oxygen-Labile Proteins
/ FILE REFERENCE: 960296, 97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ PRIOR FILING DATE: 2000-09-22
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 32
/ LENGTH: 87
/ TYPE: PRT
/ ORGANISM: Methylococcus capsulatus
US-09-955-502-32

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Query Match	50.6%	Score 239;	DB 3;	Length 87;
Best Local Similarity	51.7%	Pred. No. 8.2e-21;		
Matches	45;	Conservative	12;	Mismatches 30;
				Indels 0;
				Gaps 0

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Oy      1 MTRITWCRKQBELPGIERPPYPGAKODIFEHI SOKAMADMOHQITML INEKLNNMNA 600
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 MARRITCAKGI EADGIDAPPPPGOGORIFEHYSKEMQDWLKTML INEHLTPFEA 600

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```
QY      61 EDRKFLQAEMDKFFAGGEYAQAEGVYP 87
          ||||| : ||| : |||||
DB      61 SARKFLEGEREKFLFGGISTPQGVP 87
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RESULT 5

US-09-955-502-31
 ; Sequence 31, Application US/09955502
 ; Patent No. US20020072118A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Downs, Diana M.
 ; APPLICANT: Gralnick, Jeff A.
 ; TITLE OF INVENTION: Method For Preventing Superoxide Damage to Cells and
 ; TITLE OF INVENTION: Oxygen-Labile Proteins
 ; FILE REFERENCE: 960296, 97559
 ; CURRENT APPLICATION NUMBER: US/09/955,502
 ; CURRENT FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: 60/234,588
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ. ID NOS: 33
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 31
 ; LENGTH: 87
 ; TYPE: PR1
 ; ORGANISM: *Thiobacillus ferrooxidans*
 ; US-09-955-502-31

Query Match	50.2%;	Score 237;	DB 3;	Length 87;
Best Local Similarity	49.4%;	Pred. No. 1.4e-20;		
Matches 43;	Conservative 16;	Mismatches 28;	Indels 0;	Gaps 0;



GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocollection Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.75626 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502a-24
Perfect score: 472
Sequence: 1 MFTVWCKRYQXELPGLERP.....AEMDKFAGREYVAQAEQYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database:

Published Applications AA New:
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2: /cgn2_6/ptodaca/2/pubpaa/US06_NEW_PUB.pep:*
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6: /cgn2_6/ptodaca/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodaca/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodaca/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	46.4	88	6	US-10-467-657-968 Sequence 968, App
2	72	15.3	844	6	US-10-453-372-852 Sequence 852, App
3	72	15.3	844	6	US-10-453-372-856 Sequence 856, App
4	64.5	13.7	1560	7	US-11-059-982-1 Sequence 1, Appl1
5	61.5	13.0	689	7	US-11-121-438-2 Sequence 2, Appl1
6	61	12.9	3433	6	US-10-714-781A-67 Sequence 67, Appl1
7	60.5	12.8	645	6	US-10-510-386-32 Sequence 32, Appl1
8	60	12.7	426	6	US-10-858-730-81 Sequence 81, Appl1
9	59.5	12.6	680	6	US-10-467-657-4758 Sequence 4758, App
10	58	12.3	687	7	US-11-074-176-62 Sequence 62, Appl1
11	57	12.1	426	6	US-10-858-730-80 Sequence 80, Appl1
12	57	12.1	1386	7	US-11-091-643-6 Sequence 6, Appl1
13	57	12.1	1618	6	US-10-984-645-2 Sequence 2, Appl1
14	56	11.9	211	7	US-11-124-368A-175 Sequence 175, App
15	56	11.9	211	7	US-11-124-368A-176 Sequence 176, App
16	55.5	11.8	341	7	US-11-055-822-1054 Sequence 1054, App
17	55.5	11.8	1432	6	US-10-510-386-218 Sequence 218, App
18	55	11.7	106	7	US-11-072-512-2218 Sequence 2218, App
19	55	11.7	806	7	US-11-098-686-10278 Sequence 10278, A
20	55	11.7	1102	7	US-11-098-686-10951 Sequence 10951, A
21	54.5	11.5	310	7	US-11-198-746-88 Sequence 88, Appl1
22	54.5	11.5	310	7	US-11-198-746-88 Sequence 88, Appl1
23	54.5	11.5	315	7	US-11-198-746-91 Sequence 91, Appl1
24	54.5	11.5	315	7	US-11-198-746-91 Sequence 91, Appl1
25	54.5	11.5	320	6	US-10-467-657-3254 Sequence 3254, App

26	54.5	11.5	322	7	US-11-198-746-89 Sequence 89, Appl1
27	54.5	11.5	322	7	US-11-198-746-89 Sequence 89, Appl1
28	54.5	11.5	528	7	US-11-198-746-90 Sequence 90, Appl1
29	54.5	11.5	528	7	US-11-198-746-90 Sequence 90, Appl1
30	54.5	11.5	548	7	US-11-198-746-86 Sequence 86, Appl1
31	54.5	11.5	548	7	US-11-198-746-86 Sequence 86, Appl1
32	54.5	11.5	577	7	US-11-072-175-187 Sequence 187, App
33	54.5	11.5	648	6	US-10-467-657-2802 Sequence 2802, App
34	54.5	11.5	665	7	US-11-113-837-19 Sequence 19, Appl1
35	54.5	11.5	665	7	US-11-113-837-19 Sequence 19, Appl1
36	54.5	11.5	695	7	US-11-198-746-87 Sequence 87, Appl1
37	54.5	11.5	832	7	US-11-065-943-100 Sequence 100, App
38	54.5	11.5	832	7	US-11-065-943-100 Sequence 100, App
39	54.5	11.5	832	7	US-11-007-797A-11 Sequence 11, Appl1
40	54.5	11.5	832	7	US-11-007-797A-11 Sequence 11, Appl1
41	54.5	11.5	832	7	US-11-198-746-4 Sequence 4, Appl1
42	54.5	11.5	832	7	US-11-242-730-1 Sequence 1, Appl1
43	54.5	11.5	833	7	US-11-198-746-85 Sequence 85, Appl1
44	54.5	11.5	833	7	US-11-198-746-85 Sequence 85, Appl1
45	54	11.4	312	6	US-10-986-501-124 Sequence 124, App
46	54	11.4	313	7	US-11-156-084-335 Sequence 335, App
47	54	11.4	362	6	US-10-517-939-88 Sequence 88, Appl1
48	53.5	11.3	203	6	US-10-454-437-326 Sequence 326, App
49	53.5	11.3	233	7	US-11-072-512-2088 Sequence 2088, App
50	53.5	11.3	432	6	US-10-454-437-140 Sequence 140, App
51	53.5	11.3	432	7	US-11-055-822-184 Sequence 184, App
52	53.5	11.3	453	7	US-11-072-512-3394 Sequence 3394, App
53	53.5	11.3	691	7	US-11-098-686-11189 Sequence 11189, A
54	53.5	11.3	746	7	US-11-072-175-169 Sequence 169, App
55	53.5	11.3	919	6	US-10-821-234-1144 Sequence 1144, App
56	53.5	11.3	2335	6	US-10-821-234-1610 Sequence 1610, App
57	53	11.2	289	7	US-11-093-118-37 Sequence 37, Appl1
58	53	11.2	327	7	US-11-093-118-37 Sequence 37, Appl1
59	53	11.2	876	7	US-11-242-730-5 Sequence 5, Appl1
60	53	11.2	1506	7	US-11-060-005-4 Sequence 4, Appl1
61	52.5	11.1	215	6	US-10-131-826A-488 Sequence 488, App
62	52.5	11.1	215	7	US-11-080-921-112 Sequence 112, App
63	52.5	11.1	736	6	US-10-467-657-4780 Sequence 4780, App
64	52.5	11.1	926	6	US-11-332-405A-34 Sequence 34, Appl1
65	52	11.0	226	6	US-10-927-641-72 Sequence 72, Appl1
66	52	11.0	370	6	US-10-873-528-160 Sequence 160, App
67	52	11.0	381	7	US-11-072-512-3313 Sequence 3313, App
68	52	11.0	401	6	US-10-131-826A-486 Sequence 486, App
69	52	11.0	505	6	US-10-514-878A-3 Sequence 3, Appl1
70	52	11.0	505	6	US-10-514-878A-5 Sequence 5, Appl1
71	52	11.0	505	6	US-10-514-878A-7 Sequence 7, Appl1
72	52	11.0	505	6	US-10-514-878A-13 Sequence 13, Appl1
73	52	11.0	505	7	US-11-179-478-2 Sequence 2, Appl1
74	52	11.0	593	7	US-11-194-246-317 Sequence 317, App
75	52	11.0	924	6	US-10-467-657-4290 Sequence 4290, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWInd9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 46.4%; Score 219; DB 6; Length 88;
Best Local Similarity 44.8%; Pred. No. 1,2e-18;
Matches 39; Conservative 19; Mismatches 29; Indels 0; Gaps 0;

QY 1 MTTVMCRKYOELPGLERPPYPCAKGODIFEHISQKAMADWQHQITMLINERLNMNA 60
DB 1 MAMVFCVKNKAEKMGKPPPLPHEIGKRIFFENVSGQAMAMTRHQITMLINERLSIADP 60
QY 61 EDRKFLQAEKDFPAGERYAQAEGYVP 87
DB 61 RAREYLAQMEQYFFGDDADAVOGYVP 87

RESULT 2

US-10-453-372-852
Sequence 852, Application US/10453372
Publication No. US2006003323A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 852
LENGTH: 844
TYPE: PRT
ORGANISM: Homo sapiens
US-10-453-372-852

Query Match 15.3%; Score 72; DB 6; Length 844;
Best Local Similarity 26.6%; Pred. No. 1.6;
Matches 29; Conservative 16; Mismatches 32; Indels 32; Gaps 6;
QY 4 TWVCR-----KYOEELPGLERPPY-----PGAKGODIFEHISQKA 38
DB 515 TQCCRTTHPISLKYTEDMTPTQTPRGSMESLALSNATGLSADGAKQO---EHLSRFS 571
QY 39 WADWQKHQITMLINERLNM--MNAEDRKFLQAE-MDKFPAGEERYAQAEG 84
DB 572 MPDLSKDSGMNVSEKLSNMGTINS-SMOPRSASVSRLSLAQQOYQMEG 619

RESULT 3
US-10-453-372-856

Sequence 856, Application US/10453372
Publication No. US2006003323A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 856
LENGTH: 844
TYPE: PRT
ORGANISM: Homo sapiens
US-10-453-372-856

Query Match 15.3%; Score 72; DB 6; Length 844;
Best Local Similarity 26.6%; Pred. No. 1.6;
Matches 29; Conservative 16; Mismatches 32; Indels 32; Gaps 6;

QY 4 TWVCR-----KYOEELPGLERPPY-----PGAKGODIFEHISQKA 38
DB 515 TQCCRTTHPISLKYTEDMTPTQTPRGSMESLALSNATGLSADGAKQO---EHLSRFS 571
QY 39 WADWQKHQITMLINERLNM--MNAEDRKFLQAE-MDKFPAGEERYAQAEG 84
DB 572 MPDLSKDSGMNVSEKLSNMGTINS-SMOPRSASVSRLSLAQQOYQMEG 619

RESULT 4
US-11-059-982-1
Sequence 1, Application US/11059982
Publication No. US2005025507A1
GENERAL INFORMATION:
APPLICANT: Jenkins, Robert B.
APPLICANT: Thibodeau, Steve
APPLICANT: Wang, Liang
APPLICANT: Schaid, Daniel
TITLE OF INVENTION: CYTOGENETICALLY DETERMINED DIAGNOSIS AND
TITLE OF INVENTION: PROGNOSIS OF PROLIFERATIVE DISORDERS
FILE REFERENCE: 07039-505001
CURRENT APPLICATION NUMBER: US/11/059,982
CURRENT FILING DATE: 2005-02-17
PRIOR APPLICATION NUMBER: US 60/545,573
PRIOR FILING DATE: 2004-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1560
TYPE: PRT
ORGANISM: Homo sapiens

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 / Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502a-25

Perfect score: 477
Sequence: 1 MSRTVMCRKYHEELPGLDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	87	5	ABB78170
2	477	100.0	122	7	ABO74609
3	408	85.5	90	5	ABB78168
4	400	83.9	87	5	ABB78169
5	262.5	55.0	92	6	ADA34169
6	242	50.7	87	5	ABB78176
7	241	50.5	89	9	ABE41576
8	240	50.5	95	9	ABE38294
9	240	50.3	87	5	ABB78148
10	240	50.3	87	5	ABB78147
11	236	49.5	87	5	ABB78152
12	235	49.3	87	5	ABB78177
13	235	49.3	88	5	ABB78154
14	235	49.3	110	8	ADL05173
15	233	48.8	91	5	ABB78150
16	231	48.4	91	5	ABB78158
17	231	48.4	91	5	ABB78157
18	231	48.4	91	5	ABB78156
19	230	48.2	87	5	ABB78151
20	230	48.2	93	7	ADP05158
21	228	47.8	88	5	ABB78160
22	228	47.8	91	5	ABB78161
23	228	47.8	91	5	ABB78159
24	228	47.8	91	5	ABB78162

25	227	47.6	87	5	ABB78175	Abb78175 Amino aci
26	223	46.8	90	5	ABB78155	Abb78155 Amino aci
27	223	46.8	107	7	ABO65445	ABO65445 Klebsiell
28	222.5	46.6	86	5	ABB78149	Abb78149 Amino aci
29	222	46.5	87	5	ABB78153	Abb78153 Amino aci
30	221	46.3	87	5	ABB78174	Abb78174 Amino aci
31	221	46.3	91	5	ABB78163	Abb78163 Amino aci
32	220	46.1	88	5	ABB78178	Abb78178 Amino aci
33	211	44.2	78	5	ABB78164	Abb78164 Amino aci
34	210	44.0	90	5	ABB78165	Abb78165 Amino aci
35	207	43.4	88	5	ABB78171	Abb78171 Amino aci
36	207	43.4	88	5	ABB78172	Abb78172 Amino aci
37	207	43.4	88	5	ABB78173	Abb78173 Amino aci
38	207	43.4	88	6	ABP77219	ABP77219 N. gonorr
39	182.5	38.3	90	5	ABB78167	Abb78167 Amino aci
40	175	36.7	76	5	ABB78166	Abb78166 Amino aci
41	175	36.7	68	8	ADN73327	ADN73327 Thale cre
42	173	35.7	158	3	AAE10836	AAE10836 Arabidops
43	173	35.3	487	8	ADN74065	ADN74065 Thale cre
44	173	35.3	500	5	AAE27877	AAE27877 Arabidops
45	172.5	35.2	333	4	ABB63075	ABB63075 Drosophil
46	172	35.1	314	7	AAO23396	AAO23396 Pseudom
47	172	35.1	732	8	ADX92564	ADX92564 plant ful
48	172	35.1	1043	8	ADM48031	ADM48031 Polypepti
49	15.0	15.0	506	2	AAR97281	AAR97281 Helicobac
50	71.5	15.0	2000	6	ABR52698	ABR52698 Protein s
51	71.5	15.0	2000	7	ADK61900	ADK61900 Disease t
52	70.5	14.8	401	6	ABU24966	ABU24966 Protein e
53	70	14.7	148	2	AAE60188	AAE60188 Human end
54	70	14.7	171	8	ADP64626	ADP64626 Human onc
55	70	14.7	185	8	ADP64627	ADP64627 Human onc
56	70	14.7	381	7	ADB65159	ADB65159 Human pro
57	70	14.7	400	3	AAE24352	AAE24352 Human pro
58	70	14.7	400	6	ABR47475	ABR47475 Breast ca
59	70	14.7	400	7	ADB75332	ADB75332 Prostata
60	70	14.7	400	9	ADY72549	ADY72549 Human GP7
61	70	14.7	401	3	AAE93668	AAE93668 Human sec
62	70	14.7	401	3	AAE93668	AAE93668 Human PRO
63	70	14.7	401	4	AAE66117	AAE66117 Protein o
64	70	14.7	401	4	AAU24214	AAU24214 Human PRO
65	70	14.7	401	4	ABA97770	ABA97770 Amyloid-b
66	70	14.7	401	4	ABA93295	ABA93295 Human mem
67	70	14.7	401	4	ABA88480	ABA88480 Human mem
68	70	14.7	401	5	ABP65020	ABP65020 Human pro
69	70	14.7	401	6	ABO17858	ABO17858 Novel hum
70	70	14.7	401	6	ABU81112	ABU81112 Human PRO
71	70	14.7	401	6	ABU66812	ABU66812 Human PRO
72	70	14.7	401	6	ABU59893	ABU59893 Novel sec
73	70	14.7	401	6	ABO25083	ABO25083 Human sec
74	70	14.7	401	6	ABU67088	ABU67088 Human sec
75	70	14.7	401	6	ADA46005	ADA46005 Novel hum

ALIGNMENTS

RESULT 1	ABB78170	standard; protein; 87 AA.
ID	ABB78170	
XX	ABB78170	
AC	ABB78170	
XX	05-NOV-2002	(first entry)
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a Yggx homologue.	
XX		
KW	Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;	
KM	hydroxyl radical; DNA damage; Yggx homologue.	
XX		
OS	Unidentified.	
XX		
PN	US2002072116-A1.	
XX		

PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.
 PI Downs D, Gralnck JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 87 AA;
 Query Match 100.0%; Score 477; DB 5; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.9e-52;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTVMCRKYHELPGLDRPPYPGAKGEDIYNNVSRKAWDEMOKHOTMLINERLNMMNA 60
 DB 1 MSRTVMCRKYHELPGLDRPPYPGAKGEDIYNNVSRKAWDEMOKHOTMLINERLNMMNA 60
 QY 61 EDRKFLQEMDKFLSGEDYAKADGYVP 87
 DB 61 EDRKFLQEMDKFLSGEDYAKADGYVP 87
 RESULT 2
 ABO74609
 ID ABO74609 standard; protein; 122 AA.
 XX
 AC ABO74609;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE *Pseudomonas aeruginosa* polypeptide #6784.
 XX
 KM *Pseudomonas aeruginosa* polypeptide #6784.
 XX
 OS Bacterial infection; *Pseudomonas aeruginosa* infection; antibacterial.
 XX
 PN *Pseudomonas aeruginosa*.
 XX
 US6551795-B1.
 XX
 PD 22-APR-2003.
 XX
 PF 18-FEB-1999; 99US-00252991.
 XX
 PR 18-FEB-1998; 98US-0074788P.
 XX
 PR 27-JUL-1998; 98US-0094190P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
 XX
 DR WPI; 2003-615309/58.

DR N-PSDB; ABD08180.
 XX
 XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of
 PT pathological conditions resulting from bacterial infection.
 XX
 XX Disclosure; SEQ ID NO 23355; 455pp; English.
 XX
 CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the
 CC polynucleotides encoding them. The sequences are useful in diagnosis and
 CC therapy of pathological conditions, as molecular targets for diagnostics,
 CC prophylaxis and treatment of pathological conditions resulting from a
 CC bacterial infection, for evaluating a compound, such as a polypeptide,
 CC for the ability to bind a P. *aeruginosa* nucleic acid, as components of
 CC effective antibacterial targets, as targets for antibacterial drugs,
 CC including anti-P. *aeruginosa* drugs, as templates for recombinant
 CC production of P. *aeruginosa*-derived peptides or polypeptides, as target
 CC components for diagnosis and/or treatment of P. *aeruginosa*-caused
 CC infection, and in detection of P. *aeruginosa* sequences or other sequences
 CC of *Pseudomonas* species using bioclip technology. Sequences ABO67826-
 CC ABO84396 represent P. *aeruginosa* polypeptides of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification but was obtained in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html
 XX
 SQ Sequence 122 AA;
 Query Match 100.0%; Score 477; DB 7; Length 122;
 Best Local Similarity 100.0%; Pred. No. 3e-52;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTVMCRKYHELPGLDRPPYPGAKGEDIYNNVSRKAWDEMOKHOTMLINERLNMMNA 60
 DB 33 MSRTVMCRKYHELPGLDRPPYPGAKGEDIYNNVSRKAWDEMOKHOTMLINERLNMMNA 92
 QY 61 EDRKFLQEMDKFLSGEDYAKADGYVP 87
 DB 93 EDRKFLQEMDKFLSGEDYAKADGYVP 119
 RESULT 3
 ABB78168
 ID ABB78168 standard; protein; 90 AA.
 XX
 AC ABB78168;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.
 XX
 KM Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.
 XX
 OS *Pseudomonas syringae*.
 XX
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.
 PI Downs D, Gralnck JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 seconds
(without alignments)
879,982 Million cell updates/sec

Title: US-09-955-502a-25

Perfect score: 477
Sequence: 1 MSRTWCKRYHELPGLDRP.....QEMDKFLSGEDYAKADGYP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	90	2 H83003	conserved hypothet
2	236	49.5	90	2 C64013	hypothetical prote
3	231	48.4	91	2 A85954	hypothetical prote
4	231	48.4	91	2 A65082	hypothetical prote
5	231	48.4	91	2 F91108	hypothetical prote
6	228	47.8	91	2 AH0879	conserved hypothet
7	223	46.8	90	2 C82320	conserved hypothet
8	210	44.0	90	2 A10116	conserved hypothet
9	207	43.4	88	2 H81014	conserved hypothet
10	192	40.3	105	2 C82624	conserved hypothet
11	175	36.7	93	2 E84994	conserved hypothet
12	80.5	16.9	314	2 JC5534	catechol 2,3-dioxy
13	73	15.3	500	2 B96739	hypothetical prote
14	72	15.1	435	2 D82905	hypothetical prote
15	71.5	15.0	314	2 S31402	catechol 2,3-dioxy
16	71.5	15.0	2748	2 S57976	nuclear migration
17	69	14.5	926	2 T24923	hypothetical prote
18	68.5	14.4	506	2 H64618	sigma-54 interacti
19	68	14.3	1083	1 S53048	alpha-mannosidase
20	68	14.3	1148	2 D85360	hypothetical prote
21	67	14.0	282	2 D97138	DNA replication pr
22	66.5	13.9	532	2 H72730	probable acyl-CoA
23	66	13.8	1638	2 D87749	protein unc-73b (f
24	66	13.8	2488	2 T42739	guanine nucleotide
25	65.5	13.7	314	2 JE0127	catechol 2,3-dioxy
26	65.5	13.7	342	2 T19021	probable inositol
27	65.5	13.6	2485	1 H71621	serine/threonine-s
28	65	13.6	468	2 T33857	hypothetical prote
29	64.5	13.5	523	2 S23384	protein kinase (EC

30	64.5	13.5	766	2 T48463	hypothetical prote
31	64	13.4	283	2 H86839	hypothetical prote
32	64	13.4	642	2 D96777	hypothetical prote
33	64	13.4	670	2 T29898	kinesin protein OS
34	64	13.4	1553	2 S67483	adenosinetriphosph
35	63.5	13.3	613	2 AH2398	hypothetical prote
36	63	13.2	331	2 G84646	hypothetical prote
37	63	13.2	506	2 F71895	hypothetical prote
38	63	13.2	900	2 T33734	hypothetical prote
39	63	13.2	1645	2 A37792	spectrin beta-H ch
40	62.5	13.1	316	2 T50027	annexin-like prote
41	62.5	13.1	433	2 G70345	hypothetical prote
42	62.5	13.1	637	2 S66236	acetylcholinestera
43	62.5	13.1	985	2 T10339	DNA-directed DNA p
44	62	13.0	244	2 C90580	DNA processing pro
45	62	13.0	442	2 B81418	adenylsuccinate 1
46	62	13.0	830	2 S56940	factor arrest prot
47	62	13.0	921	2 A83968	isoletucyl-tRNA syn
48	62	13.0	1290	1 DVBYS6	matrig pheromone a
49	62	13.0	4063	2 T42993	probable spectrin
50	62	13.0	4101	2 T23630	hypothetical prote
51	61.5	12.9	218	2 C70536	hypothetical prote
52	61.5	12.9	455	2 D75043	seeryl-tRNA synthet
53	61.5	12.9	509	2 T21512	hypothetical prote
54	61.5	12.9	767	2 T31558	hypothetical prote
55	61.5	12.9	1090	2 AG1749	glycosidase homolo
56	61.5	12.9	1091	2 AP1380	probable arabinosy
57	61.5	12.9	1111	2 A86922	protein P54D8.1 (f
58	61.5	12.9	1120	2 H88449	hypothetical prote
59	61	12.8	284	2 G72662	probable membrane
60	61	12.8	367	2 H81379	mannitol-1-phospha
61	61	12.8	378	2 H95045	hypothetical prote
62	61	12.8	389	2 T14751	transposase (12) B
63	61	12.8	552	2 C83965	arginine-tRNA ligase
64	61	12.8	583	2 A70380	reverse transcript
65	61	12.8	964	2 T01860	DNA-directed RNA p
66	61	12.8	1203	2 A39607	cobalamin biosynth
67	61	12.8	1232	2 D64413	K12H4.8 protein -
68	61	12.8	1822	2 S44849	hypothetical prote
69	60.5	12.7	71	2 H97137	protein SPB-11 - C
70	60.5	12.7	299	2 T29546	modification methy
71	60.5	12.7	303	2 A64423	serine-tRNA ligase
72	60.5	12.7	460	2 G71117	probable DNA polym
73	60.5	12.7	1067	2 D96545	probable reverse t
74	60.5	12.7	1142	2 E96519	hypothetical prote
75	60	12.6	150	2 F90212	

ALIGNMENTS

RESULT 1
H83003 conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: H83003
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lapid, K.; Lam,
.; Lory, S.; Olson, M.V.
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A:Reference number: A82950; MUID:20437377; PMID:10984043
A:Accession: H83003
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: UNIPARC:UPI000000CFR26; GB:AB004927; GB:AB004091; NID:99951437; PIDN:f
A:Experimental source: strain PA01
A:Genetics:
A:Gene: PA5148
C:Superfamily: fe(II) trafficking protein Y95X

Query Match 100.0%; Score 477; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.1e-42;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60
 DB 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
 DB 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87

RESULT 2
 C64013
 hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
 C/Species: Haemophilus influenzae
 C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
 C/Accession: C64013
 R./Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Puhmann, J.L.; Geoghegan, N.S.M.; Science 269, 496-512, 1995
 A./Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A./Reference number: A64000; MUID:95350630; PMID:7542800
 A./Accession: C64013
 A./Status: nucleic acid sequence not shown; translation not shown
 A./Molecule type: DNA
 A./Residues: 1-90 <RTGR>
 A./Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:915
 A./Superfamily: Fe(II) trafficking protein YggX

Query Match 49.5%; Score 236; DB 2; Length 90;
 Best Local Similarity 54.5%; Pred. No. 1.3e-17;
 Matches 48; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

QY 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60
 DB 1 MATTVCSEYIKKABGLDPOLYFGLGKRIYFDSVSKQNGEWIKKQOTMLINEKKLNNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
 DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTP 87

RESULT 3
 A85954
 hypothetical protein y99X [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
 C/Species: Escherichia coli
 C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
 C/Accession: A85954
 R./Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.; Miller, L.J.; Groblich, E.U.; Davis, N.W.; Llim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
 A./Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A./Reference number: A85480; MUID:21074935; PMID:11206551
 A./Accession: A85954
 A./Status: preliminary
 A./Molecule type: DNA
 A./Residues: 1-91 <STO>
 A./Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:G12517511; F
 A./Experimental source: strain O157:H7, substrain EDL933
 C/Genetics:
 A./Gene: y99X
 A./Superfamily: Fe(II) trafficking protein YggX

Query Match 48.4%; Score 231; DB 2; Length 91;
 Best Local Similarity 51.7%; Pred. No. 4.2e-17;
 Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60
 DB 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60

DB 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60
 QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
 DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTP 87

RESULT 4
 A65082
 hypothetical protein b2962 - Escherichia coli (strain K-12)
 C/Species: Escherichia coli
 C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
 C/Accession: A65082
 R./Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coi, A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
 A./Title: The complete genome sequence of Escherichia coli K-12.
 A./Reference number: A64720; MUID:97426617; PMID:9278503
 A./Accession: A65082
 A./Status: preliminary; nucleic acid sequence not shown; translation not shown
 A./Molecule type: DNA
 A./Residues: 1-91 <BLAT>
 A./Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:91
 A./Experimental source: strain K-12, substrain MG1655
 A./Superfamily: Fe(II) trafficking protein YggX

Query Match 48.4%; Score 231; DB 2; Length 91;
 Best Local Similarity 51.7%; Pred. No. 4.2e-17;
 Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60
 DB 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
 DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTP 87

RESULT 5
 F91108
 hypothetical protein Ecs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1A)
 C/Species: Escherichia coli
 C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
 C/Accession: F91108
 R./Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasaawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H. DNA Res. 8, 11-22, 2001
 A./Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
 A./Reference number: A99629; MUID:21156231; PMID:11258796
 A./Accession: F91108
 A./Status: preliminary
 A./Molecule type: DNA
 A./Residues: 1-91 <NAV>
 A./Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA037261.1;
 A./Experimental source: strain O157:H7, substrain R1A
 C/Genetics:
 A./Gene: Ecs3838
 A./Superfamily: Fe(II) trafficking protein YggX

Query Match 48.4%; Score 231; DB 2; Length 91;
 Best Local Similarity 51.7%; Pred. No. 4.2e-17;
 Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60
 DB 1 MSRTWCRKRYHELPGLDRPPYGAAGEDIYNNVSRKADWQKHQOTMLINERLNNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
 DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTP 87

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502a-25

Perfect score: 477
Sequence: 1.MSRTVMCKRYHEBPLGLDRP.....QEMDKFLSGEDYKADGYVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	100.0	90	1	FETP_PSEAB
2	420	88.1	90	2	Q4J228 AZOVI
3	408	85.5	90	1	FETP_PSESM
4	408	85.5	90	2	Q4ZLB3_PSESY
5	401	84.1	90	2	Q4KJT2_PSEFS
6	400	83.9	90	1	FETP_PSEPK
7	383	80.3	90	2	Q6T7F6_PSEFL
8	258.5	54.2	90	1	FETP_PSEAD
9	250	52.4	96	2	Q4FVJ7_9GAMW
10	245	51.4	90	1	FETP_IDILO
11	244	51.2	91	1	FETP_MANSW
12	241	50.5	89	1	FETP_LBQPA
13	241	50.5	89	1	FETP_LBQPA
14	240	50.3	90	1	FETP_LBQPL
15	240	50.3	90	1	FETP_LBQPL
16	240	50.3	90	1	FETP_LBQPL
17	240	50.3	90	1	FETP_LBQPL
18	236	49.5	90	2	Q4QMD9_HAIR8
19	236	49.5	90	2	Q4QMD9_HAIR8
20	235	49.3	92	1	FETP_METCA
21	235	49.3	92	1	FETP_SHEON
22	233	48.8	90	1	FETP_VIBRI
23	230	48.2	90	1	FETP_PASMU
24	230	48.2	90	1	FETP_PASMU
25	229	48.0	90	1	FETP_PASMU
26	228	47.8	90	1	FETP_PASMU
27	228	47.8	91	1	FETP_PASMU
28	227	47.6	90	1	FETP_PASMU
29	227	47.6	90	1	FETP_PASMU
30	227	47.6	90	1	FETP_PASMU
31	227	47.6	91	1	FETP_PASMU

32	227	47.6	91	1	FETP_PASMU	Q6B14 burkholderi
33	226	47.4	90	1	FETP_PASMU	Q6B14 burkholderi
34	226	47.4	90	1	FETP_PASMU	Q6B14 burkholderi
35	226	47.4	90	1	FETP_PASMU	Q6B14 burkholderi
36	224	47.0	91	2	Q4LS19_9BURK	Q6B14 burkholderi
37	223	46.8	90	1	FETP_PASMU	Q6B14 burkholderi
38	223	46.8	90	1	FETP_PASMU	Q6B14 burkholderi
39	223	46.8	90	1	FETP_PASMU	Q6B14 burkholderi
40	223	46.8	90	1	FETP_PASMU	Q6B14 burkholderi
41	223	46.8	90	1	FETP_PASMU	Q6B14 burkholderi
42	222	46.5	90	1	FETP_PASMU	Q6B14 burkholderi
43	222	46.5	90	1	FETP_PASMU	Q6B14 burkholderi
44	222	46.5	90	1	FETP_PASMU	Q6B14 burkholderi
45	220	46.1	90	1	FETP_PASMU	Q6B14 burkholderi
46	218	45.7	90	1	FETP_PASMU	Q6B14 burkholderi
47	215	45.1	78	1	FETP_PASMU	Q6B14 burkholderi
48	210	44.0	90	1	FETP_PASMU	Q6B14 burkholderi
49	210	44.0	90	1	FETP_PASMU	Q6B14 burkholderi
50	208	43.6	92	1	FETP_PASMU	Q6B14 burkholderi
51	207	43.4	88	1	FETP_PASMU	Q6B14 burkholderi
52	207	43.4	88	1	FETP_PASMU	Q6B14 burkholderi
53	207	43.4	88	1	FETP_PASMU	Q6B14 burkholderi
54	204	42.8	91	1	FETP_PASMU	Q6B14 burkholderi
55	202	42.3	87	1	FETP_PASMU	Q6B14 burkholderi
56	197	41.3	92	2	Q4UW14_XANCP	Q6B14 burkholderi
57	197	41.3	92	2	Q4UW14_XANCP	Q6B14 burkholderi
58	195	40.9	78	1	FETP_PASMU	Q6B14 burkholderi
59	193	40.5	90	1	FETP_PASMU	Q6B14 burkholderi
60	192	40.3	90	1	FETP_PASMU	Q6B14 burkholderi
61	190	39.8	79	1	FETP_PASMU	Q6B14 burkholderi
62	175	36.7	77	1	FETP_PASMU	Q6B14 burkholderi
63	174	36.5	87	1	FETP_PASMU	Q6B14 burkholderi
64	171	35.8	92	2	Q4NMQ4_9DELT	Q6B14 burkholderi
65	81.5	17.1	326	2	Q5SGT4_DICDI	Q6B14 burkholderi
66	80.5	16.9	314	2	Q7MR6_BURCH	Q6B14 burkholderi
67	79	16.6	703	2	Q4MPT2_ASPTU	Q6B14 burkholderi
68	78.5	16.5	1097	1	KIFID_RAT	Q6B14 burkholderi
69	78	16.4	410	2	Q8SRF4_ENCCU	Q6B14 burkholderi
70	76.5	16.0	314	2	Q9RBS5_9BURK	Q6B14 burkholderi
71	75.5	15.8	280	2	Q81BK9_BACRC	Q6B14 burkholderi
72	75	15.7	681	2	Q9LV16_ARATH	Q6B14 burkholderi
73	74	15.5	525	2	Q6BNV8_DEBHA	Q6B14 burkholderi
74	73.5	15.4	307	2	Q6BFB3_PARTE	Q6B14 burkholderi
75	73.5	15.4	549	2	Q6BKE2_DEBHA	Q6B14 burkholderi

ALIGNMENTS

RESULT 1
FETP_PSEAB
ID FETP_PSEAB STANDARD; PRT; 90 AA.
AC Q9HJ36;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SRP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocName=PA5148;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino B., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sater M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PA01, an

RT opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AB004927; AAC08533.1; -; Genomic_DNA.
 DR PDB; 1T07; X-ray; A=1-90.
 DR SMR; O9HU36; 1-79.
 DR HAMAP; MF_006866; -; 1.
 DR InterPro; IPR007457; Yg9X.
 DR Pfam; PF04362; DUF495; 1.
 DR PIRSF; PIRSF029827; Fe traffic_Yg9X; 1.
 DR Prodom; PD029191; DUF495; 1.
 DR 3D-structure; Complete proteome; Iron.
 KM SEQUENCE 90 AA; 10625 MW; 02BB6CEBF7AEF39 CRC64;
 SQ
 Query Match 100.0%; Score 477; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 6.6e-42;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTVMCRKRYHEELPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHQTMLINERRLNMNNA 60
 DB 1 MSRTVMCRKRYHEELPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHQTMLINERRLNMNNA 60
 QY 61 EDRKFLQEMDKFLSGEDYAKADGYV 87
 DB 61 EDRKFLQEMDKFLSGEDYAKADGYV 87
 Db
 RESULT 2
 Q4J228_AZOVI PRELIMINARY; PRT; 90 AA.
 AC Q4J228;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AvindRAFT_6916;
 OS Acetobacter vinelandii AVOP.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Acetobacter.
 OX NCBI_TaxID=322710;
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP.
 RG US DOE Joint Genome Institute (JGI-RGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.,
 RT "Sequencing of the draft genome assembly of Acetobacter vinelandii
 RT AVOP.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.,
 RT "Annotation of the draft genome assembly of Acetobacter vinelandii
 RT AVOP.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute;
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN
 RT

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AVOP;
 RG US DOE Joint Genome Institute (JGI-RGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.,
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAU0300001; EAM08363.1; -; Genomic_DNA.
 DR Hypothetical protein
 KM SEQUENCE 90 AA; 10777 MW; F6F766143D3B5B1 CRC64;
 SQ
 Query Match 88.1%; Score 420; DB 2; Length 90;
 Best Local Similarity 88.4%; Pred. No. 5.7e-36;
 Matches 76; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MSRTVMCRKRYHEELPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHQTMLINERRLNMNNA 60
 DB 1 MSRTVMCRKRYHEELPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHQTMLINERRLNMNNA 60
 QY 61 EDRKFLQEMDKFLSGEDYAKADGYV 86
 DB 61 EDRKFLQEMDKFLSGEDYAKADGYV 86
 Db
 RESULT 3
 PEPF_PFSM STANDARD; PRT; 90 AA.
 AC 087UF5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 GN OrderedListNames=PSPT05343;
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=DC3000;
 RX MEDLINE=2834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
 RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
 RA Medugu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Knout H.M., Fedorova N.B., Tran B., Russell D., Berry K.U.,
 RA Utechtack T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
 RA Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,
 RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
 RA Bender C.L., White O., Fraser C.M., Collier A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 RT Pseudomonas syringae pv. tomato DC3000."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
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 CC removed.
 CC -----
 DR EMBL; AB016853; AA058769.1; -; Genomic_DNA.
 DR SMR; O87UF5; 1-79.
 DR TIGR; PSP05343; -
 DR HAMAP; MF_006866; -; 1.
 DR InterPro; IPR007457; Yg9X.
 DR Pfam; PF04362; DUF495; 1.
 DR PIRSF; PIRSF029827; Fe traffic_Yg9X; 1.

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-25

Perfect score: 477
Sequence: 1 MSRTVMCRKHYRELPGLDRP.....QEMDKFLSGHDYAKAGSYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	122	US-09-252-991A-23355	Sequence 23355, A
2	262.5	55.0	92	US-09-328-352-5456	Sequence 5456, Ap
3	235	49.3	110	US-09-540-236-2859	Sequence 2859, Ap
4	230	48.2	93	US-09-543-681A-5443	Sequence 5443, Ap
5	223	46.8	107	US-09-489-039A-11962	Sequence 11962, A
6	72	15.1	314	US-09-716-865-4	Sequence 4, Appl1
7	71.5	15.0	506	US-08-849-480A-5	Sequence 5, Appl1
8	70	14.7	148	US-09-673-395A-389	Sequence 389, Appl
9	70	14.7	381	US-10-104-047-3313	Sequence 3313, Ap
10	70	14.7	401	US-09-489-847-202	Sequence 202, App
11	70	14.7	401	US-10-012-31A-100	Sequence 100, App
12	70	14.7	401	US-10-015-389A-100	Sequence 100, App
13	70	14.7	401	US-10-006-768A-100	Sequence 100, App
14	70	14.7	401	US-10-015-671A-100	Sequence 100, App
15	70	14.7	401	US-10-015-393A-100	Sequence 100, App
16	70	14.7	401	US-10-011-833A-100	Sequence 100, App
17	70	14.7	401	US-10-006-041A-100	Sequence 100, App
18	70	14.7	401	US-10-012-064A-100	Sequence 100, App
19	70	14.7	401	US-10-010-269A-8	Sequence 8, Appl
20	70	14.7	422	US-09-489-847-357	Sequence 357, Appl
21	68	14.3	443	US-09-248-796A-16816	Sequence 16816, A
22	67.5	14.2	505	US-09-543-681A-7151	Sequence 7151, Ap
23	67	14.0	563	US-09-902-540-14552	Sequence 14552, A
24	66	13.8	361	US-09-134-001C-3862	Sequence 3862, Ap
25	65.5	13.7	375	US-09-583-110-4950	Sequence 4950, Ap
26	65.5	13.7	382	US-09-107-433-3837	Sequence 3837, Ap
27	65	13.6	163	US-09-270-767-33714	Sequence 33714, A

28	65	13.6	420	US-09-248-796A-15323	Sequence 15323, A
29	65	13.6	1042	US-09-792-024-106	Sequence 106, App
30	64.5	13.5	327	US-09-902-540-10864	Sequence 10864, A
31	64.5	13.5	343	US-09-270-767-41701	Sequence 41701, A
32	64.5	13.5	839	US-09-758-282B-232	Sequence 232, App
33	64.5	13.5	839	US-09-577-304A-232	Sequence 232, App
34	64	13.4	1103	US-09-162-373-1	Sequence 1, Appl1
35	64	13.4	1103	US-09-467-946-1	Sequence 1, Appl1
36	64	13.4	1123	US-09-949-016-9935	Sequence 9935, Ap
37	63.5	13.3	403	US-09-543-681A-6083	Sequence 6083, Ap
38	63.5	13.3	1967	US-09-849-602-16	Sequence 16, Appl
39	63	13.2	254	US-09-586-106D-111	Sequence 111, App
40	63	13.2	254	US-10-799-870-111	Sequence 111, App
41	62.5	13.1	3542	US-10-087-013-2	Sequence 2, Appl1
42	62	13.0	595	US-09-902-540-16334	Sequence 16334, A
43	61	12.8	193	US-09-252-991A-17828	Sequence 17828, A
44	61	12.8	378	US-09-583-110-3941	Sequence 3941, Ap
45	61	12.8	378	US-09-107-433-5197	Sequence 5197, Ap
46	61	12.8	381	US-09-949-016-9788	Sequence 9788, Ap
47	61	12.8	381	US-09-964-899-13	Sequence 13, Appl
48	60.5	12.7	302	US-09-902-540-13084	Sequence 13084, A
49	60.5	12.7	315	US-10-164-595-12	Sequence 12, Appl
50	60	12.6	243	US-09-248-796A-20306	Sequence 20306, A
51	60	12.6	286	US-09-248-796A-20057	Sequence 20057, A
52	60	12.6	331	US-08-961-083-212	Sequence 212, App
53	60	12.6	331	US-09-536-784-212	Sequence 212, App
54	60	12.6	331	US-09-765-372A-212	Sequence 212, App
55	60	12.6	331	US-09-765-372A-212	Sequence 212, App
56	60	12.6	338	US-09-328-352-7427	Sequence 7427, Ap
57	60	12.6	341	US-09-252-991A-32797	Sequence 32797, A
58	60	12.6	344	US-08-961-083-192	Sequence 192, App
59	60	12.6	344	US-09-536-784-192	Sequence 192, App
60	60	12.6	344	US-09-765-371-192	Sequence 192, App
61	60	12.6	344	US-09-765-371-192	Sequence 192, App
62	60	12.6	370	US-09-583-110-5251	Sequence 5251, Ap
63	60	12.6	370	US-09-583-110-5251	Sequence 5251, Ap
64	60	12.6	370	US-09-769-787-160	Sequence 160, App
65	60	12.6	375	US-09-107-433-4121	Sequence 4121, Ap
66	60	12.6	454	US-09-771-161A-95	Sequence 95, Appl
67	60	12.6	504	US-09-538-092-1170	Sequence 1170, Ap
68	60	12.6	505	US-09-949-016-6117	Sequence 6117, Ap
69	60	12.6	505	US-09-771-161A-186	Sequence 186, App
70	60	12.6	513	US-09-949-016-11517	Sequence 11517, A
71	60	12.6	531	US-09-540-236-2072	Sequence 2072, Ap
72	59.5	12.5	1122	US-10-146-704-2	Sequence 2, Appl1
73	59.5	12.5	488	US-08-911-824-95	Sequence 95, Appl
74	59.5	12.5	491	US-08-912-129A-56	Sequence 56, Appl
75	59.5	12.5	491	US-08-911-824-56	Sequence 56, Appl
			599	US-08-911-824-108	Sequence 108, App

ALIGNMENTS

RESULT 1
US-09-252-991A-23355
Sequence 23355, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23355
LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23355

Query Match 100.0%; Score 477; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.6e-55;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNA 60
DB 33 MSRTVMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNA 92

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
DB 93 EDRKFLQOEMDKFLSGEDYAKADGYVP 119

RESULT 2

US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT

US-09-328-352-5456
; ORGANISM: Acinetobacter baumannii

Query Match 55.0%; Score 262.5; DB 2; Length 92;
Best Local Similarity 52.3%; Pred. No. 5.9e-27;
Matches 46; Conservative 19; Mismatches 22; Indels 1; Gaps 1;

QY 1 MSRTVMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNA 60
DB 4 MSRTVMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNA 63

QY 61 EDRKFLQOEMDKFLSG-EDYAKADGYVP 87
DB 64 EDRKFLQOEMDKFLSG-EDYAKADGYVP 91

RESULT 3

US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT

US-09-540-236-2859
; ORGANISM: M. catarrhalis

Query Match 49.3%; Score 235; DB 2; Length 110;
Best Local Similarity 48.2%; Pred. No. 3.3e-23;
Matches 40; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 5 VMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNAADRK 64
DB 25 VMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNAADRK 84

QY 65 FLOEMDKFLSGEDYAKADGYVP 87

DB 85 YLNEQREKFLDNGDYKPAKGYKP 107

RESULT 4
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT

US-09-543-681A-5443
; ORGANISM: Proteus mirabilis

Query Match 48.2%; Score 230; DB 2; Length 93;
Best Local Similarity 51.1%; Pred. No. 1.2e-22;
Matches 45; Conservative 14; Mismatches 27; Indels 2; Gaps 2;

QY 1 MSRTVMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNA 60
DB 4 MSRTVMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNA 63

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
DB 64 EDRKFLQOEMDKFLSGEDYAKADGYVP 90

RESULT 5

US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT

US-09-489-039A-11962
; ORGANISM: Klebsiella pneumoniae

Query Match 46.8%; Score 223; DB 2; Length 107;
Best Local Similarity 51.1%; Pred. No. 1.2e-21;
Matches 45; Conservative 13; Mismatches 28; Indels 2; Gaps 2;

QY 1 MSRTVMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNA 60
DB 17 MSRTVMCRKYHEBLPGIDRPPYPGAKGEDIYNNVSRKAMDEWQKHOTMLINERLNNMNA 76

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
DB 77 EDRKFLQOEMDKFLSGEDYAKADGYVP 103

RESULT 6
US-09-716-865-4
; Sequence 4, Application US/09716865

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
DB 77 EDRKFLQOEMDKFLSGEDYAKADGYVP 103

US-09-716-865-4
; Sequence 4, Application US/09716865

US-09-955-502-25

Query Match	100.0%;	Score 477;	DB 3;	length 87;
Best Local Similarity	100.0%;	Pred. No. 8.1e-49;		
Matches	87;	Conservative	0;	Mismatches 0;
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			Gaps	0;

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Db 1 MSRTWCRKHYEELPGIDRPPYGAKEGDIYNNVSRKAMDEWQKQTMLINERLLNNNA 600

QY 61 EDRKFLQEQEMDKFLSGEDYAKADGYVP 87
Db 61 EDRKFLQEQEMDKFLSGEDYAKADGYVP 87

RESULT 2

US-09-955-502-23
Sequence 23, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT APPLICATION DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ. ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ. ID NO 23
LENGTH: 90
TYPE: PRT
ORGANISM: *Pseudomonas syringae*
US-09-955-502-23

Query Match	85.5%	Score 408;	DB 3;	Length 90;
Best Local Similarity	83.9%	Pred. No. 1.4e-40;		
Matches 73;	Conservative 10;	Mismatches 4;	Indels 0;	Gaps 0;

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Db 1 MTRTWVCRKYHEELPGIERAPYPAKGEDIFNNHSQKAMADWQKQTMILINERLLNMNA 600

QY 61 EDRKFLQGEIMDKFLSGEDYAKADGYVP 87
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Db 61 EDRKFLQTEIMDKFLSGEYEAQAEGYVP 87

RESULT 3

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US-09-955-502-24
; Sequence 24, Application US/09355502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 87
; TYPE: FRT
; ORGANISM: Pseudomonas putida
US-09-955-502-24

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Query Match 83.9%; Score 400; DB 3; Length 87;

Best Local Similarity 79.3%; Pred. No. 1.2e-39;
Matches 63; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

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Oy      1 MSRTWCRKTHEELPGILDRPPYPGAAGEDIYNNVSRKAWDEWOXQYTLINERLNMNA    60
        :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 MTRTWCRCRKGQELPGLERPPYPGAKODIFEHISQKAMADWQHQTMLINEKRNLNMNA    60
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Qy 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
||| : : : : :
Db 61 EDRKFLQOEMDKFLPAGEBYAQAEGYVP 87

RESULT 4

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US-09-955-502-31
Sequence 31, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCES: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 87
TYPE: PRT
ORGANISM: Thiobacillus ferrooxidans
US-09-955-502-31

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Query Match 50.7%; Score 242; DB 3; Length 87;
Best Local Similarity 51.7%; Pred. No. 8e-21;
Matches 45; Conservative 13; Mismatches 29; Indels 0; Gaps 0;

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Db      1 MSRHWQCVKLGHAEGLDRPPYPGALGARITYGVSKEMQGWLKHQTMLINEYRLSPDP    600
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QY      61 EDRKFLQQEMDKFLSGEDYAKADGYVP 87  
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DB      61 KSRFTLEKQMEAYFFPGDAQSPREGYVP 87
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RESULT

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US-09-955-502-2
; Sequence 2, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OR INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OR INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIORITY FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIORITY FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-955-502-2

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Query Match 50.3%; Score 240; DB 3; Length 87;
Best Local Similarity 50.6%; Pred. No. 1.4e-20;
Matches 44; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Title: US-09-955-502A-25

Perfect score: 477

Sequence: 1 MSRTWCRKRYHEHLPGLDRP.....QEMDKFLSGEDYAKADGYVP 87

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	70	14.7	381	US-11-072-512-3313	Sequence 3313, App
3	70	14.7	401	US-10-131-826A-486	Sequence 486, App
4	65	13.6	353	US-11-098-686-10774	Sequence 10774, A
5	64.5	13.5	1560	US-11-059-982-1	Sequence 1, Appl1
6	60	12.6	370	US-10-873-528-160	Sequence 160, App
7	58.5	12.3	310	US-11-198-746-88	Sequence 88, Appl
8	58.5	12.3	310	US-11-198-794-88	Sequence 88, Appl
9	58.5	12.3	315	US-11-198-746-91	Sequence 91, Appl
10	58.5	12.3	315	US-11-198-794-91	Sequence 91, Appl
11	58.5	12.3	322	US-11-198-746-89	Sequence 89, Appl
12	58.5	12.3	322	US-11-198-794-89	Sequence 89, Appl
13	58.5	12.3	528	US-11-198-746-90	Sequence 90, Appl
14	58.5	12.3	548	US-11-198-794-90	Sequence 90, Appl
15	58.5	12.3	548	US-11-198-746-86	Sequence 86, Appl
16	58.5	12.3	548	US-11-198-794-86	Sequence 86, Appl
17	58.5	12.3	695	US-11-198-746-87	Sequence 87, Appl
18	58.5	12.3	695	US-11-198-794-87	Sequence 87, Appl
19	58.5	12.3	832	US-11-065-943-100	Sequence 100, App
20	58.5	12.3	832	US-11-007-797A-11	Sequence 11, Appl
21	58.5	12.3	832	US-11-007-642B-11	Sequence 11, Appl
22	58.5	12.3	832	US-11-198-746-4	Sequence 4, Appl1
23	58.5	12.3	832	US-11-198-794-4	Sequence 4, Appl1
24	58.5	12.3	832	US-11-242-730-1	Sequence 1, Appl1
25	58.5	12.3	833	US-11-198-746-85	Sequence 85, Appl

26	58.5	12.3	833	7	US-11-198-794-85	Sequence 85, Appl
27	58	12.2	589	7	US-11-072-512-2914	Sequence 2914, App
28	58	12.2	1206	6	US-10-467-657-72	Sequence 72, Appl
29	58	12.2	1206	6	US-10-467-657-3892	Sequence 3892, App
30	57.5	12.1	383	6	US-10-793-626-2426	Sequence 2426, App
31	57.5	12.1	1077	6	US-11-054-281-110	Sequence 110, App
32	57	11.9	426	6	US-10-858-730-81	Sequence 81, Appl
33	57	11.9	456	7	US-11-069-642-8	Sequence 8, Appl1
34	57	11.9	600	7	US-11-072-512-3845	Sequence 3845, App
35	57	11.9	645	6	US-10-510-386-32	Sequence 32, Appl
36	57	11.9	3748	8	US-11-132-686-8	Sequence 8, Appl1
37	57	11.9	3749	7	US-11-132-686-6	Sequence 6, Appl1
38	57	11.9	3749	7	US-11-132-686-12	Sequence 12, Appl
39	57	11.9	3912	7	US-11-132-686-7	Sequence 7, Appl1
40	57	11.9	3913	7	US-11-132-686-5	Sequence 5, Appl1
41	57	11.9	3913	7	US-11-132-686-9	Sequence 9, Appl1
42	56.5	11.8	2871	7	US-11-124-367A-264	Sequence 264, App
43	56	11.7	315	6	US-10-878-556A-178	Sequence 178, App
44	56	11.7	333	6	US-10-821-234-1036	Sequence 1036, App
45	56	11.7	647	7	US-11-000-463-1222	Sequence 722, App
46	56	11.7	1897	6	US-10-821-234-1635	Sequence 1635, App
47	56	11.7	1907	7	US-11-000-463-250	Sequence 250, App
48	55.5	11.6	357	7	US-11-053-100-33	Sequence 33, Appl
49	55.5	11.6	400	7	US-11-202-566-27	Sequence 27, Appl
50	55.5	11.6	526	7	US-11-055-822-124	Sequence 124, Appl
51	55.5	11.6	657	7	US-11-053-100-35	Sequence 35, Appl
52	55	11.5	211	7	US-11-124-368A-175	Sequence 175, App
53	55	11.5	211	7	US-11-124-368A-176	Sequence 176, App
54	55	11.5	395	6	US-10-793-626-656	Sequence 656, App
55	55	11.5	701	6	US-10-467-657-7872	Sequence 7872, App
56	55	11.5	805	6	US-10-485-517-198	Sequence 198, App
57	55	11.5	1386	7	US-11-091-643-6	Sequence 6, Appl1
58	54.5	11.4	339	6	US-10-841-956A-3	Sequence 3, Appl1
59	54.5	11.4	39	7	US-11-029-003-3	Sequence 3, Appl1
60	54.5	11.4	40	7	US-11-112-277-34	Sequence 34, Appl
61	54.5	11.4	203	6	US-10-454-437-326	Sequence 326, App
62	54.5	11.4	415	6	US-10-763-712A-25	Sequence 25, Appl
63	54.5	11.4	436	6	US-10-763-712A-5	Sequence 5, Appl1
64	54.5	11.4	746	7	US-11-072-175-169	Sequence 169, App
65	54	11.3	426	6	US-10-858-730-80	Sequence 80, Appl
66	54	11.3	3433	6	US-10-714-781A-67	Sequence 67, Appl
67	53.5	11.2	612	6	US-10-467-657-3988	Sequence 3988, App
68	53.5	11.2	1717	7	US-11-182-016-20	Sequence 20, Appl
69	53	11.1	120	6	US-10-793-626-958	Sequence 958, App
70	53	11.1	120	6	US-10-793-626-1444	Sequence 1444, App
71	53	11.1	383	7	US-11-072-512-3140	Sequence 3140, App
72	53	11.1	532	6	US-10-793-626-546	Sequence 546, App
73	53	11.1	618	7	US-11-110-082-25	Sequence 25, Appl
74	53	11.1	744	7	US-11-186-284-37	Sequence 37, Appl
75	53	11.1	744	7	US-11-186-284-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PIZZANI Maria Rita
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 43.4%; Score 207; DB 6; Length 88;
Best Local Similarity 42.5%; Pred. No. 1.4e-16;
Matches 37; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

Qy 1 MSRTYMKRYHELPGLRPPYPAKSGEDYNNVSRKAWDEMOKHQTMLINERLNNMNA 60
Db 1 MARWVFCVKNLKEAGMCPPLPNELGRIFENVSQEMAAWTRHQTMLINERLNLSDP 60

Qy 61 EDRKPLQOEMDKFLSGEDYAKADGYVP 87
Db 61 RARETLAQOEMEYFFPGDADAVQGYVP 87

RESULT 2
US-11-072-512-3313

Sequence 3313, Application US/11072512
Publication No. US20060029945A1

GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISOMO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, KYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3313
LENGTH: 381
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3313

Query Match 14.7%; Score 70; DB 7; Length 381;
Best Local Similarity 35.9%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 14; Conservative 8; Mismatches 17;

Qy 26 KGEDYNNVSRKAWDEMOKHQTMLINERLNNMNAEDRK 64
Db 326 RGEDYNNMDENEAESFTDKQALAGNDNRNDIVFNVEDQK 364

RESULT 3
US-10-131-826A-486

Sequence 486, Application US/10131826A
Publication No. US20050245730A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeNovoys, Inc
APPLICANT: Pilyaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 486
LENGTH: 401
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-486

Query Match 14.7%; Score 70; DB 6; Length 401;
Best Local Similarity 35.9%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 14; Conservative 8; Mismatches 17;

Qy 26 KGEDYNNVSRKAWDEMOKHQTMLINERLNNMNAEDRK 64
Db 346 RGEDYNNMDENEAESFTDKQALAGNDNRNDIVFNVEDQK 384

RESULT 4
US-11-098-686-10774

Sequence 10774, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
FROM LAMSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 19:03:38 ; Search time 72.164 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502a-26

Perfect score: 467

Sequence: 1 MAWVFCVKNLKEAEGKFP.....QMEQYFGDADAVGVTPQ 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database:

A_Geneseq_21.*
1: geneseqp1980a.*
2: geneseqp1990a.*
3: geneseqp2000a.*
4: geneseqp2001a.*
5: geneseqp2002a.*
6: geneseqp2003a.*
7: geneseqp2003b.*
8: geneseqp2004a.*
9: geneseqp2005a.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	5	ABB78171
2	467	100.0	88	5	ABB78172
3	467	100.0	88	5	ABB78173
4	467	100.0	88	6	ABP77219
5	339	72.6	87	5	ABB78175
6	333	71.3	87	5	ABB78174
7	294	63.0	87	5	ABB78176
8	290	62.1	87	5	ABB78148
9	272.5	58.4	87	5	ABB78147
10	271	58.0	89	9	ABB78149
11	271	58.0	95	9	ABB781576
12	258	55.2	88	5	ABB78178
13	243	52.0	87	5	ABB78177
14	240	51.4	90	5	ABB78155
15	235	50.3	87	5	ABB78153
16	230	49.3	88	5	ABB78154
17	228	48.8	91	5	ABB78150
18	227	48.6	87	5	ABB78152
19	227	48.6	107	7	ABO65445
20	225	48.3	92	7	ADP34169
21	221	47.3	93	7	ADP05158
22	219	46.9	87	5	ABB78169
23	217	46.5	87	5	ABB78151

25	213	45.6	91	5	ABB78158	Abb78158 Amino aci
26	213	45.6	91	5	ABB78157	Abb78157 Amino aci
27	213	45.6	91	5	ABB78156	Abb78156 Amino aci
28	211	45.2	88	5	ABB78160	Abb78160 Amino aci
29	211	45.2	91	5	ABB78161	Abb78161 Amino aci
30	211	45.2	91	5	ABB78159	Abb78159 Amino aci
31	211	45.2	91	5	ABB78162	Abb78162 Amino aci
32	210	45.0	87	5	ABB78164	Abb78164 Amino aci
33	207	44.3	87	5	ABB78170	Abb78170 Amino aci
34	207	44.3	122	7	ABO74609	Abb74609 Pseudomon
35	202	43.3	91	5	ABB78163	Abb78163 Amino aci
36	198	42.4	90	5	ABB78165	Abb78165 Amino aci
37	198	42.4	90	5	ABB78168	Abb78168 Amino aci
38	193.5	41.4	90	5	ABB78167	Abb78167 Amino aci
39	182	39.0	110	8	ADL05173	Adl05173 M. catarr
40	158	33.8	76	5	ABB78166	Abb78166 Amino aci
41	74	15.8	1122	6	ABU22044	Abu22044 Protein e
42	70	15.0	202	7	ABM90380	Abm90380 Rice abio
43	70	15.0	1079	8	ADN19463	Adn19463 Bacterial
44	69	14.8	774	4	ABG29304	Abg29304 Novel hum
45	68.5	14.7	361	7	ABO76259	AbO76259 Pseudomon
46	68	14.6	189	9	ADM18357	Adm18357 Pimus rad.
47	67.5	14.5	466	7	ABO84015	AbO84015 Pseudomon
48	66.5	14.2	401	6	ABU19221	Abu19221 Protein e
49	66	14.1	418	7	ABO66638	AdG4671 E. faeciu
50	65.5	14.0	1443	7	ADJ68530	Adj68530 Human hea
51	65.5	14.0	1935	7	ADJ70260	Adj70260 Human hea
52	65.5	14.0	3830	5	ABB81168	Abb81168 TRRAP pro
53	65.5	14.0	3830	8	ADJ78499	Adj78499 PAF/TRRAP
54	65.5	14.0	3830	8	ADQ19749	Adq19749 Human sof
55	65.5	14.0	3830	8	ADQ89826	Adq89826 Antagonis
56	65.5	14.0	3830	8	ADJ68548	Adj68548 Human hea
57	65.5	14.0	3859	7	ADJ68548	Adj68548 Human hea
58	65.5	14.0	3859	7	ADJ68548	Adj68548 Human pro
59	65	13.9	255	7	ADM27073	Adm27073 Hyperther
60	65	13.9	296	4	AUJ35611	AuJ35611 Haemophil
61	65	13.9	296	6	AUJ35611	AuJ35611 Protein e
62	65	13.9	438	2	AAV11015	AaV11015 H. pylori
63	65	13.9	442	2	AAW20830	AaW20830 H. pylori
64	65	13.9	465	2	AAW20303	AaW20303 H. pylori
65	64.5	13.8	207	6	ABM73508	Abm73508 Scaphyloc
66	64.5	13.8	207	9	ADV16859	Adv16859 Staphyloc
67	64.5	13.8	207	9	ADW94758	Adw94758 Prolifera
68	64.5	13.8	362	7	ADF89476	Adf89476 Human ery
69	64.5	13.8	362	8	ADK48858	Adk48858 Human tra
70	64.5	13.8	362	8	ADP12457	Adp12457 Protein e
71	64	13.7	260	4	AAW38702	AaW38702 Human pol
72	64	13.7	378	4	AAW40488	AaW40488 Human tes
73	64	13.7	656	8	ABU53239	Abu53239 Human tes
74	64	13.7	656	8	ADJ28417	Adj28417 Human nuc
75	64	13.7	2426	2	ADH11285	Adh11285 Vertebrat

ALIGNMENTS

RESULT 1
ABB78171
ID ABB78171 standard; protein; 88 AA.
XX
XX ABB78171;
AC
XX 29-AUG-2003 (revised)
DT 05-NOV-2002 (first entry)
DT
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
XX Neisseria gonorrhoeae.
XX
PN US2002072118-A1.

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XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
PR (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PA Downs D, Gralnicks JA;
XX WPI; 2002-589476/63.
DR Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
PS Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues. (Updated on 25-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 88 AA;
Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARWVCVLTNKEAEKMKPPPLPNEIGKRIFFENVSOEAMAAWTRHOTMLINENRSLADP 60
DB 1 MARWVCVLTNKEAEKMKPPPLPNEIGKRIFFENVSOEAMAAWTRHOTMLINENRSLADP 60
QY 61 RAREVLAQOMEQYFFGDGADAVQGYVPQ 88
DB 61 RAREVLAQOMEQYFFGDGADAVQGYVPQ 88
RESULT 2
AB878172
ID ABB78172 standard; protein; 88 AA.
XX
AC ABB78172;
XX
DE 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar Typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
XX Neisseria meningitidis.
OS
XX US2002072118-A1.
PN 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
PR (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PA Downs D, Gralnicks J A.
XX
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PI Downs D, Gralnicks JA;
XX WPI; 2002-589476/63.
DR Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
PS Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 88 AA;
Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARWVCVLTNKEAEKMKPPPLPNEIGKRIFFENVSOEAMAAWTRHOTMLINENRSLADP 60
DB 1 MARWVCVLTNKEAEKMKPPPLPNEIGKRIFFENVSOEAMAAWTRHOTMLINENRSLADP 60
QY 61 RAREVLAQOMEQYFFGDGADAVQGYVPQ 88
DB 61 RAREVLAQOMEQYFFGDGADAVQGYVPQ 88
RESULT 3
AB878173
ID ABB78173 standard; protein; 88 AA.
XX
AC ABB78173;
XX
DE 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar Typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
XX Neisseria meningitidis.
OS
XX US2002072118-A1.
PN 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
PR (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PA Downs D, Gralnicks JA;
XX WPI; 2002-589476/63.
DR Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
PS Example; Fig 1A; 16pp; English.
XX The specification describes a method for reducing superoxide damage to a
```


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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.62187 Seconds
(without alignments)
879,982 Million cell updates/sec

Title: US-09-955-502a-26

Perfect score: 467
Sequence: 1 MAMWFCVKLNKEAEGKFP.....QMEQYFGDADAVGVPPQ 88

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	2 H81014	conserved hypochet
2	240	51.4	90	2 C68230	conserved hypochet
3	227	48.6	90	2 C64013	hypochetrical prote
4	213	45.6	91	2 A85954	hypochetrical prote
5	213	45.6	91	2 A65082	hypochetrical prote
6	213	45.6	91	2 F91108	hypochetrical prote
7	211	45.2	91	2 AH0879	conserved hypochet
8	207	44.3	90	2 H83003	conserved hypochet
9	201	43.0	105	2 C82624	conserved hypochet
10	198	42.4	90	2 A10116	conserved hypochet
11	158	33.8	93	2 E84594	hypochetrical prote
12	72	15.4	1041	2 A81960	probable DNA helic
13	70	15.0	1079	2 T38913	translation initia
14	68.5	14.7	338	2 A83389	probable permease
15	68.5	14.7	349	2 A11457	ABC transporter ol
16	68	14.6	195	2 S74714	hypochetrical prote
17	67.5	14.5	899	2 A83019	conserved hypochet
18	66.5	14.2	401	2 C70159	translation elonga
19	66	14.1	598	1 RGECKX	nitrate/nitrite elon
20	66	14.1	598	1 F85702	nitrate/nitrite se
21	66	14.1	598	2 G90844	nitrate/nitrite se
22	65	13.9	296	2 A64110	cell division inh
23	65	13.9	465	2 C71870	hypochetrical prote
24	65	13.9	590	2 E85057	probable transposo
25	64.5	13.8	362	2 T45072	conserved hypochet
26	64.5	13.8	362	2 T45072	erythroid Kruppel-
27	64.5	13.8	400	2 A39254	inositol-1,4-bisph
28	64.5	13.8	1553	2 S67483	adenosinetriphosph
29	64	13.7	676	2 A45984	sperm-binding glyco

30	64	13.7	677	2 S33664	flagella-associate
31	63.5	13.6	288	2 H95018	transcription regu
32	63.5	13.6	301	2 H82446	transcription regu
33	63	13.5	282	2 D97138	DNA replication pr
34	63	13.5	388	1 JC5461	cellulase (EC 3.2.
35	63	13.5	388	1 S43920	cellulase (EC 3.2.
36	62	13.3	120	2 G97833	hypochetrical prote
37	62	13.3	200	2 B82203	transcription regu
38	62	13.3	259	2 S55033	transcription init
39	62	13.3	570	2 D83177	probable phosphot
40	62	13.3	2314	2 T38698	hypochetrical prote
41	61.5	13.2	211	2 T38645	hypochetrical prote
42	61.5	13.2	288	2 B95122	transcription regu
43	61.5	13.2	374	2 A96502	probable acyl-acyl
44	61.5	13.2	412	2 G81581	tyrosyl-tRNA synth
45	61.5	13.2	422	2 G86535	tyrosyl-tRNA synth
46	61.5	13.2	432	2 D72088	tyrosine-tRNA liga
47	61.5	13.2	589	2 AE3530	flagellar biosynth
48	61	13.1	455	2 T50184	mammalian swi/bnf
49	61	13.1	553	2 P97028	arginyl-tRNA synth
50	61	13.1	969	2 T33156	hypochetrical prote
51	61	13.1	1639	2 T50119	probable sensory t
52	60.5	13.0	186	1 WMR219	19k globulin precu
53	60.5	13.0	186	2 UC4784	alpha-globulin pre
54	60.5	13.0	261	2 S14875	dnak-type molecula
55	60.5	13.0	357	2 F82892	heat-inducible tra
56	60.5	13.0	448	2 T45145	glutamate-ammonia
57	60.5	13.0	1888	2 T39009	hypochetrical prote
58	60	12.8	292	2 A10422	conserved hypochet
59	60	12.8	306	2 A97249	Zn-binding lipopro
60	60	12.8	309	2 D95843	probable transcrip
61	60	12.8	323	2 D35734	probable antiopept
62	60	12.8	335	2 D83142	hypochetrical prote
63	60	12.8	397	2 A75503	hypochetrical prote
64	60	12.8	410	2 T39115	formidase-like p
65	60	12.8	508	2 T02486	hypochetrical prote
66	60	12.8	615	2 E81451	1-deoxyxylulose-5-
67	60	12.8	67	2 E75206	alpha-amylose (or
68	60	12.8	859	2 T29630	hypochetrical prote
69	60	12.8	1006	2 A59384	oxycotinase/innu
70	60	12.8	1021	2 AC2202	hypochetrical prote
71	60	12.8	1025	2 A59383	oxycotinase/innu
72	60	12.8	3788	2 T30851	lysosomal traffick
73	59.5	12.7	157	1 HHPM17	heat shock protein
74	59.5	12.7	237	2 A55218	atp homolog gap -
75	59.5	12.7	295	2 T35330	probable RNA polym

ALIGNMENTS

RESULT 1
H81014
conserved hypochetrical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58 :
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014, F81958
R/Retelin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: AB10000, M01D:2015755, PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TEXT>
A/Cross-references: UNIPARC:UPI000000C487P; GB:AB002553; GB:AB002098; NID:97222729; P1DN:/;
A/Experimental source: Serogroup B, strain MC58
R/Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churche, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.9476 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502a-26

Perfect score: 467
Sequence: 1 MAMVFCVKLNKEAGMKFP.....QMEQYFGDADAVGGVPPQ 88

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	1	FETP_NEIG1
2	467	100.0	88	1	FETP_NEIMA
3	467	100.0	88	1	FETP_NEIMB
4	354	75.8	91	1	FETP_RALSO
5	348	74.5	91	2	Q4LS19_9BURK
6	339	72.6	91	1	FETP_BURMA
7	339	72.6	91	1	FETP_BURPS
8	335	71.7	90	1	FETP_CHRVO
9	319	68.3	90	1	FETP_NITRU
10	290	62.1	90	1	FETP_NITRU
11	290	62.1	90	1	FETP_BORBP
12	290	62.1	90	1	FETP_BORBP
13	275	58.9	89	1	FETP_LBGPL
14	271	58.0	89	1	FETP_LBGPL
15	271	58.0	89	1	FETP_LBGPL
16	258	55.2	90	1	FETP_LBGPL
17	254	54.4	90	1	FETP_COXBU
18	252	54.0	92	2	Q4NM04_9DELT
19	243	52.0	90	1	FETP_METCA
20	242	51.8	90	1	FETP_METCA
21	240	51.4	90	1	FETP_VIBCH
22	239	51.2	90	1	FETP_VIBCH
23	239	51.2	90	1	FETP_VIBCH
24	239	51.2	90	1	FETP_VIBCH
25	235	50.3	91	1	FETP_XANAC
26	235	50.3	91	1	FETP_XANAC
27	233	49.9	92	1	FETP_XANOR
28	230	49.3	92	1	FETP_XANOR
29	227	48.6	90	1	FETP_XANOR
30	227	48.6	90	2	Q4QMD9_HAE18
31	225	48.2	92	1	FETP_XANCP

32	225	48.2	92	2	Q4UW14_XANCP
33	224	48.0	91	1	FETP_MANSM
34	220.5	47.2	90	1	FETP_ACIAD
35	220	47.1	90	1	FETP_PHOPR
36	219	46.9	90	1	FETP_PSRPK
37	217	46.5	90	1	FETP_PASMU
38	217	46.5	90	1	FETP_PASMU
39	211	45.2	90	2	Q6T7F6_PSEBL
40	209	44.8	90	1	FETP_XYLFT
41	208	44.5	87	1	FETP_PATRT
42	208	44.5	90	1	FETP_ECO57
43	208	44.5	90	1	FETP_ECOLI
44	208	44.5	90	1	FETP_ERWCT
45	208	44.5	90	1	FETP_SHIFL
46	207	44.3	90	1	FETP_PSRAP
47	207	44.3	90	2	Q4KJ22_PSEFS
48	206	44.1	90	1	FETP_SALCH
49	206	44.1	90	1	FETP_SALCH
50	206	44.1	90	1	FETP_SALTI
51	206	44.1	90	1	FETP_SALTY
52	206	44.1	90	1	FETP_YERPS
53	206	44.1	96	2	Q4PV07_9GAMM
54	204	43.7	90	1	FETP_ECOL6
55	201	43.0	90	1	FETP_XYLFA
56	198	42.4	90	1	FETP_PSRSM
57	198	42.4	90	1	FETP_YERPE
58	198	42.4	90	2	Q4ZLB3_PSESY
59	196	42.0	90	2	Q4J228_AZOV1
60	186	39.8	79	1	FETP_CANBF
61	186	39.8	78	1	FETP_BUCAP
62	167	35.8	78	1	FETP_WIGBR
63	158	33.8	77	1	FETP_BUCAT
64	127	27.2	87	1	FETP_BUCBP
65	75	16.1	359	2	Q7VKN4_HAEPU
66	74	15.8	453	2	Q4PBL1_USTVA
67	74	15.8	1598	2	Q6ZCB0_BURMA
68	74	15.8	1599	2	Q63KS1_BURPS
69	73	15.6	820	2	Q52IA7_MAGGR
70	72.5	15.5	301	2	Q6LNI9_PHOPR
71	72	15.4	203	2	Q56W66_BRARE
72	72	15.4	1041	2	Q9UWD5_NEIMA
73	71	15.2	346	2	Q8ER42_SHEON
74	70.5	15.1	320	2	Q6PKY5_XENILA
75	70	15.0	1079	1	IF2P_SCHPO

ALIGNMENTS

RESULT 1	FETP_NEIG1	STANDARD;	PRT;	88 AA.
ID	FETP_NEIG1			
AC	Q5F533			
DT	13-SEP-2005 (Rel. 48, Created)			
DT	13-SEP-2005 (Rel. 48, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	OrderedLocustNames=NGO2083;			
OS	Neisseria gonorrhoeae (strain ATCC 700825 / PA 1090).			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=242231;			
RN	[1]			
RP	NOCLROTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RA	Lewis L.A., Gillaspy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,			
RA	Omney T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,			
RA	Song L., Lin S., Yuan X., Najaf F., Zhan M., Ren Q., Zhu H., Qi S.,			
RA	Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;			
RT	"The complete genome sequence of Neisseria gonorrhoeae."			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Could be a mediator in iron transactions between iron			
CC	acquisition and iron-regulating processes, such as synthesis and/or			
CC	repair of Fe-S clusters in biosynthetic enzymes (By similarity).			

```

CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB004969; AAM90684.1; -; Genomic_DNA.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; DUF495; 1.
CC PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
CC Prodom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC Sequence 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVKLNKEAGMKFPPLPNEIGKRIFFENVSGEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVKLNKEAGMKFPPLPNEIGKRIFFENVSGEAMAAWTRHQTMLINENRLSLADP 60
QY 61 RAREVLAQOMEQYFFGDGADAVQGYVPQ 88
DB 61 RAREVLAQOMEQYFFGDGADAVQGYVPQ 88

RESULT 2
PFTP_NEIIMB STANDARD; PRT; 88 AA.
ID PFTP_NEIIMB
AC P67615; Q9J0P5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=NMB0419;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=65699;

[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Baaham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jørgensen K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skellern J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RT Nature 404:502-506(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL162753; CAB83718.1; -; Genomic_DNA.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; DUF495; 1.
CC PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
CC Prodom; PD029191; DUF495; 1.

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KW Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVKLNKEAGMKFPPLPNEIGKRIFFENVSGEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVKLNKEAGMKFPPLPNEIGKRIFFENVSGEAMAAWTRHQTMLINENRLSLADP 60
QY 61 RAREVLAQOMEQYFFGDGADAVQGYVPQ 88
DB 61 RAREVLAQOMEQYFFGDGADAVQGYVPQ 88

RESULT 3
PFTP_NEIIMB STANDARD; PRT; 88 AA.
ID PFTP_NEIIMB
AC P67616; Q9J0P5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=NMB2021;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=491;

[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., Deboy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Clecko A., Parksey D.S., Blair E.,
RA Clifton H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.V., Gill J., Scarlato V., Maignant V., Pizzia M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappunli R.,
RA Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RT Science 287:1809-1815(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB002098; AAF42344.1; -; Genomic_DNA.
CC TIGR; NME2021; -; 1.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; DUF495; 1.
CC Prodom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC Sequence 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVKLNKEAGMKFPPLPNEIGKRIFFENVSGEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVKLNKEAGMKFPPLPNEIGKRIFFENVSGEAMAAWTRHQTMLINENRLSLADP 60

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: February 28, 2006, 20:20:31 ; Search time 17.8405 Seconds
(Without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-26
Perfect score: 467
Sequence: 1 MARWFCVLTNKEAEKMPK.....QNEQYFGDGAADVGVYQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/iaa/5/COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6/COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/H/COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCMTUS/COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	227	48.6	107	2	US-09-489-039A-11962	Sequence 11962, A
2	225.5	48.3	92	2	US-09-328-352-5456	Sequence 5456, Ap
3	221	47.3	93	2	US-09-543-681A-5443	Sequence 5443, Ap
4	207	44.3	122	2	US-09-252-991A-23355	Sequence 23355, A
5	182	39.0	110	2	US-09-540-236-2859	Sequence 2859, Ap
6	68.5	14.7	361	2	US-09-252-991A-25005	Sequence 25005, A
7	67.5	14.5	466	2	US-09-252-991A-32761	Sequence 32761, A
8	66	14.1	418	2	US-09-489-039A-13155	Sequence 13155, A
9	65.5	14.0	649	2	US-09-107-532A-4298	Sequence 4298, Ap
10	64.5	13.8	3838	2	US-09-949-016-10853	Sequence 10853, A
11	64.5	13.8	361	2	US-08-874-569B-21	Sequence 21, Appl
12	64.5	13.8	361	2	US-09-955-518-21	Sequence 21, Appl
13	63	13.5	351	2	US-09-248-796A-19129	Sequence 19129, A
14	63	13.5	461	1	US-08-672-571A-3	Sequence 3, Appl
15	63	13.5	490	1	US-08-672-571A-1	Sequence 1, Appl
16	62.5	13.4	263	2	US-09-252-991A-22230	Sequence 22230, A
17	62	13.3	360	2	US-09-543-681A-7067	Sequence 7067, Ap
18	62	13.3	671	2	US-09-252-991A-18020	Sequence 18020, A
19	61.5	13.2	422	2	US-09-198-452A-377	Sequence 377, App
20	61.5	13.2	423	2	US-09-438-185A-363	Sequence 363, App
21	60.5	13.0	478	2	US-09-489-039A-7300	Sequence 7300, Ap
22	60.5	13.0	596	2	US-09-902-540-10121	Sequence 10121, A
23	60	12.8	621	2	US-09-489-039A-10378	Sequence 10378, A
24	60	12.8	2186	1	US-08-822-445-2	Sequence 2, Appl
25	60	12.8	2186	2	US-09-396-540-2	Sequence 2, Appl
26	59.5	12.7	315	2	US-09-461-325-297	Sequence 297, App
27	59.5	12.7	315	2	US-10-012-542-297	Sequence 297, App

28	59.5	12.7	315	2	US-10-115-123-297	Sequence 297, App
29	59.5	12.7	346	2	US-09-808-701A-32	Sequence 32, Appl
30	59.5	12.7	420	2	US-09-302-540-16463	Sequence 16463, A
31	59.5	12.7	431	2	US-09-461-325-146	Sequence 146, App
32	59.5	12.7	431	2	US-10-012-542-146	Sequence 146, App
33	59.5	12.7	431	2	US-09-311-021-178	Sequence 178, App
34	59.5	12.7	431	2	US-10-115-123-146	Sequence 146, App
35	59.5	12.7	848	2	US-09-538-092-33	Sequence 33, Appl
36	59.5	12.7	977	2	US-08-335-844A-22	Sequence 22, Appl
37	59.5	12.7	977	2	US-09-129-366-22	Sequence 22, Appl
38	59	12.6	366	2	US-09-252-991A-31958	Sequence 31958, A
39	59	12.6	563	2	US-09-583-110-4195	Sequence 4195, Ap
40	59	12.6	577	2	US-09-107-433-3424	Sequence 3424, Ap
41	59	12.6	5069	2	US-10-042-665A-5	Sequence 5, Appl
42	58.5	12.5	213	2	US-09-959-873B-16	Sequence 16, Appl
43	58.5	12.5	213	2	US-09-949-016-5955	Sequence 5955, Ap
44	58.5	12.5	284	1	US-08-061-889-2	Sequence 2, Appl
45	58.5	12.5	284	1	US-08-462-611-2	Sequence 2, Appl
46	58.5	12.5	284	2	US-08-623-428D-2	Sequence 2, Appl
47	58.5	12.5	284	2	US-09-949-016-11673	Sequence 11673, A
48	58.5	12.5	284	4	PCT-US94-05378-2	Sequence 2, Appl
49	58.5	12.5	340	2	US-09-270-767-42358	Sequence 42358, A
50	58.5	12.5	396	2	US-09-800-729-207	Sequence 207, App
51	58.5	12.5	397	2	US-09-079-030-123	Sequence 123, App
52	58.5	12.5	401	2	US-09-252-991A-17272	Sequence 17272, A
53	58	12.4	303	2	US-09-543-681A-7924	Sequence 7924, Ap
54	58	12.4	318	2	US-09-489-039A-8369	Sequence 8369, Ap
55	58	12.4	331	2	US-08-849-751-4	Sequence 4, Appl
56	58	12.4	331	2	US-09-478-816-4	Sequence 4, Appl
57	58	12.4	486	2	US-08-906-743-4	Sequence 4, Appl
58	58	12.4	531	2	US-09-489-039A-12406	Sequence 12406, A
59	58	12.4	563	2	US-08-906-743-2	Sequence 2, Appl
60	58	12.4	720	2	US-09-604-605-2	Sequence 2, Appl
61	58	12.4	720	2	US-10-101-080-2	Sequence 2, Appl
62	58	12.4	1178	2	US-09-489-039A-9944	Sequence 9944, Ap
63	57.5	12.3	163	2	US-09-198-452A-103	Sequence 103, App
64	57.5	12.3	180	2	US-09-640-211A-834	Sequence 834, App
65	57.5	12.3	200	2	US-09-710-279-1186	Sequence 1186, Ap
66	57.5	12.3	200	2	US-09-710-279-2390	Sequence 2390, Ap
67	57.5	12.3	208	2	US-09-134-001C-3785	Sequence 3785, Ap
68	57.5	12.3	210	2	US-09-438-185A-86	Sequence 86, Appl
69	57.5	12.3	282	2	US-09-543-681A-4715	Sequence 4715, Ap
70	57.5	12.3	451	2	US-09-543-681A-7401	Sequence 7401, Ap
71	57.5	12.3	879	2	US-09-107-433-4058	Sequence 4058, Ap
72	57.5	12.3	890	2	US-09-583-110-4739	Sequence 4739, Ap
73	57	12.2	157	2	US-09-802-540-15203	Sequence 15203, A
74	57	12.2	384	2	US-10-094-944-19	Sequence 19, Appl
75	57	12.2	412	2	US-09-538-092-709	Sequence 709, App

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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 Best Local Similarity 48.9%; Pred. No. 5.7e-24;
 Matches 43; Conservative 16; Mismatches 27; Indels 2; Gaps 2;

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 DB 17 MSRTICTFLORBADQDFQLYPGEIGKRIYNEISKEAMWQMOHKQTMLINEKSLMNDP 76
 QY 61 RAREYLAQOMEQYFFGDGADA-VQGYVP 87
 DB 77 EHRKLEQEWQFLF-EGKDVHIEGYTP 103

RESULT 2

US-09-328-352-5456
 ; Sequence 5456, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 5456
 ; LENGTH: 92
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 ; US-09-328-352-5456

Query Match 48.3%; Score 225.5; DB 2; Length 92;
 Best Local Similarity 44.9%; Pred. No. 7.5e-24;
 Matches 40; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

QY 1 MARWFCVTKLKEAGMKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRSLADP 60
 DB 4 MSRQVFCRKXQKEMEGIDFAPFGAKQEFFENVSKQAWQEWLQHTTLINEKRLNVEFP 63
 QY 61 RAREYLAQOMEQYFFGD-GADAVQGYVP 88
 DB 64 EAKKFLQEKREKFNDESVKAEKGRPE 92

RESULT 3

US-09-543-681A-5443
 ; Sequence 5443, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 5443
 ; LENGTH: 93
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 ; US-09-543-681A-5443

Query Match 47.3%; Score 221; DB 2; Length 93;
 Best Local Similarity 48.9%; Pred. No. 3.3e-23;
 Matches 43; Conservative 15; Mismatches 28; Indels 2; Gaps 2;

QY 1 MARWFCVTKLKEAGMKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRSLADP 60
 DB 4 MSRTICTFLORBADQDFQLYPGEIGKRIYNEISKEAMWQMOHKQTMLINEKSLMNDP 63
 QY 61 RAREYLAQOMEQYFFGDGADA-VQGYVP 87

DB 64 DRRKLEQEWQFLF-EGHDVHIDGYTP 90

RESULT 4

US-09-252-991A-23355
 ; Sequence 23355, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 23355
 ; LENGTH: 122
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-23355

Query Match 44.3%; Score 207; DB 2; Length 122;
 Best Local Similarity 42.5%; Pred. No. 4.5e-21;
 Matches 37; Conservative 19; Mismatches 31; Indels 0; Gaps 0;

QY 1 MARWFCVTKLKEAGMKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRSLADP 60
 DB 33 MSRTWCRXHYBELPGLDRPYPAKAGEDIVNNVERKAWDEWQKHQTMLINEKRLNMNNA 92
 QY 61 RAREYLAQOMEQYFFGDGADAVQGYVP 87
 DB 93 EDRKFLQEMDKFLSGEDYAKADGYVP 119

RESULT 5

US-09-540-236-2859
 ; Sequence 2859, Application US/09540236
 ; Patent No. 6673910
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2005-001
 ; CURRENT APPLICATION NUMBER: US/09/540,236
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 3840
 ; SEQ ID NO 2859
 ; LENGTH: 110
 ; TYPE: PRT
 ; ORGANISM: Moraxella catarrhalis
 ; US-09-540-236-2859

Query Match 39.0%; Score 182; DB 2; Length 110;
 Best Local Similarity 41.7%; Pred. No. 1.3e-17;
 Matches 35; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

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 DB 24 MWFCKRYQONLPTLPPFPFNKAGQIQTITAKAMNALLQTMLINEKSLMIDPOAK 83
 QY 64 EYLAQOMEQYFFGDGADAVQGYVP 87
 DB 84 KYLINEQREKFLDNGDYKPDAGYVP 107

RESULT 6

US-09-252-991A-25005
 ; Sequence 25005, Application US/09252991A

GenCore version 5.1.7
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OM protein - protein search, using BW model

Run on: March 1, 2006, 00:24:18 ; Search time 55.5262 Seconds
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662.192 Million cell updates/sec

Title: US-09-955-502a-26

Perfect score: 467

Sequence: 1 MARWFCVTLNKEAEKMPK.....QMEQYFEGDAVAGGVQ 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	467	100.0	88	3	US-09-955-502-27
3	467	100.0	88	3	US-09-955-502-28
4	339	72.6	87	3	US-09-955-502-29
5	339	72.6	87	3	US-09-955-502-30
6	294	63.0	87	3	US-09-955-502-31
7	290	62.1	87	3	US-09-955-502-32
8	272.5	58.4	86	3	US-09-955-502-33
9	272.5	58.4	86	3	US-09-955-502-34
10	258	55.2	88	3	US-09-955-502-35
11	243	52.0	87	3	US-09-955-502-36
12	240	51.4	87	3	US-09-955-502-37
13	235	50.3	87	3	US-09-955-502-38
14	230	49.3	88	3	US-09-955-502-39
15	228	48.8	87	3	US-09-955-502-40
16	227	48.6	87	3	US-09-955-502-41
17	219	46.9	87	3	US-09-955-502-42
18	217	46.5	87	3	US-09-955-502-43
19	213	45.6	91	3	US-09-955-502-44
20	213	45.6	91	3	US-09-955-502-45
21	213	45.6	91	3	US-09-955-502-46
22	211	45.2	88	3	US-09-955-502-47
23	211	45.2	91	3	US-09-955-502-48
24	211	45.2	91	3	US-09-955-502-49
25	211	45.2	91	3	US-09-955-502-50
26	210	45.0	78	3	US-09-955-502-51
27	207	44.3	87	3	US-09-955-502-52

28	202	43.3	91	3	US-09-955-502-18	Sequence 18, Appl
29	201	43.0	89	3	US-09-955-502-22	Sequence 22, Appl
30	198	42.4	90	3	US-09-955-502-20	Sequence 20, Appl
31	198	42.4	90	3	US-09-955-502-23	Sequence 23, Appl
32	158	33.8	76	3	US-09-955-502-21	Sequence 21, Appl
33	158	33.8	76	3	US-09-955-502-21	Sequence 21, Appl
34	70	15.0	1079	4	US-10-282-122A-49968	Sequence 49968, A
35	69	14.8	774	5	US-10-369-493-2116	Sequence 2116, Ap
36	67.5	14.5	205	4	US-10-450-763-59663	Sequence 59663, A
37	66.5	14.2	401	4	US-10-424-599-191747	Sequence 191747, A
38	66.5	14.2	1055	4	US-10-282-122A-47145	Sequence 47145, A
39	65.5	14.0	228	4	US-10-437-963-131308	Sequence 131308, A
40	65.5	14.0	246	4	US-10-425-115-191304	Sequence 191304, A
41	65.5	14.0	246	4	US-10-767-701-42494	Sequence 42494, A
42	65.5	14.0	246	4	US-10-425-115-191308	Sequence 191308, A
43	65.5	14.0	866	4	US-10-087-887-73	Sequence 66, Appl
44	65.5	14.0	1443	4	US-10-087-887-73	Sequence 73, Appl
45	65.5	14.0	1935	4	US-10-408-765A-336	Sequence 336, Appl
46	65.5	14.0	3830	5	US-10-408-765A-2066	Sequence 2066, Ap
47	65.5	14.0	3830	5	US-10-723-860-2568	Sequence 2568, Ap
48	65.5	14.0	3859	4	US-10-745-237-256	Sequence 256, Ap
49	65	13.9	296	3	US-09-815-242-11204	Sequence 354, App
50	65	13.9	296	4	US-10-335-977-8913	Sequence 11204, A
51	65	13.9	432	4	US-10-282-122A-58445	Sequence 58445, A
52	65	13.9	432	4	US-10-335-977-8910	Sequence 8910, Ap
53	65	13.9	442	4	US-10-335-977-9043	Sequence 9043, Ap
54	65	13.9	465	4	US-10-335-977-8912	Sequence 8912, Ap
55	65	13.9	465	4	US-10-335-977-8913	Sequence 8913, Ap
56	64.5	13.8	207	5	US-10-857-625-698	Sequence 698, App
57	64.5	13.8	361	3	US-09-955-518-21	Sequence 21, Appl
58	64.5	13.8	361	4	US-10-289-152-21	Sequence 21, Appl
59	64.5	13.8	1501	5	US-10-732-923-22706	Sequence 22706, A
60	64.5	13.8	1553	5	US-10-732-923-22705	Sequence 22705, A
61	64.5	13.8	1555	5	US-10-732-923-22584	Sequence 22584, A
62	63.5	13.6	94	4	US-10-425-115-281438	Sequence 281438, A
63	63.5	13.6	288	5	US-10-472-928-132	Sequence 132, App
64	63	13.5	417	4	US-10-156-761-8759	Sequence 8759, App
65	62.5	13.4	126	4	US-10-437-963-172448	Sequence 172448, A
66	62	13.3	360	4	US-10-282-122A-68811	Sequence 68811, A
67	62	13.3	519	4	US-10-369-493-4727	Sequence 4727, Ap
68	62	13.3	532	4	US-10-369-493-7486	Sequence 7486, Ap
69	62	13.3	570	3	US-09-815-242-11951	Sequence 11951, A
70	62	13.3	570	4	US-10-282-122A-66545	Sequence 66545, A
71	62	13.3	835	4	US-10-273-680-7	Sequence 7, Appl
72	62	13.3	835	4	US-10-087-887-67	Sequence 67, Appl
73	62	13.3	835	4	US-10-087-887-74	Sequence 74, Appl
74	62	13.3	835	5	US-10-889-340-7	Sequence 7, Appl
75	62	13.3	1025	4	US-10-424-599-149485	Sequence 149485, A

ALIGNMENTS

RESULT 1
US-09-955-502-26
Sequence 26, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downy, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

US-09-955-502-26

Query Match	100.0%;	Score 467;	DB 3;	Length 88;
Best Local Similarity	100.0%;	Pred. No. 2.6e-50;		
Matches 88;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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DB 1 MARWVFCVKLNKEAEGMKFPPLPLENELGKRI FENVSQEAAMAAWTRQTMLINENRSLADP 600

QY 61 RAREYLAQQMEQYFFGDGADAVQGYVPQ 88
DB 61 RAREYLAQQMEQYFFGDGADAVQGYVPQ 88

RESULT 2
US-09-955-502-27
Sequence 27, Application US/09955502

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; GENERAL INFORMATION:
;
; APPLICANT: Downs, Diana M.
; APPLICANT: Grainick, Jeff A.
;
; NAME OF APPLICANT: Downs, Diana M.

```

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; TITLE OF INVENTION: Oxygen-Labile Protein  
; FILE REFERENCE: 960296.97559  
; CURRENT APPLICATION NUMBER: US/09/955,502  
; PRIORITY DATE: 2004-08-10
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; PRIOR APPLICATION NUMBER: 60/234,588
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 33
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; SEQ ID NO 27
; LENGTH: 88
; TYPE: PRT
;
ORIGIN      1

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US-09-955-502-27

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Qy 61 RAREYLAQOMEQYFFGGGADAVQGVPO 88

Db 61 RAREYLAQQMEQYFFGDGADAVQSYVQ 88

; Sequence 28, Application US/09955502
 ; Patent No. US20020072118A1
 ; GENERAL INFORMATION:
 ; ADDITIONAL DOCUMENTS:

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; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; PTE REFERENCE: 960296 97559

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;
; CURRENT APPLICATION NUMBER: US/09/955,502
;
; CURRENT FILING DATE: 2001-09-18
;
; PRIOR APPLICATION NUMBER: 60/234,588
;
; PRIOR FILING DATE: 2000-09-22

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; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 88

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;      TYPE: PRT
;      ORGANISM: Neisseria meningitidis
US-09-955-502-28

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Query match

100.0%; Score 467; DB 3; Length 88;

Best Local Similarity 100.0%; Pred. No. 2.6e-50;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARNVFCVLTNKEAGMKFPPLPNELGKRI FENVSGEAWAATRHQTM LINENRSLADP 600

QY 61 RAREYLAQQMEQYFFGGDADAVQGYVQ 88
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RESULT 4
US-09-955-502-29
; Sequence 29, Application US/09955502

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; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.

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; TITLE OF INVENTION: Oxygen-Labile Protein
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
;

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; PRIOR APPLICATION NUMBER: 60/234,588
 ;
 ; PRIOR FILING DATE: 2000-09-22
 ;
 ; NUMBER OF SEQ ID NOS: 33
 ;

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; SEQ ID NO 29
;
; LENGTH: 87
; TYPE: PRT
ORIGIN: 1

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US-09-955-502-25

Query Match	72.6%	Score 339;	DB 3;	Length 87;
Best Local Similarity	67.8%	Pred. No. 2.6e-34;		
Matches 59;	Conservative 14;	Mismatches 14;	Indels 0;	Gaps 0;

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DB      1 MARMTHCAKCKEAEGLDFFPLPGELGKRLYESISKQMWDWLKQOTMNLINENRLINAVDP    60C
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QY      61 RAREYLAAQOMBQYFFEGDADAVQGYVP 87
      |||:::|:||||:||||
DB      61 RARQYLMKQTEKYFFEGADQASGYVP 87
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RESULT 5
US-09-955-502-30
; Sequence 30, Application US/09955502

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; GENERAL INFORMATION:
;
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.

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; TITLE OF INVENTION: Oxygen-Labile Protein
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502

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; PRIOR APPLICATION NUMBER: 60/234,588
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 33

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: SEQ ID NO 30  
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: TYPE: PRT
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ORGANISM: B
US-09-955-502-30

Query Match	72.6%;	Score 339;	DB 3;	Length 87;
Best Local Similarity	67.8%;	Pred. No. 2.6e-34;		
Matches	59;	Conservative 14;	Mismatches 14;	Indels 0;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Run on: March 1, 2006, 00:25:12 ; Search time 4.81093 Seconds
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Title: US-09-955-502a-26

Perfect score: 467
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 75 summaries

Database :

Published Applications_AA_New:*

- 1: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
- 5: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
- 6: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	100.0	88	US-10-467-657-968	Sequence 968, App
2	60	12.8	1092	US-10-821-234-999	Sequence 999, App
3	58	12.4	380	US-10-525-674-28	Sequence 28, App1
4	58	12.4	614	US-11-165-576-2	Sequence 2, App1
5	58	12.4	614	US-11-165-576-4	Sequence 4, App1
6	57.5	12.3	200	US-10-793-626-1186	Sequence 1186, App
7	57.5	12.3	200	US-10-793-626-2390	Sequence 2390, App
8	57.5	12.3	204	US-11-098-686-10498	Sequence 10498, App
9	57.5	12.3	655	US-11-098-686-10464	Sequence 10464, App
10	57	12.2	384	US-11-219-282-19	Sequence 19, App1
11	57	12.2	620	US-10-131-826A-324	Sequence 324, App
12	56.5	12.1	575	US-11-098-686-10635	Sequence 10635, App
13	56.5	12.1	688	US-11-165-226-124	Sequence 124, App
14	56	12.0	1124	US-11-090-617-688	Sequence 688, App
15	56	12.0	1375	US-10-995-561-809	Sequence 809, App
16	56	12.0	1376	US-11-100-640-32	Sequence 32, App1
17	55.5	11.9	403	US-11-009-658-14	Sequence 14, App1
18	55.5	11.9	408	US-10-821-234-1100	Sequence 1100, App
19	55.5	11.9	449	US-11-098-686-10535	Sequence 10535, App
20	55	11.8	258	US-11-090-439-38	Sequence 38, App
21	55	11.8	261	US-10-467-657-400	Sequence 400, App
22	55	11.8	611	US-10-454-437-54	Sequence 54, App1
23	55	11.8	633	US-11-193-561-13	Sequence 13, App1
24	55	11.8	633	US-11-193-771-13	Sequence 13, App1
25	55	11.8	633	US-11-193-789-13	Sequence 13, App1

26	55	11.8	633	7	US-11-193-806-13	Sequence 13, App1
27	55	11.8	633	7	US-11-193-857-13	Sequence 13, App1
28	55	11.8	925	6	US-10-454-437-50	Sequence 50, App1
29	55	11.8	967	7	US-11-202-268-6	Sequence 6, App1
30	55	11.8	1011	7	US-11-202-268-2	Sequence 2, App1
31	54.5	11.7	719	7	US-11-087-227-14	Sequence 14, App1
32	54	11.6	307	6	US-10-793-626-522	Sequence 522, App
33	54	11.6	685	7	US-11-098-686-10574	Sequence 10574, App
34	54	11.6	738	7	US-11-140-625-11	Sequence 11, App1
35	53.5	11.5	291	6	US-10-883-512-103	Sequence 103, App
36	53.5	11.5	310	7	US-11-055-163-7	Sequence 7, App1
37	53.5	11.5	344	7	US-11-055-163-6	Sequence 6, App1
38	53.5	11.5	432	6	US-10-933-115-8	Sequence 8, App1
39	53.5	11.5	432	7	US-11-056-354-4	Sequence 4, App1
40	53.5	11.5	440	6	US-10-933-115-2	Sequence 2, App1
41	53.5	11.5	473	6	US-10-131-826A-382	Sequence 382, App
42	53	11.3	288	6	US-10-467-657-3426	Sequence 3426, App
43	53	11.3	291	7	US-11-120-308-24	Sequence 24, App1
44	53	11.3	710	7	US-11-124-367A-354	Sequence 354, App
45	53	11.3	710	7	US-11-124-367A-359	Sequence 359, App
46	53	11.3	713	7	US-11-124-367A-355	Sequence 355, App
47	53	11.3	713	7	US-11-124-367A-356	Sequence 356, App
48	53	11.3	713	7	US-11-124-367A-358	Sequence 358, App
49	53	11.3	734	6	US-10-821-234-1056	Sequence 1056, App
50	53	11.3	3507	7	US-11-075-185-7	Sequence 7, App1
51	52.5	11.2	197	6	US-10-986-501-296	Sequence 296, App
52	52.5	11.2	229	6	US-10-793-626-2818	Sequence 2818, App
53	52.5	11.2	335	7	US-11-072-175-245	Sequence 245, App
54	52.5	11.2	754	7	US-11-140-625-10	Sequence 10, App1
55	52.5	11.2	1476	6	US-10-647-956A-4	Sequence 4, App1
56	52.5	11.2	4128	6	US-10-770-726-77	Sequence 77, App1
57	52	11.1	223	7	US-11-018-868-140	Sequence 140, App
58	52	11.1	381	7	US-11-024-959-418	Sequence 418, App
59	52	11.1	390	7	US-11-019-711-65	Sequence 65, App1
60	52	11.1	390	7	US-11-219-282-12	Sequence 12, App1
61	52	11.1	1022	7	US-11-156-084-118	Sequence 118, App
62	51.5	11.0	396	5	US-09-995-493-94	Sequence 94, App
63	51.5	11.0	403	7	US-11-202-731-2	Sequence 2, App1
64	51.5	11.0	408	7	US-11-074-176-354	Sequence 354, App
65	51.5	11.0	408	7	US-11-074-176-186	Sequence 186, App
66	51.5	11.0	447	7	US-11-024-959-286	Sequence 286, App
67	51.5	11.0	479	6	US-10-821-234-871	Sequence 871, App
68	51.5	11.0	1034	7	US-10-613-744-12	Sequence 12, App1
69	51.5	11.0	1159	6	US-10-613-744-12	Sequence 12, App1
70	51.5	11.0	1159	6	US-10-957-116-9	Sequence 9, App1
71	51	10.9	326	7	US-11-098-686-10173	Sequence 10173, App
72	51	10.9	387	7	US-11-219-282-20	Sequence 20, App1
73	50.5	10.8	124	7	US-11-069-642-10	Sequence 10, App1
74	50.5	10.8	347	6	US-10-853-807A-45	Sequence 45, App1
75	50.5	10.8	352	6	US-10-878-556A-40	Sequence 40, App1

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: MONACT Elisabetta
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 100.0%; Score 467; DB 6; Length 88;
Best Local Similarity 100.0%; Pred. No. 1,7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMVFCVKLNKAEKPPPLNNEIGKRIFFENVSOEAMAAWTRHQTMLINENRSLADP 60
DB 1 MAMVFCVKLNKAEKPPPLNNEIGKRIFFENVSOEAMAAWTRHQTMLINENRSLADP 60

QY 61 RAREYLAQOMEQYFFGADAVOGYVPO 88
DB 61 RAREYLAQOMEQYFFGADAVOGYVPO 88

RESULT 2

US-10-821-234-999
Sequence 999, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes version 1.0
SEQ ID NO 999
LENGTH: 1092
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-999

Query Match 12.8%; Score 60; DB 6; Length 1092;
Best Local Similarity 30.6%; Pred. No. 28;
Matches 15; Conservative 12; Mismatches 20; Indels 2; Gaps 2;

QY 31 FENVSOEAMAAWTRHQTMLINENRSLADP-AREYLAQOMEQYFFGD 77
DB 492 FEAGAMENMGILTFREETLLYDSNTSSMADRKIIVTKIIAHIAHWQFNG 540

RESULT 3
US-10-525-674-28
Sequence 28, Application US/10525674
Publication No. US2006003425A1
GENERAL INFORMATION:
APPLICANT: Kroger, Burkhard
APPLICANT: Zelder, Oskar
APPLICANT: Kolprogge, Corinna
APPLICANT: Schröder, Hartwig
APPLICANT: Hafner, Stefan
TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
FILE REFERENCE: 13111-00002-US
CURRENT APPLICATION NUMBER: US/10/525,674
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: PCT/EP 2003/009452
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: DE 102 39 073.8
PRIOR FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.3
SEQ ID NO 28

LENGTH: 380
TYPE: PRT
ORGANISM: Thermus thermophilus
US-10-525-674-28

Query Match 12.4%; Score 58; DB 6; Length 380;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 15; Conservative 14; Mismatches 22; Indels 6; Gaps 2;

QY 34 VSOEAMAAWTRHQTMLINENR--LSLADPRAREYLAQOMEQYFFGADAVOGYVPO 88
DB 1 MSBIALSAWGEHIALKPPRSPSLIPPKXTAVLFPKRGFTYE---LGGTPE 53

RESULT 4

US-11-165-576-2
Sequence 2, Application US/11165576
Publication No. US20060009388A1
GENERAL INFORMATION:
APPLICANT: Mc Coy, John
APPLICANT: Pedinsky, R. Blake
TITLE OF INVENTION: Treatment of Conditions Involving Demyelination
FILE REFERENCE: 2159.0460004
CURRENT APPLICATION NUMBER: US/11/165,576
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: 60/680,475
PRIOR FILING DATE: 2005-05-13
PRIOR APPLICATION NUMBER: 60/628,435
PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 60/617,297
PRIOR FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: 60/582,966
PRIOR FILING DATE: 2004-06-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 614
TYPE: PRT
ORGANISM: Homo sapiens
US-11-165-576-2

Query Match 12.4%; Score 58; DB 7; Length 614;
Best Local Similarity 27.4%; Pred. No. 24;
Matches 17; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

QY 3 RMVFCYLNKAE--EGMKPPPLNNEIGKRIFFENVSOEAMAAWTRHQTMLINENRSLADP 60
DB 47 RAVLCHRRKRFVAVBEGIPETRIILDLGNRIKIKTINODEFASFPHLRELEINENIVASVEP 106

QY 61 RA 62
DB 107 GA 108

RESULT 5
US-11-165-576-4
Sequence 4, Application US/11165576
Publication No. US20060009388A1
GENERAL INFORMATION:
APPLICANT: Mc Coy, John
APPLICANT: Pedinsky, R. Blake
TITLE OF INVENTION: Treatment of Conditions Involving Demyelination
FILE REFERENCE: 2159.0460004
CURRENT APPLICATION NUMBER: US/11/165,576
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: 60/680,475
PRIOR FILING DATE: 2005-05-13
PRIOR APPLICATION NUMBER: 60/628,435
PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 60/617,297
PRIOR FILING DATE: 2004-10-07

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 / Search time 72.164 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502a-27

Perfect score: 467

Sequence: 1 MARWFCVKLNKEAKENKFP.....QMEQYFGDADAVGYVPQ 88

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database: A_Geneseq_21.*

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8: geneseqp2004s.*

9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	5	ABB78171
2	467	100.0	88	5	ABB78172
3	467	100.0	88	5	ABB78173
4	467	100.0	88	6	ABP77219
5	339	72.6	87	5	ABB78175
6	333	71.3	87	5	ABB78174
7	294	63.0	87	5	ABB78176
8	290	62.1	87	5	ABB78148
9	290	62.1	87	5	ABB78147
10	272.5	58.4	86	5	ABB78149
11	271	58.0	89	9	ABE41576
12	271	58.0	95	9	ABE38294
13	258	55.2	88	5	ABB78178
14	243	52.0	87	5	ABB78177
15	240	51.4	87	5	ABB78155
16	235	50.3	87	5	ABB78153
17	230	49.3	88	5	ABB78154
18	228	48.8	91	5	ABB78150
19	227	48.6	87	5	ABB78152
20	227	48.6	107	7	ABO65445
21	225.5	48.3	92	6	ADA34169
22	221	47.3	93	7	ADF05158
23	219	46.9	87	5	ABB78169
24	217	46.5	87	5	ABB78151

25	213	45.6	91	5	ABB78158	Abb78158 Amino aci
26	213	45.6	91	5	ABB78157	Abb78157 Amino aci
27	213	45.6	91	5	ABB78156	Abb78156 Amino aci
28	211	45.2	88	5	ABB78160	Abb78160 Amino aci
29	211	45.2	91	5	ABB78161	Abb78161 Amino aci
30	211	45.2	91	5	ABB78159	Abb78159 Amino aci
31	211	45.2	91	5	ABB78162	Abb78162 Amino aci
32	210	45.0	78	5	ABB78164	Abb78164 Amino aci
33	207	44.3	87	5	ABB78170	Abb78170 Amino aci
34	207	44.3	122	7	ABO74609	AbO74609 Pseudomon
35	202	43.3	91	5	ABB78163	Abb78163 Amino aci
36	198	42.4	90	5	ABB78165	Abb78165 Amino aci
37	198	42.4	90	5	ABB78168	Abb78168 Amino aci
38	193.5	41.4	90	5	ABB78167	Abb78167 Amino aci
39	182	39.0	110	8	ADL05173	AdL05173 M. catarr
40	158	33.8	76	5	ABB78166	Abb78166 Amino aci
41	158	33.8	1122	6	ABU22044	Abu22044 Protein e
42	158	33.8	202	7	ABW90380	Abw90380 Rice abio
43	158	33.8	1079	8	ADN19463	Adn19463 Bacterial
44	158	33.8	774	4	ABG29304	Abg29304 Novel hum
45	158	33.8	361	7	ABO76259	AbO76259 Pseudomon
46	158	33.8	189	9	ADM18357	Adm18357 Pinus rad
47	158	33.8	466	7	ABO84015	AbO84015 Pseudomon
48	158	33.8	401	6	ABU19221	Abu19221 Protein e
49	158	33.8	418	7	ABO66638	AbO66638 Klebsiell
50	158	33.8	649	7	ADC94671	AdC94671 E. faeciu
51	158	33.8	1443	7	ADJ68530	AdJ68530 Human hea
52	158	33.8	1935	7	ADJ70260	AdJ70260 Human hea
53	158	33.8	3830	5	ABB81168	Abb81168 TRAP pro
54	158	33.8	3830	8	ADJ78499	AdJ78499 PAV/TRAP
55	158	33.8	3830	8	ADQ19749	AdQ19749 Human sof
56	158	33.8	3830	8	ADQ98926	AdQ98926 Antagonis
57	158	33.8	3859	7	ADJ68548	AdJ68548 Human hea
58	158	33.8	3859	7	ADJ68548	AdJ68548 Human hea
59	158	33.8	255	7	ADM27073	Adm27073 Hyperther
60	158	33.8	296	4	AUJ35611	AuJ35611 Haemophil
61	158	33.8	296	6	AUJ35611	AuJ35611 Haemophil
62	158	33.8	438	2	AAV11015	AaV11015 H. pylori
63	158	33.8	442	2	AAW20830	AaW20830 H. pylori
64	158	33.8	465	2	AAW20303	AaW20303 H. pylori
65	158	33.8	207	6	ABW73508	AbW73508 Staphyloc
66	158	33.8	207	9	ADV16859	AdV16859 Staphyloc
67	158	33.8	207	9	ADW94758	AdW94758 Prolifera
68	158	33.8	362	7	ADP89476	AdP89476 Human ery
69	158	33.8	362	8	ADK48858	AdK48858 Human tra
70	158	33.8	362	8	ADP12457	AdP12457 Protein e
71	158	33.8	260	4	AAW38702	AaW38702 Human pol
72	158	33.8	378	4	AAW40488	AaW40488 Human tes
73	158	33.8	656	8	ADJ28417	AdJ28417 Human nuc
74	158	33.8	2426	2	ADH11285	AdH11285 Vertebrat
75	158	33.8	2426	2	ADH11285	AdH11285 Vertebrat

ALIGNMENTS

RESULT 1
ABB78171
ID ABB78171 standard; protein; 88 AA.
XX
AC ABB78171;
XX
DT 29-AUG-2003 (revised)
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
OS Neisseria gonorrhoeae.
XX
PN US2002072118-A1.

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XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YgX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YgX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YgX homologues. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
XX Sequence 88 AA;
XX
XX Query Match 100.0%; Score 467; DB 5; Length 88;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-54;
XX Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 MARWVCVKLNKEAEKMKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60
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XX 61 RAREYLAQOMEOYFFGADAVOGYVPQ 88
XX 61 RAREYLAQOMEOYFFGADAVOGYVPQ 88
XX
XX RESULT 2
XX ABB78172
XX ID ABB78172 standard; protein; 88 AA.
XX
XX ABB78172;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YgX homologue.
XX
XX Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
XX
XX Neisseria meningitidis.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX
XX

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```

PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YgX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YgX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YgX homologues
XX
XX Sequence 88 AA;
XX
XX Query Match 100.0%; Score 467; DB 5; Length 88;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-54;
XX Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MARWVCVKLNKEAEKMKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60
XX 1 MARWVCVKLNKEAEKMKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60
XX
XX 61 RAREYLAQOMEOYFFGADAVOGYVPQ 88
XX 61 RAREYLAQOMEOYFFGADAVOGYVPQ 88
XX
XX RESULT 3
XX ABB78173
XX ID ABB78173 standard; protein; 88 AA.
XX
XX ABB78173;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YgX homologue.
XX
XX Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
XX
XX Neisseria meningitidis.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a

```

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.62187 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-27

Perfect score: 467
Sequence: 1 MARWFCYKLNKAEQMKP.....QMEQYFGDADAVQGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	467	100.0	88 2 H81014	conserved hypotnet
2	240	51.4	90 2 C82320	conserved hypotnet
3	227	48.6	90 2 C64013	hypothetical prote
4	213	45.6	91 2 A85954	hypothetical prote
5	213	45.6	91 2 A85082	hypothetical prote
6	213	45.6	91 2 F91108	hypothetical prote
7	211	45.2	91 2 AH0879	conserved hypotnet
8	207	44.3	90 2 H83003	conserved hypotnet
9	201	43.0	105 2 C82624	conserved hypotnet
10	198	42.4	90 2 A10116	conserved hypotnet
11	158	33.8	93 2 E84994	hypothetical prote
12	72	15.4	1041 2 A81960	probable DNA helic
13	70	15.0	1079 2 T38913	translational initia
14	68.5	14.7	338 2 A83389	probable permease
15	68.5	14.7	549 2 A11457	ABC transporter Ol
16	68	14.6	195 2 S74714	hypothetical prote
17	67.5	14.5	899 2 A83019	conserved hypotnet
18	66.5	14.2	401 2 C70159	translational elonga
19	66	14.1	598 1 R8RCMX	nitrate/nitrite se
20	66	14.1	598 2 P85702	nitrate/nitrite se
21	66	14.1	598 2 G90844	nitrate/nitrite se
22	65	13.9	296 2 A64110	cell division inh
23	65	13.9	465 2 C71870	hypothetical prote
24	65	13.9	590 2 E85057	probable transpos
25	64.5	13.8	207 2 E89952	conserved hypotnet
26	64.5	13.8	362 2 T45072	erythroid Kruppel
27	64.5	13.8	400 2 A33254	inositol-1,4-bisph
28	64.5	13.8	1553 2 S67483	adenosinetriphosph
29	64	13.7	676 2 A45984	sperm-binding glyc

30	64	13.7	677	2	S33664	flagella-associate
31	63.5	13.6	288	2	H95018	transcription regu
32	63.5	13.6	301	2	F82446	transcription regu
33	63	13.5	282	2	D97138	DNA replication pr
34	63	13.5	388	1	JC5461	cellulase (EC 3.2.
35	63	13.5	388	1	S43920	cellulase (EC 3.2.
36	62	13.3	120	2	G97833	hypothetical prote
37	62	13.3	200	2	B82203	transcription regu
38	62	13.3	259	2	S55033	transcription init
39	62	13.3	570	2	D83177	probable phosphotr
40	62	13.3	2314	2	T28698	hypothetical prote
41	61.5	13.2	211	2	T38645	hypothetical prote
42	61.5	13.2	288	2	B95122	transcription regu
43	61.5	13.2	374	2	A96502	probable acyl-acyl
44	61.5	13.2	412	2	G81581	tyrosyl-CRNA synth
45	61.5	13.2	422	2	G86535	tyrosyl-CRNA synth
46	61.5	13.2	422	2	D72088	lysosomal traifick
47	61.5	13.2	589	2	A83530	flagellar biosynth
48	61	13.1	425	2	T50184	mammalian swi/snf
49	61	13.1	563	2	F97028	arginyl-CRNA synth
50	61	13.1	969	2	T33156	hypothetical prote
51	61	13.1	1639	2	T50119	probable sensory t
52	60.5	13.0	186	1	WKR239	10k globulin precu
53	60.5	13.0	186	2	UC4784	alpha-globulin pre
54	60.5	13.0	261	2	S14875	dnak-type molecula
55	60.5	13.0	357	2	F82892	heat-inducible tra
56	60.5	13.0	448	2	T45145	glutamate-ammonia
57	60.5	13.0	1888	2	T39009	hypothetical prote
58	60	12.8	292	2	A10422	conserved hypotnet
59	60	12.8	306	2	A97249	Zn-binding lipopro
60	60	12.8	309	2	D95843	probable transcrip
61	60	12.8	323	2	T35734	probable aminopept
62	60	12.8	335	2	D83142	hypothetical prote
63	60	12.8	397	2	A75503	hypothetical prote
64	60	12.8	410	2	T39115	formamidase-like p
65	60	12.8	508	2	T02466	hypothetical prote
66	60	12.8	615	2	E81451	1-deoxyxylulose-5-
67	60	12.8	655	2	E75206	alpha-amyase (or
68	60	12.8	859	2	T29630	hypothetical prote
69	60	12.8	1006	2	A59384	oxycocinase/insuli
70	60	12.8	1021	2	AC2282	hypothetical prote
71	60	12.8	1025	2	A59383	oxycocinase/insuli
72	60	12.8	3788	2	T30851	lysosomal traifick
73	59.5	12.7	157	1	HHPM17	heat shock protein
74	59.5	12.7	237	2	A55218	slp homolog gsp -
75	59.5	12.7	295	2	T35330	probable RNA polym

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58)
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
R/Retain: H., Saunders, N.U.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; et al.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Piazza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; M01D:2015755; PMID:10710307
A/Accession: H81014
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TEXT>
A/Cross-references: UNIPARC:UP100000C4E7F; GB:AE002552; GB:AE002098; NID:G7227279; PMID:
A/Experimental source: serogroup B, strain MC58
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R/Holroyd, S.; Jørgensen, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.9476 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502a-27

Perfect score: 467
Sequence: 1 MARWFCVTLNKEABGMKEP.....QMEQYFEGDADAVGVYVQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :
1: uniprot_05.80: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	467	100.0	88 1	FETP_NEIG1
2	467	100.0	88 1	FETP_NEIMA
3	467	100.0	88 1	FETP_NEIMB
4	354	75.8	91 1	FETP_PALSO
5	348	74.5	91 2	Q4LS19_9BORK
6	339	72.6	91 1	FETP_BURMA
7	339	72.6	91 1	FETP_BURPS
8	335	71.7	90 1	FETP_CHRYO
9	319	68.3	90 1	FETP_NITRU
10	290	62.1	90 1	FETP_BORER
11	290	62.1	90 1	FETP_BORPA
12	290	62.1	90 1	FETP_BORPE
13	275	58.9	89 1	FETP_LEGPL
14	271	58.0	89 1	FETP_LEGPA
15	271	58.0	89 1	FETP_LEGPH
16	258	55.2	90 1	FETP_COXBU
17	254	54.4	90 1	FETP_VIBF1
18	252	54.0	92 2	Q4NMQ4_9DBLT
19	243	52.0	90 1	FETP_METCA
20	242	51.8	90 1	FETP_IDILO
21	240	51.4	90 1	FETP_VIBCH
22	239	51.2	90 1	FETP_VIBPA
23	239	51.2	90 1	FETP_VIBVU
24	239	51.2	90 1	FETP_VIBVY
25	235	50.3	91 1	FETP_XANAC
26	235	50.3	91 1	FETP_XANBY
27	233	49.9	92 1	FETP_XANOR
28	230	49.3	92 1	FETP_XANOR
29	227	48.6	90 1	FETP_XANON
30	227	48.6	90 2	Q4QMD9_HABE8
31	225	48.2	92 1	FETP_XANCP

32	225	48.2	92 2	Q4UW14_XANCP	Q4UW14 xanthomonas
33	224	48.0	91 1	FETP_MANSN	Q65V77 mannheimia
34	220.5	47.2	90 1	FETP_ACIAH	Q6F6b3 acinetobact
35	220	47.1	90 1	FETP_PHOBR	Q61mk7 photobacter
36	219	46.9	90 1	FETP_PSEBK	Q88r49 pseudomonas
37	217	46.5	90 1	FETP_PASWU	Q961b9 pasteurella
38	217	46.5	90 1	FETP_PHOHL	Q7n711 photoxhabu
39	211	45.2	90 2	Q6r7f6_PSEFL	Q6r7f6 pseudomonas
40	209	44.8	90 1	FETP_XYLFT	Q5nhj8 xyliella fas
41	208	44.5	87 1	FETP_FRATU	Q5nhj8 frincisella
42	208	44.5	90 1	FETP_ECOS7	Q5nhj8 escherichia
43	208	44.5	90 1	FETP_ECOTL	Q5nhj8 escherichia
44	208	44.5	90 1	FETP_ERWCT	Q6d8j3 erwina car
45	208	44.5	90 1	FETP_SHIRL	Q6d8j3 shigella fl
46	207	44.3	90 1	FETP_PSEBA	Q9nu36 pseudomonas
47	207	44.3	90 2	Q4KJ28_PSEFS	Q4KJ28 pseudomonas
48	206	44.1	90 1	FETP_SALPH	Q57K04 salmonella
49	206	44.1	90 1	FETP_SALPA	Q57K04 salmonella
50	206	44.1	90 1	FETP_SALTY	Q57K04 salmonella
51	206	44.1	90 1	FETP_SALTY	Q57K04 salmonella
52	206	44.1	90 1	FETP_YERPS	Q66m3 yersinia ps
53	206	44.1	96 2	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
54	204	43.7	90 1	FETP_ECOT6	Q8f6i3 escherichia
55	201	43.0	90 1	FETP_XYLPA	Q9pc73 xyliella fas
56	198	42.4	90 1	FETP_PSEBM	Q87uf5 pseudomonas
57	198	42.4	90 1	FETP_YERPE	Q87he7 yersinia pe
58	198	42.4	90 2	Q4ZLF3_PSESY	Q4ZLF3 pseudomonas
59	196	42.0	90 2	Q4J228_AZOVI	Q4J228 azotobacter
60	186	39.8	79 1	FETP_CANBP	Q7vrg9 candidatus
61	167	35.8	78 1	FETP_BUCAP	Q8K925 buchnera ap
62	167	35.8	78 1	FETP_WIGBR	Q8d3c5 wigleswort
63	158	33.8	77 1	FETP_BUCAI	Q57618 buchnera ap
64	127	27.2	87 1	FETP_BUCBP	Q89n44 buchnera ap
65	75	16.1	359 2	Q7VKN4_HABDU	Q7VKN4 haemophilus
66	74	15.8	453 2	Q4PBL1_USDMA	Q4PBL1 usellago ma
67	74	15.8	1598 2	Q62C80_BURMA	Q62C80 burkholderi
68	74	15.8	1599 2	Q63KX1_BURPS	Q63KX1 burkholderi
69	73	15.6	820 2	Q521A7_MAGGR	Q521A7 magnaporthe
70	72.5	15.5	301 2	Q6L1N9_PHOPR	Q6L1N9 photobacter
71	72	15.4	203 2	Q568W6_BRARE	Q568W6 brachydanto
72	72	15.4	1041 2	Q5JWDS_NEIMA	Q5JWDS neisseria m
73	71	15.2	346 2	Q6BFA2_SHEON	Q6BFA2 shewanella
74	70.5	15.1	320 2	Q6PKY5_XENLA	Q6PKY5 xenopus lae
75	70	15.0	1079 1	IR2P_SCHPO	Q10251 schizosacch

ALIGNMENTS

RESULT 1	
FETP_NEIG1	STANDARD: PRT: 88 AA.
AC	Q5F553;
DT	13-SEP-2005 (Rel. 48, Created)
DT	13-SEP-2005 (Rel. 48, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Probable Fe(2+) trafficking protein.
GN	Ordered locus names=NG02083;
OS	Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
CC	Neisseriaceae; Neisseria.
OX	NCBI_TaxID=242231;
RN	NCUB071DB SEQUENCE [LARGE SCALE GENOMIC DNA].
RA	Lewis L.A., Gillaspay A.F., McLaughlin R.E., Gispson M., Ducey T.F.,
RA	Owensby T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA	Song L., Lin S., Yuan X., Najjar F., Zhan Q., Zhu H., Qi S.,
RA	Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.,
RT	"The complete genome sequence of Neisseria gonorrhoeae."
RL	Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
CC	-1- FUNCTION: Could be a mediator in iron transactions between iron
CC	acquisition and iron-regulating processes, such as synthesis and/or
CC	repair of Fe-S clusters in biosynthetic enzymes (By similarity).

CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE004699; AAW90684.1; -; Genomic_DNA.
CC
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; YggX.
CC DR Pfam; PF04362; DUF495; 1.
CC DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
CC DR Prodom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC KM Complete proteome; Iron.
CC SQ SEQUENCE 88 AA; 10180 MW; EBC6F2BF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVLANKEAGKMKFPPLPNELGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVLANKEAGKMKFPPLPNELGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
QY 61 RAREYLAQOMEQYFFGDGADAVOGYVPQ 88
DB 61 RAREYLAQOMEQYFFGDGADAVOGYVPQ 88

RESULT 2
FETP_NEIMA
ID FETP_NEIMA STANDARD; PRT; 88 AA.
AC P67615; O9JQP5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=NMA0419;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RT [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=22491 / Serogroup A / Serotype 4A;
RC MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parthill J., Achtmann M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holtroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajadaram M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrett B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491."
RL Nature 404:502-506(2000).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AL162753; CAB83718.1; -; Genomic_DNA.
CC
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; YggX.
CC DR Pfam; PF04362; DUF495; 1.
CC DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
CC DR Prodom; PD029191; DUF495; 1.

KM Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2BF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVLANKEAGKMKFPPLPNELGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVLANKEAGKMKFPPLPNELGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
QY 61 RAREYLAQOMEQYFFGDGADAVOGYVPQ 88
DB 61 RAREYLAQOMEQYFFGDGADAVOGYVPQ 88

RESULT 3
FETP_NEIMB
ID FETP_NEIMB STANDARD; PRT; 88 AA.
AC P67616; O9JQP5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=NMB2021;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RT [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=MC58 / Serogroup B;
RC MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettein H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Khouri H.M.,
RA Citrone H., Clark E.B., Cotton M.D., Uterback T.R., Khouiri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignant V., Piazza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC removed.
CC -----
CC EMBL: AE002098; AAF42344.1; -; Genomic_DNA.
CC
CC DR TIGR; NMB2021; -;
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; YggX.
CC DR Pfam; PF04362; DUF495; 1.
CC DR Prodom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC KM Complete proteome; Iron.
CC SQ SEQUENCE 88 AA; 10180 MW; EBC6F2BF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVLANKEAGKMKFPPLPNELGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVLANKEAGKMKFPPLPNELGKRIFENVSOEAMAAWTRHQTMLINENRLSLADP 60

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.8405 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-27
Perfect score: 467
Sequence: 1 MARWFCVKLNKAEKMKFP.....QMEQYFPDGDADVGVYVQ 88

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: /cgn2_6/ptodata/1/iaa/5.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	225.5	48.3	92	US-09-328-352-5456	Sequence 5456, Ap
3	221	47.3	93	US-09-543-681A-5443	Sequence 5443, Ap
4	207	44.3	122	US-09-252-991A-23355	Sequence 23355, A
5	182	39.0	110	US-09-540-236-2859	Sequence 2859, Ap
6	68.5	14.7	361	US-09-252-991A-25005	Sequence 25005, A
7	67.5	14.5	466	US-09-252-991A-32761	Sequence 32761, A
8	66	14.1	418	US-09-489-039A-13155	Sequence 13155, A
9	65.5	14.0	649	US-09-107-532A-4298	Sequence 4298, A
10	65.5	14.0	3838	US-09-949-016-10853	Sequence 10853, A
11	64.5	13.8	361	US-08-874-5698-21	Sequence 21, Appl
12	64.5	13.8	361	US-09-955-518-21	Sequence 21, Appl
13	63	13.5	351	US-09-248-796A-19129	Sequence 19129, A
14	63	13.5	461	US-08-672-571A-1	Sequence 1, Appl1
15	63	13.5	490	US-08-672-571A-1	Sequence 1, Appl1
16	62.5	13.4	263	US-09-252-991A-22230	Sequence 22230, A
17	62	13.3	360	US-09-543-681A-7067	Sequence 7067, Ap
18	62	13.3	671	US-09-252-991A-18020	Sequence 18020, A
19	61.5	13.2	422	US-09-198-452A-377	Sequence 377, App
20	61.5	13.2	422	US-09-438-185A-363	Sequence 363, App
21	60.5	13.0	478	US-09-489-039A-7300	Sequence 7300, Ap
22	60.5	13.0	596	US-09-902-540-10121	Sequence 10121, A
23	60	12.8	621	US-09-489-039A-10378	Sequence 10378, A
24	60	12.8	2186	US-08-822-445-2	Sequence 2, Appl1
25	60	12.8	2186	US-09-396-540-2	Sequence 2, Appl1
26	59.5	12.7	315	US-09-461-325-297	Sequence 297, App
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ALIGNMENTS

28	59.5	12.7	315	2	US-10-115-123-297	Sequence 297, App
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33	59.5	12.7	431	2	US-09-311-021-178	Sequence 178, App
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36	59.5	12.7	977	2	US-08-335-844A-22	Sequence 22, Appl
37	59.5	12.7	977	2	US-09-129-366-22	Sequence 22, Appl
38	59	12.6	366	2	US-09-252-991A-13958	Sequence 13958, A
39	59	12.6	553	2	US-09-583-110-4195	Sequence 4195, Ap
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54	58	12.4	318	2	US-09-489-039A-8369	Sequence 8369, Ap
55	58	12.4	331	2	US-08-849-751-4	Sequence 4, Appl1
56	58	12.4	331	2	US-09-478-816-4	Sequence 4, Appl1
57	58	12.4	466	2	US-08-906-743-4	Sequence 4, Appl1
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59	58	12.4	553	2	US-08-906-743-2	Sequence 2, Appl1
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61	58	12.4	720	2	US-10-101-080-2	Sequence 2, Appl1
62	58	12.4	1178	2	US-09-489-039A-9944	Sequence 9944, Ap
63	57.5	12.3	163	2	US-09-198-452A-103	Sequence 103, App
64	57.5	12.3	180	2	US-09-640-211A-834	Sequence 834, App
65	57.5	12.3	200	2	US-09-710-279-1186	Sequence 1186, Ap
66	57.5	12.3	200	2	US-09-710-279-2390	Sequence 2390, Ap
67	57.5	12.3	208	2	US-09-134-001C-3785	Sequence 3785, Ap
68	57.5	12.3	210	2	US-09-438-185A-88	Sequence 88, Appl
69	57.5	12.3	282	2	US-09-543-681A-4715	Sequence 4715, Ap
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71	57.5	12.3	879	2	US-09-583-110-4739	Sequence 4739, Ap
72	57.5	12.3	890	2	US-09-802-540-15203	Sequence 15203, A
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Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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Title: US-09-955-502a-27

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	294	63.0	87	3	US-09-955-502-31
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11	243	52.0	87	3	US-09-955-502-36
12	240	51.4	90	3	US-09-955-502-37
13	235	50.3	87	3	US-09-955-502-38
14	230	49.3	88	3	US-09-955-502-39
15	228	48.8	91	3	US-09-955-502-40
16	227	48.6	87	3	US-09-955-502-41
17	219	46.9	87	3	US-09-955-502-42
18	217	46.5	87	3	US-09-955-502-43
19	213	45.6	91	3	US-09-955-502-44
20	213	45.6	91	3	US-09-955-502-45
21	213	45.6	91	3	US-09-955-502-46
22	211	45.2	88	3	US-09-955-502-47
23	211	45.2	91	3	US-09-955-502-48
24	211	45.2	91	3	US-09-955-502-49
25	211	45.2	91	3	US-09-955-502-50
26	210	45.0	78	3	US-09-955-502-51
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28	202	43.3	91	3	US-09-955-502-18	Sequence 18, Appl
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31	198	42.4	90	3	US-09-955-502-23	Sequence 23, Appl
32	158	33.8	76	3	US-09-955-502-21	Sequence 21, Appl
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34	70	15.0	1079	4	US-10-369-493-2116	Sequence 2116, Ap
35	69	14.8	774	5	US-10-450-763-59663	Sequence 59663, A
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37	66.5	14.2	401	4	US-10-282-122A-47145	Sequence 47145, A
38	66.5	14.2	1055	4	US-10-437-963-131308	Sequence 131308, A
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47	65.5	14.0	3830	5	US-10-745-237-256	Sequence 256, Appl
48	65.5	14.0	3859	4	US-10-408-765A-354	Sequence 354, Appl
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61	64.5	13.6	94	4	US-10-425-115-281438	Sequence 281438, A
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67	62	13.3	532	4	US-10-369-493-7486	Sequence 7486, Appl
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69	62	13.3	570	4	US-10-282-122A-66545	Sequence 66545, A
70	62	13.3	835	4	US-10-273-680-7	Sequence 7, Appl
71	62	13.3	835	4	US-10-087-887-67	Sequence 67, Appl
72	62	13.3	835	4	US-10-087-887-74	Sequence 74, Appl
73	62	13.3	835	5	US-10-889-340-7	Sequence 7, Appl
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ALIGNMENTS

RESULT 1
US-09-955-502-26
Sequence 26, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

US-09-955-502-26

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Best Local Similarity 100.0%; Pred. No. 2.6e-50;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAMVFCVTKLKEAGMKPPPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88
DB 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88

RESULT 2

US-09-955-502-27
; Sequence 27, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria meningitidis B
US-09-955-502-27

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Best Local Similarity 100.0%; Pred. No. 2.6e-50;
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QY 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88
DB 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88

RESULT 3

US-09-955-502-28
; Sequence 28, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 88
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; ORGANISM: Neisseria meningitidis A
US-09-955-502-28

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DB 61 RAREYLAQOMEQYFFGADAVQGYVPQ 88

RESULT 4

US-09-955-502-29
; Sequence 29, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-09-955-502-29

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Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

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QY 61 RAREYLAQOMEQYFFGADAVQGYVPQ 87
DB 61 RAREYLAQOMEQYFFGADAVQGYVPQ 87

RESULT 5

US-09-955-502-30
; Sequence 30, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

Query Match 72.6%; Score 339; DB 3; Length 87;
Best Local Similarity 67.8%; Pred. No. 2.6e-34;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

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Title: US-09-955-502a-27

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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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11	57	12.2	620	US-10-131-826A-324	Sequence 324, App
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16	56	12.0	1376	US-11-100-640-32	Sequence 32, App
17	55.5	11.9	403	US-11-009-658-14	Sequence 14, Appl
18	55.5	11.9	408	US-10-821-234-1100	Sequence 1100, Appl
19	55.5	11.9	449	US-11-098-686-10535	Sequence 10535, A
20	55	11.8	258	US-11-090-439-38	Sequence 38, Appl
21	55	11.8	261	US-10-467-657-400	Sequence 400, App
22	55	11.8	611	US-10-454-437-54	Sequence 54, Appl
23	55	11.8	633	US-11-193-561-13	Sequence 13, Appl
24	55	11.8	633	US-11-193-771-13	Sequence 13, Appl
25	55	11.8	633	US-11-193-789-13	Sequence 13, Appl

26	55	11.8	633	7	US-11-193-806-13	Sequence 13, Appl
27	55	11.8	633	7	US-11-193-857-13	Sequence 13, Appl
28	55	11.8	925	6	US-10-454-437-50	Sequence 50, Appl
29	55	11.8	967	7	US-11-202-268-6	Sequence 6, Appl
30	55	11.8	1011	7	US-11-202-268-2	Sequence 2, Appl
31	54.5	11.7	719	7	US-11-087-227-14	Sequence 14, Appl
32	54	11.6	307	6	US-10-793-626-322	Sequence 322, App
33	54	11.6	685	7	US-11-098-686-10574	Sequence 10574, A
34	54	11.6	738	7	US-11-140-625-11	Sequence 11, Appl
35	53.5	11.5	291	6	US-10-883-512-103	Sequence 103, App
36	53.5	11.5	310	7	US-11-055-163-7	Sequence 7, Appl
37	53.5	11.5	344	7	US-11-055-163-6	Sequence 6, Appl
38	53.5	11.5	432	6	US-10-933-115-8	Sequence 8, Appl
39	53.5	11.5	432	7	US-11-056-354-4	Sequence 4, Appl
40	53.5	11.5	440	6	US-10-933-115-2	Sequence 2, Appl
41	53.5	11.5	473	6	US-10-131-826A-382	Sequence 382, App
42	53	11.3	288	6	US-10-467-657-326	Sequence 326, App
43	53	11.3	291	7	US-11-120-308-24	Sequence 24, Appl
44	53	11.3	710	7	US-11-124-367A-354	Sequence 354, App
45	53	11.3	710	7	US-11-124-367A-359	Sequence 359, App
46	53	11.3	713	7	US-11-124-367A-355	Sequence 355, App
47	53	11.3	713	7	US-11-124-367A-356	Sequence 356, App
48	53	11.3	713	7	US-11-124-367A-358	Sequence 358, App
49	53	11.3	734	6	US-10-821-234-1056	Sequence 1056, App
50	53	11.3	3507	7	US-11-075-185-7	Sequence 7, Appl
51	52.5	11.2	197	6	US-10-986-501-296	Sequence 296, App
52	52.5	11.2	229	6	US-10-793-626-2818	Sequence 2818, App
53	52.5	11.2	335	7	US-11-072-175-245	Sequence 245, App
54	52.5	11.2	754	7	US-11-140-625-10	Sequence 10, Appl
55	52.5	11.2	1476	6	US-10-647-956A-4	Sequence 4, Appl
56	52.5	11.2	4128	6	US-10-770-726-7	Sequence 7, Appl
57	52	11.1	223	7	US-11-018-868-140	Sequence 140, App
58	52	11.1	381	7	US-11-024-959-418	Sequence 418, App
59	52	11.1	390	7	US-11-019-711-65	Sequence 65, Appl
60	52	11.1	390	7	US-11-219-282-12	Sequence 12, Appl
61	52	11.1	1022	7	US-11-156-084-118	Sequence 118, App
62	51.5	11.0	209	5	US-09-995-493-94	Sequence 94, Appl
63	51.5	11.0	396	7	US-11-202-731-2	Sequence 2, Appl
64	51.5	11.0	403	7	US-11-074-176-354	Sequence 354, App
65	51.5	11.0	408	7	US-11-074-176-186	Sequence 186, App
66	51.5	11.0	447	7	US-11-024-959-286	Sequence 286, App
67	51.5	11.0	479	6	US-10-821-234-871	Sequence 871, App
68	51.5	11.0	1034	7	US-11-072-512-2343	Sequence 2343, App
69	51.5	11.0	1159	6	US-10-613-744-12	Sequence 12, Appl
70	51.5	11.0	1159	6	US-10-957-116-9	Sequence 9, Appl
71	51	10.9	326	7	US-11-098-686-10173	Sequence 10173, A
72	51	10.9	387	7	US-11-219-282-20	Sequence 20, Appl
73	50.5	10.8	124	7	US-11-069-642-10	Sequence 10, Appl
74	50.5	10.8	347	6	US-10-853-807A-45	Sequence 45, Appl
75	50.5	10.8	352	6	US-10-878-556A-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
Sequence 968, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASTIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 100.0%; Score 467; DB 6; Length 88;
Best Local Similarity 100.0%; Pred. No. 1,7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARNVFCVKNKEABGKMPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRSLADP 60
DB 1 MARNVFCVKNKEABGKMPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRSLADP 60

QY 61 RAREYLAQOMEOYFFGGADAVOGYVPQ 88
DB 61 RAREYLAQOMEOYFFGGADAVOGYVPQ 88

RESULT 2
US-10-821-234-999
Sequence 999, Application US/10821234
Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andermani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes Version 1.0
SEQ ID NO 999
LENGTH: 1092
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-999

Query Match 12.8%; Score 60; DB 6; Length 1092;
Best Local Similarity 30.6%; Pred. No. 28;
Matches 15; Conservative 12; Mismatches 20; Indels 2; Gaps 2;

QY 31 FENVSOEAMAAWTRHQTMLINENRSLADP-RAREYLAQOMEOYFFGD 77
DB 492 FEAGAMENWGLTFRFEETLVDSTSSMADRGLVTKIAHLELAHQWFGN 540

RESULT 3
US-10-525-674-28
Sequence 28, Application US/10525674
Publication No. US20060003425A1

GENERAL INFORMATION:
APPLICANT: Kroger, Burkhard
APPLICANT: Zelder, Oskar
APPLICANT: Kolp-Proge, Corinna
APPLICANT: Schroeder, Hartwig
APPLICANT: Hafner, Stefan
TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
FILE REFERENCE: 13111-00002-US
CURRENT APPLICATION NUMBER: US/10/525,674
CURRENT FILING DATE: 2005-02-24
PRIOR APPLICATION NUMBER: PCT/EP 2003/009452
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: DE 102 39 073.8
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.3
SEQ ID NO 28

LENGTH: 380
TYPE: PRT
ORGANISM: Thermus thermophilus
US-10-525-674-28

Query Match 12.4%; Score 58; DB 6; Length 380;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 15; Conservative 14; Mismatches 22; Indels 6; Gaps 2;

QY 34 VSOEAMAAWTRHQTMLINER--LSLADPARAREYLAQOMEOYFFGGADAVOGYVPQ 88
DB 1 MSRIALBAWGBHEHLLKPPRSLIPPKRTAVLPFRREGVTE---LGGVLP 53

RESULT 4
US-11-165-576-2
Sequence 2, Application US/11165576
Publication No. US20060009388A1

GENERAL INFORMATION:
APPLICANT: Mi, Sha
APPLICANT: Pepinsky, R. Blake
APPLICANT: McCoy, John
TITLE OF INVENTION: Treatment of Conditions Involving Demyelination
FILE REFERENCE: 2159, 0460004
CURRENT APPLICATION NUMBER: US/11/165,576
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: 60/680,475
PRIOR FILING DATE: 2005-05-13
PRIOR APPLICATION NUMBER: 60/628,435
PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 60/617,297
PRIOR FILING DATE: 2004-10-07
PRIOR APPLICATION NUMBER: 60/582,966
PRIOR FILING DATE: 2004-06-24
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 614
TYPE: PRT
ORGANISM: Homo sapiens
US-11-165-576-2

Query Match 12.4%; Score 58; DB 7; Length 614;
Best Local Similarity 27.4%; Pred. No. 24;
Matches 17; Conservative 15; Mismatches 28; Indels 2; Gaps 1;

QY 3 RMVFCVKLNKEA--EGKMPPLPNEIGKRIFENVSOEAMAAWTRHQTMLINENRSLADP 60
DB 47 RAVLCHRKFVAVDEGIPTETRLADLGKNRKTLNODFASFPIELEINENIVSAVEP 106

QY 61 RA 62
DB 107 GA 108

RESULT 5
US-11-165-576-4
Sequence 4, Application US/11165576
Publication No. US20060009388A1

GENERAL INFORMATION:
APPLICANT: Mi, Sha
APPLICANT: Pepinsky, R. Blake
APPLICANT: McCoy, John
TITLE OF INVENTION: Treatment of Conditions Involving Demyelination
FILE REFERENCE: 2159, 0460004
CURRENT APPLICATION NUMBER: US/11/165,576
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: 60/680,475
PRIOR FILING DATE: 2005-05-13
PRIOR APPLICATION NUMBER: 60/628,435
PRIOR FILING DATE: 2004-11-15
PRIOR APPLICATION NUMBER: 60/617,297
PRIOR FILING DATE: 2004-10-07

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 72.164 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502a-28

Perfect score: 467

Sequence: 1 MARMVFCVLRKAEKMKFP.....QMEQYFFGDAVQGYVQ 88

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database :

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2: geneseq1990s.*
3: geneseq2000s.*
4: geneseq2001s.*
5: geneseq2002s.*
6: geneseq2003as.*
7: geneseq2003bs.*
8: geneseq2004s.*
9: geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	467	100.0	88	5	ABB781172
3	467	100.0	88	5	ABB781173
4	467	100.0	88	6	ABP77219
5	339	72.6	87	5	ABB781175
6	333	71.3	87	5	ABB781174
7	294	63.0	87	5	ABB781176
8	290	62.1	87	5	ABB781148
9	290	62.1	87	5	ABB781147
10	272.5	58.4	86	5	ABB781149
11	271	58.0	89	9	AE841576
12	271	58.0	95	9	AE838294
13	258	55.2	88	5	ABB781178
14	243	52.0	87	5	ABB781177
15	240	51.4	90	5	ABB781155
16	235	50.3	87	5	ABB781153
17	230	49.3	88	5	ABB781154
18	228	48.8	91	5	ABB781150
19	227	48.6	87	5	ABB781152
20	227	48.6	107	6	ADA34169
21	225.5	48.3	93	7	ADF05158
22	221	47.3	93	7	ABB781169
23	219	46.9	87	5	ABB781169
24	217	46.5	87	5	ABB781151

25	213	45.6	91	5	ABB781158	Abb781158	Amino aci
26	213	45.6	91	5	ABB781157	Abb781157	Amino aci
27	213	45.6	91	5	ABB781156	Abb781156	Amino aci
28	211	45.2	88	5	ABB781160	Abb781160	Amino aci
29	211	45.2	91	5	ABB781161	Abb781161	Amino aci
30	211	45.2	91	5	ABB781159	Abb781159	Amino aci
31	211	45.2	91	5	ABB781162	Abb781162	Amino aci
32	210	45.0	78	5	ABB781164	Abb781164	Amino aci
33	207	44.3	87	5	ABB781170	Abb781170	Amino aci
34	207	44.3	122	7	ABO74609	Abb74609	Pseudomon
35	202	43.3	91	5	ABB781163	Abb781163	Amino aci
36	198	42.4	90	5	ABB781165	Abb781165	Amino aci
37	198	42.4	90	5	ABB781168	Abb781168	Amino aci
38	193.5	41.4	90	5	ABB781167	Abb781167	Amino aci
39	182	39.0	110	8	ADL05173	Adl05173	M. catarr
40	158	33.8	76	5	ABB781166	Abb781166	Amino aci
41	74	15.8	1122	6	ABU22044	Abu22044	Protein e
42	70	15.0	202	7	ABM90380	Abm90380	Rice abio
43	70	15.0	1079	8	ADN19463	Adn19463	Bacterial
44	69	14.8	774	4	ABG29304	Abg29304	Novel hum
45	68.5	14.7	361	7	ABO76259	AbO76259	Pseudomon
46	68	14.6	189	9	ADM18357	Adm18357	Pinus rad
47	67.5	14.5	466	7	ABO84015	AbO84015	Pseudomon
48	66.5	14.2	401	6	ABU19221	Abu19221	Protein e
49	66	14.1	418	7	ABO66638	AbO66638	Klebsiell
50	65.5	14.0	649	7	ADC94671	AdC94671	E. faeciu
51	65.5	14.0	1443	7	ADJ68530	Adj68530	Human hea
52	65.5	14.0	1935	7	ADJ70260	Adj70260	Human hea
53	65.5	14.0	3830	5	ABB81168	Abb81168	TRRAP pro
54	65.5	14.0	3830	8	ADJ78499	Adj78499	PAF/TRRAP
55	65.5	14.0	3830	8	ADQ19749	Adq19749	Human bof
56	65.5	14.0	3830	8	ADQ89826	AdQ89826	Antagonis
57	65.5	14.0	3859	7	ADJ68548	Adj68548	Human hea
58	65.5	14.0	3859	8	ADS88242	AdS88242	Human pro
59	65	13.9	255	7	ADM27073	Adm27073	Hyperther
60	65	13.9	296	6	AAU35611	Aau35611	Haemophil
61	65	13.9	296	6	ABU30521	Abu30521	Protein e
62	65	13.9	438	2	AAV11015	Aav11015	H. pylori
63	65	13.9	442	2	AAW20830	Aaw20830	H. pylori
64	65	13.9	465	2	AAW20303	Aaw20303	H. pylori
65	64.5	13.8	207	6	ABW73508	Abw73508	Staphyloc
66	64.5	13.8	207	9	ADV16859	Adv16859	Staphyloc
67	64.5	13.8	207	9	ADM94758	Adm94758	Prolifera
68	64.5	13.8	362	7	ADP89476	Adp89476	Human ery
69	64.5	13.8	362	8	ADK48858	Adk48858	Human tra
70	64.5	13.8	362	8	ADP12457	Adp12457	Protein e
71	64	13.7	260	4	AAW38702	Aaw38702	Human pol
72	64	13.7	378	4	AAW40488	Aaw40488	Human tes
73	64	13.7	656	4	ABU53239	Abu53239	Human tes
74	64	13.7	656	8	ADJ28417	Adj28417	Human nuc
75	64	13.7	2426	2	ADH11285	Adh11285	Vertebrat

ALIGNMENTS

RESULT 1	ABB781171	standard; protein; 88 AA.
ID	ABB781171	
XX	ABB781171;	
AC	29-AUG-2003	(revised)
XX	05-NOV-2002	(first entry)
DT	05-NOV-2002	(first entry)
XX	Amino acid sequence of a YggX homologue.	
DE	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX	Neisseria gonorrhoeae.	
OS	US2002072118-A1.	
PN		

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XX 13-JUN-2002.
PD
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
PI
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PR protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 88 AA;
XX
XX Query Match 100.0%; Score 467; DB 5; Length 88;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-54;
XX Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MARWFCVTKLNKEAEKGKFPPLPNEIGKRIFFENVSGEAMAWTRHOTMLINENRSLADP 60
DB 1 MARWFCVTKLNKEAEKGKFPPLPNEIGKRIFFENVSGEAMAWTRHOTMLINENRSLADP 60
QY 61 RAREYLAQOMEQYFFGADGADAVOGYVPQ 88
DB 61 RAREYLAQOMEQYFFGADGADAVOGYVPQ 88
XX
XX RESULT 2
XX ABB78172
XX ID ABB78172 standard; protein; 88 AA.
XX AC ABB78172;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YgX homologue.
XX
XX Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
XX
XX Neisseria meningitidis.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
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PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PR protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YgX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YgX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YgX homologues
XX
XX Sequence 88 AA;
XX
XX Query Match 100.0%; Score 467; DB 5; Length 88;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-54;
XX Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MARWFCVTKLNKEAEKGKFPPLPNEIGKRIFFENVSGEAMAWTRHOTMLINENRSLADP 60
DB 1 MARWFCVTKLNKEAEKGKFPPLPNEIGKRIFFENVSGEAMAWTRHOTMLINENRSLADP 60
QY 61 RAREYLAQOMEQYFFGADGADAVOGYVPQ 88
DB 61 RAREYLAQOMEQYFFGADGADAVOGYVPQ 88
XX
XX RESULT 3
XX ABB78173
XX ID ABB78173 standard; protein; 88 AA.
XX AC ABB78173;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YgX homologue.
XX
XX Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
XX
XX Neisseria meningitidis.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
PI
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PR protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.62187 Seconds

(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-28

Perfect score: 467

Sequence: 1 MARWFCVYLNKRAKMKFP.....QMEQYFEGDADAVGVVPO 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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1: pirl:*

2: pirl:*

3: pirl:*

4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	467	100.0	88 2 H81014	conserved hypothe
2	240	51.4	90 2 C82320	conserved hypothe
3	227	48.6	90 2 C64013	hypothetical prote
4	213	45.6	91 2 A85954	hypothetical prote
5	213	45.6	91 2 A65082	hypothetical prote
6	213	45.6	91 2 P91108	hypothetical prote
7	211	45.2	91 2 AH0879	conserved hypothe
8	207	44.3	90 2 H83003	conserved hypothe
9	201	43.0	105 2 C82624	conserved hypothe
10	198	42.4	90 2 A10116	conserved hypothe
11	158	33.8	93 2 E84994	hypothetical prote
12	72	15.4	1041 2 A81960	probable DNA helic
13	70	15.0	1079 2 T38913	translational initia
14	68.5	14.7	338 2 A83389	probable pernaase
15	68.5	14.7	549 2 A11457	ABC transporter ol
16	68	14.6	195 2 S74714	hypothetical prote
17	67.5	14.5	899 2 A83019	conserved hypothe
18	66.5	14.2	401 2 C70159	translational elonga
19	66	14.1	598 1 RGECKX	nitrate/nitrite se
20	66	14.1	598 2 P85702	nitrate/nitrite se
21	66	14.1	598 2 G90844	cell division inhi
22	65	13.9	296 2 A64110	hypothetical prote
23	65	13.9	465 2 C71870	probable transposo
24	64.5	13.8	590 2 E85057	hypothetical prote
25	64.5	13.8	207 2 E89952	erythroid kruppel-
26	64.5	13.8	362 2 T45072	inositol-1,4-bisph
27	64.5	13.8	400 2 A39254	adenosinetriphosph
28	64.5	13.8	1553 2 S67483	sperm-binding glyc
29	64	13.7	676 2 A45984	

30	64	13.7	677	2	S33664	flagella-associate
31	63.5	13.6	288	2	H95018	transcription regu
32	63.5	13.6	301	2	P82446	transcription regu
33	63	13.5	282	2	D97138	DNA replication pr
34	63	13.5	388	1	JC5461	cellulase (EC 3.2.
35	63	13.5	388	1	S43920	cellulase (EC 3.2.
36	62	13.3	120	2	G97833	hypothetical prote
37	62	13.3	200	2	B82203	transcription regu
38	62	13.3	259	2	S55033	transcription init
39	62	13.3	570	2	D83177	probable phosphor
40	62	13.3	2314	2	T28698	hypothetical prote
41	61.5	13.2	211	2	T38645	hypothetical prote
42	61.5	13.2	288	2	B95122	transcription regu
43	61.5	13.2	374	2	A96502	probable acyl-acyl
44	61.5	13.2	412	2	G81581	tyrosyl-tRNA synth
45	61.5	13.2	422	2	G86535	tyrosyl-tRNA synth
46	61.5	13.2	422	2	D72088	tyrosine-tRNA liga
47	61.5	13.2	589	2	A83530	flagellar biosynth
48	61	13.1	425	2	T50184	mammalian swi/snf
49	61	13.1	563	2	P97028	arginyl-tRNA synth
50	61	13.1	969	2	T33156	hypothetical prote
51	61	13.1	1639	2	T50119	probable sensory t
52	60.5	13.0	186	1	WMRZ19	19k globulin precu
53	60.5	13.0	186	2	JC4784	alpha-globulin pre
54	60.5	13.0	261	2	S14875	dnak-type molecula
55	60.5	13.0	357	2	P82892	heat-inducible tra
56	60.5	13.0	448	2	T45145	glutamate-ammonia
57	60.5	13.0	1888	2	T39009	hypothetical prote
58	60	12.8	292	2	A10422	conserved hypothe
59	60	12.8	306	2	A97249	Zn-binding lipopro
60	60	12.8	309	2	D95843	probable transcrip
61	60	12.8	323	2	T35734	probable aminopept
62	60	12.8	335	2	D83142	hypothetical prote
63	60	12.8	397	2	A75503	hypothetical prote
64	60	12.8	410	2	T39115	formamide-1-like p
65	60	12.8	515	2	T02486	hypothetical prote
66	60	12.8	618	2	B81451	1-deoxyxylulose-5-
67	60	12.8	655	2	E75206	alpha-amyase (or
68	60	12.8	859	2	T29630	hypothetical prote
69	60	12.8	1006	2	A59384	oxycotinase/insuli
70	60	12.8	1021	2	AC2202	hypothetical prote
71	60	12.8	1025	2	A59383	oxycotinase/insuli
72	60	12.8	3788	2	T30851	lysosomal traffick
73	59.5	12.7	157	1	HHPM17	heat shock protein
74	59.5	12.7	237	2	A55218	sfp homolog gsp -
75	59.5	12.7	295	2	T35330	probable RNA polym

ALIGNMENTS

RESULT 1
H81014
conserved hypotheical protein NMB2021 [imported] - Neisseria meningitidis (strain MCS8 ;
C.Species: Neisseria meningitidis
C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C.Accession: H81014, F81958
R.Fletcher, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Plaza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A:Reference number: A81000, MUID:2015755, PMID:10710307
A:Accession: H81014
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-88 <TET>
A:Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:G7227279; PIDN:
A:Experimental source: serogroup B, strain MCS8
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R; Holtroyd, S.; Jorgels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

A>Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A/Reference number: A81775; MUID:20222556; PMID:10761919
A/Accession: F81958
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <PAE>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:97379120; PIDN:
A/Experimental source: serogroup A, strain Z2491
A/Genetic:
A/Gene: NMD2021; NMA0419
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 100.0%; Score 467; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 2,7e-46;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGADGADAVOGYVPQ 88
DB 61 RAREYLAQOMEQYFFGADGADAVOGYVPQ 88

RESULT 2
C82320
hypotheetical protein VC0451 [imported] - *Vibrio cholerae* (strain N16961 serogr
C/Species: *Vibrio cholerae*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82320
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A/Residues: 1-90 <HEI>
A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:99654871; PIDN:
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0451
A/Map position: 1
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 51.4%; Score 240; DB 2; Length 90;
Best Local Similarity 50.6%; Pred. No. 2.5e-20;
Matches 44; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

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DB 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGADGADAVOGYVP 87
DB 61 EHRKLEQEMVNFLEFGEKVHIEGYTP 87

RESULT 3
C64013
hypotheetical protein H10760 - *Haemophilus influenzae* (strain Rd KW20)
C/Species: *Haemophilus influenzae*
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <ITIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:915;
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 48.6%; Score 227; DB 2; Length 90;
Best Local Similarity 50.0%; Pred. No. 7.8e-19;
Matches 44; Conservative 17; Mismatches 25; Indels 2; Gaps 2;

QY 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGADGADAVOGYVP 87
DB 61 EHRKLEQEMVNFLEFGEKVHIEGYTP 87

RESULT 4
A85954
hypotheetical protein Y9GX [imported] - *Escherichia coli* (strain O157:H7, substrain EDL93;
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
A/Reference number: A85940; MUID:21074935; PMID:11206551
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:912517511; P
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: Y9GX
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 45.6%; Score 213; DB 2; Length 91;
Best Local Similarity 44.3%; Pred. No. 3.1e-17;
Matches 39; Conservative 16; Mismatches 33; Indels 0; Gaps 0;

QY 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MSRTICTFLQREABEGDQFLYFGEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGADGADAVOGYVPQ 88
DB 61 EHRKLEQEMVNFLEFGEKVHIEGYTP 88

RESULT 5
A65082
hypotheetical protein b2962 - *Escherichia coli* (strain K-12)
C/Species: *Escherichia coli*
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:91
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: fe(II) trafficking protein Y9GX

A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <ITIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:915;
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 48.6%; Score 227; DB 2; Length 90;
Best Local Similarity 50.0%; Pred. No. 7.8e-19;
Matches 44; Conservative 17; Mismatches 25; Indels 2; Gaps 2;

QY 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGADGADAVOGYVP 87
DB 61 EHRKLEQEMVNFLEFGEKVHIEGYTP 87

RESULT 4
A85954
hypotheetical protein Y9GX [imported] - *Escherichia coli* (strain O157:H7, substrain EDL93;
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
A/Reference number: A85940; MUID:21074935; PMID:11206551
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:912517511; P
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: Y9GX
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 45.6%; Score 213; DB 2; Length 91;
Best Local Similarity 44.3%; Pred. No. 3.1e-17;
Matches 39; Conservative 16; Mismatches 33; Indels 0; Gaps 0;

QY 1 MARWFCVKLNKEAGMKFPPLPNEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MSRTICTFLQREABEGDQFLYFGEIGKRIFENVSGEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGADGADAVOGYVPQ 88
DB 61 EHRKLEQEMVNFLEFGEKVHIEGYTP 88

RESULT 5
A65082
hypotheetical protein b2962 - *Escherichia coli* (strain K-12)
C/Species: *Escherichia coli*
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:91
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: fe(II) trafficking protein Y9GX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.9476 Seconds
(Without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502a-28

Perfect score: 467
Sequence: 1 MARWECVXLNKEAGMKPP.....QMEQYFGGDAVAGCVTPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	1	FETP_NEIG1
2	467	100.0	88	1	FETP_NEIG1
3	467	100.0	88	1	FETP_NEIG1
4	354	75.8	91	1	FETP_RALSO
5	348	74.5	91	2	Q4LSI9_9BURK
6	339	72.6	91	1	FETP_BURMA
7	339	72.6	91	1	FETP_BURPS
8	335	71.7	90	1	FETP_BURPS
9	339	68.3	90	1	FETP_NITEU
10	290	62.1	90	1	FETP_BORBR
11	290	62.1	90	1	FETP_BORPE
12	290	62.1	90	1	FETP_BORPE
13	275	58.9	89	1	FETP_LEGPA
14	271	58.0	89	1	FETP_LEGPA
15	271	58.0	89	1	FETP_LEGPA
16	258	55.2	90	1	FETP_COXHU
17	254	54.4	90	1	FETP_VIBFI
18	252	54.0	92	2	Q4NM04_9DEBT
19	243	52.0	90	1	FETP_METCA
20	242	51.8	90	1	FETP_IDILO
21	240	51.4	90	1	FETP_VIBCH
22	239	51.2	90	1	FETP_VIBPA
23	239	51.2	90	1	FETP_VIBPA
24	239	51.2	90	1	FETP_VIBPA
25	235	50.3	91	1	FETP_VIBPA
26	235	50.3	91	1	FETP_VIBPA
27	233	49.9	92	1	FETP_XANOR
28	230	49.3	92	1	FETP_XANOR
29	227	48.6	90	1	FETP_XANOR
30	227	48.6	90	2	Q4QMD9_HABIR
31	225	48.2	92	1	FETP_XANCP

32	225	48.2	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
33	224	48.0	91	1	FETP_MANSN	Q65VC7 manheimia
34	220.5	47.2	90	1	FETP_ACTAD	Q6FDB3 actinobacter
35	220	47.1	90	1	FETP_PHOPR	Q6LAK7 photobacter
36	219	46.9	90	1	FETP_PSEPK	Q88T49 pseudomonas
37	217	46.5	90	1	FETP_PASWU	Q9CIB9 pasteurella
38	217	46.5	90	1	FETP_PASWU	Q9CIB9 pasteurella
39	211	45.2	90	2	Q6T7F6_PSEEL	Q7N711 photorhabdu
40	209	44.8	90	1	FETP_XYLEFI	Q6T7F6 pseudomonas
41	208	44.5	87	1	FETP_PRAAT	Q874D6 xylella fas
42	208	44.5	90	1	FETP_ECO57	Q5N1J8 franciella
43	208	44.5	90	1	FETP_ECOLI	Q5N1J8 franciella
44	208	44.5	90	1	FETP_ERWCT	Q5N1J8 franciella
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46	207	44.3	90	1	FETP_SHIFL	Q6B8J9 erwina car
47	207	44.3	90	1	FETP_PSEAE	Q6B8J9 erwina car
48	206	44.1	90	2	Q4KTJ2_PSEFS	Q9HJ36 pseudomonas
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54	204	43.7	90	1	FETP_ECOL6	Q57K04 salmonella
55	201	43.0	90	1	FETP_XYLEFI	Q57K04 salmonella
56	198	42.4	90	1	FETP_PSESM	Q57K04 salmonella
57	198	42.4	90	1	FETP_PSESM	Q57K04 salmonella
58	198	42.4	90	2	Q4ZLP3_PSESY	Q4ZLP3 pseudomonas
59	196	42.0	90	2	Q4Z228_AZOVI	Q4Z228 azotobacter
60	186	39.8	79	1	FETP_CANBP	Q7V9G3 candidatus
61	167	35.8	78	1	FETP_WIGBR	Q8K925 buchnera ap
62	167	35.8	78	1	FETP_WIGBR	Q8K925 buchnera ap
63	158	33.8	77	1	FETP_BUCAL	Q843C5 wigglewort
64	127	27.2	87	1	FETP_BUCAL	P57618 buchnera ap
65	75	16.1	359	2	Q7VKN4_HARDU	Q89444 buchnera ap
66	74	15.8	453	2	Q4PBL1_USTWA	Q7VKN4 haemophilus
67	74	15.8	1598	2	Q62CBO_BURMA	Q4PBL1 usellago ma
68	74	15.8	1598	2	Q62CBO_BURMA	Q62CBO burholderi
69	73	15.6	820	2	Q52IA7_MAGGR	Q63K61 burholderi
70	72.5	15.5	301	2	Q6N1A7_PHOBR	Q52IA7 magaporthe
71	72	15.4	203	2	Q568W6_BRARE	Q6N1A7 photobacter
72	72	15.4	1041	2	Q568W6_BRARE	Q568W6 brachydanio
73	71	15.2	346	2	Q8BF42_SHEON	Q568W6 brachydanio
74	70.5	15.1	320	2	Q6PKY5_XENIA	Q8BF42 shewanella
75	70	15.0	1079	1	IF2P_SCHPO	Q6PKY5 xenopus lae

ALIGNMENTS

RESULT 1	
ID FETP_NEIG1	STANDARD; PRT; 88 AA.
AC Q5F553;	
DT 13-SBP-2005 (Rel. 48, Created)	
DT 13-SBP-2005 (Rel. 48, Last sequence update)	
DT 13-SBP-2005 (Rel. 48, Last annotation update)	
DE Probable Fe(2+) trafficking protein.	
GN OrderedAccession=NG02083;	
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).	
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	
OC Neisseriaceae; Neisseria.	
OX NCBI_TaxID=242231;	
RN NCUB017DE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RA Lewis L.A., Gillespie A.F., McLaughlin R.E., Gibson M., Ducey T.F.,	
RA Omley T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,	
RA Song L., Lin S., Yuan X., Najaf F., Zhan M., Ren Q., Zhu H., Qi S.,	
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;	
RT "The complete genome sequence of Neisseria gonorrhoeae."	
CC Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.	
CC -1- FUNCTION: Could be a mediator in iron transactions between iron	
CC acquisition and iron-requiring processes, such as synthesis and/or	
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).	

```

CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE004969; AAW90684.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match      100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARMVFCVTLNKEAEGKPKPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGDGADAVGVYVPQ 88
DB 61 RAREYLAQOMEQYFFGDGADAVGVYVPQ 88

RESULT 2
FETP_NEIMA STANDARD; PRT; 88 AA.
ID FETP_NEIMA
AC P67615; O9J0P5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedocNames=MMA0419;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Z491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222555; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Baeham D., Brown D., Chillingworth T.,
RA Jørgensen K., Davies P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Rajandream M., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream S., Spratt B.G., Barrett B.G.,
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z491."
RL Nature 404:502-506(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AL162753; CAB83718.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match      100.0%; Score 467; DB 1; Length 88;
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QY 1 MARMVFCVTLNKEAEGKPKPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVTLNKEAEGKPKPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60

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KW Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match      100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVTLNKEAEGKPKPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVTLNKEAEGKPKPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGDGADAVGVYVPQ 88
DB 61 RAREYLAQOMEQYFFGDGADAVGVYVPQ 88

RESULT 3
FETP_NEIMB STANDARD; PRT; 88 AA.
ID FETP_NEIMB
AC P67616; O9J0P5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedocNames=NMB2021;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MCS8 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Velthuis A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Swinn M.L., Deboy R.T., Peterson J.D.,
RA Hickey B.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cifton H., Clark E.B., Cotton M.D., Utebbeck T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappelli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MCS8."
RL Science 287:1809-1815(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE002098; AAF42344.1; -; Genomic_DNA.
CC TIGR: NMB2021; -; 1.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match      100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVTLNKEAEGKPKPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVTLNKEAEGKPKPLPNEIGKRIFFENVSOEAMAAWTRHQTMLINENRLSLADP 60

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 / Search time 17.8405 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-28

Perfect score: 467
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	221	47.3	93 2	US-09-543-681A-5443
4	207	44.3	122 2	US-09-252-991A-23355
5	182	39.0	110 2	US-09-540-236-2859
6	68.5	14.7	361 2	US-09-252-991A-25005
7	67.5	14.5	466 2	US-09-252-991A-32761
8	66	14.1	418 2	US-09-489-039A-13155
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12	64.5	13.8	361 2	US-08-955-518-21
13	63	13.5	351 2	US-09-248-796A-19129
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18	62	13.3	671 2	US-09-252-991A-18020
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20	61.5	13.2	423 2	US-09-438-185A-363
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22	60.5	13.0	596 2	US-09-902-540-10121
23	60	12.8	621 2	US-09-489-039A-10378
24	60	12.8	2186 1	US-08-823-445-2
25	60	12.8	2186 2	US-09-396-540-2
26	59.5	12.7	315 2	US-09-461-325-297
27	59.5	12.7	315 2	US-10-012-542-297

ALIGNMENTS

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Sequence 11962, Application US/09489039A
Parent No. 6610636
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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31	59.5	12.7	431	2	US-09-461-325-146	Sequence 146, App
32	59.5	12.7	431	2	US-10-012-542-146	Sequence 146, App
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34	59.5	12.7	431	2	US-10-115-123-146	Sequence 146, App
35	59.5	12.7	431	2	US-09-538-092-33	Sequence 33, Appl
36	59.5	12.7	848	2	US-08-335-844A-22	Sequence 22, Appl
37	59.5	12.7	977	2	US-09-129-366-22	Sequence 22, Appl
38	59	12.6	366	2	US-09-252-991A-31958	Sequence 31958, A
39	59	12.6	563	2	US-09-583-110-4195	Sequence 4195, Ap
40	59	12.6	577	2	US-09-107-433-3424	Sequence 3424, Ap
41	59	12.6	5069	2	US-10-042-665A-5	Sequence 5, Appl
42	58.5	12.5	213	2	US-09-959-873B-16	Sequence 16, Appl
43	58.5	12.5	213	2	US-09-949-016-5955	Sequence 5955, Ap
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:24:18 ; Search time 55.5262 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502a-28

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	290	62.1	87	3	US-09-955-502-33
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24	211	45.2	91	3	US-09-955-502-49
25	211	45.2	91	3	US-09-955-502-50
26	210	45.0	78	3	US-09-955-502-51
27	207	44.3	87	3	US-09-955-502-52

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29	201	43.0	89	3	US-09-955-502-22	Sequence 22, Appl
30	198	42.4	90	3	US-09-955-502-20	Sequence 20, Appl
31	198	42.4	90	3	US-09-955-502-23	Sequence 23, Appl
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ALIGNMENTS

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US-09-955-502-26
Sequence 26, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 26
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 / Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502a-18
Perfect score: 488
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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7: Geneseqp2003b:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	100.0	91	5	ABB78163 Amino aci
2	474	97.1	91	5	ABB78161 Amino aci
3	474	97.1	91	5	ABB78159 Amino aci
4	474	97.1	91	5	ABB78162 Amino aci
5	458	93.9	88	5	ABB78160 Amino aci
6	455	93.2	91	5	ABB78158 Amino aci
7	455	93.2	91	5	ABB78157 Amino aci
8	455	93.2	91	5	ABB78156 Amino aci
9	431	88.3	107	7	ABO65445 Klebsiell
10	386	79.1	78	5	ABB78164 Amino aci
11	378	77.7	90	5	ABB78165 Amino aci
12	378	77.5	87	5	ABB78152 Amino aci
13	375	76.8	90	5	ABB78155 Amino aci
14	370	75.8	87	5	ABB78151 Amino aci
15	369.5	75.7	91	5	ABB78150 Amino aci
16	369	75.6	93	7	ADf05158 Bacteri
17	364	74.6	87	5	ABB78153 Amino aci
18	326	66.8	88	5	ABB78154 Amino aci
19	259	53.1	76	5	ABB78166 Amino aci
20	242	49.6	87	5	ABB78148 Amino aci
21	242	49.6	87	5	ABB78147 Amino aci
22	241	49.4	86	5	ABB78149 Amino aci
23	224.5	46.0	89	9	ABE41576 L. pneumo
24	224.5	46.0	95	9	ABE38294 L. pneumo

25	221	45.3	87	5	ABB78170 Amino aci
26	221	45.3	122	7	ABO74609 Pseudomon
27	220.5	45.2	90	5	ABB78167 Amino aci
28	214	43.9	88	5	ABB78178 Amino aci
29	212	43.4	90	5	ABB78168 Amino aci
30	211	43.2	87	5	ABB78169 Amino aci
31	202	41.4	88	5	ABB78171 Amino aci
32	202	41.4	88	5	ABB78172 Amino aci
33	202	41.4	88	5	ABB78173 Amino aci
34	202	41.4	88	6	ABB77219 N. gonorr
35	199	40.8	87	5	ABB78175 Amino aci
36	193	39.5	87	5	ABB78174 Amino aci
37	190	38.9	87	5	ABB78176 Amino aci
38	188	38.5	87	5	ABB78177 Amino aci
39	187.5	38.4	92	6	ADA34169 Acinetoba
40	124	25.4	110	8	ADf05173 M. catarr
41	72	14.8	309	8	ADN46828 Thermoco
42	72	14.8	506	3	AAV74371 Neisseria
43	72	14.8	507	6	ABU40210 Protein e
44	71.5	14.7	184	3	AAV74372 Neisseria
45	71	14.5	507	3	AAV74373 Neisseria
46	71	14.5	507	3	AAV74373 Neisseria
47	71	14.5	546	6	ABU38097 Protein e
48	71	14.5	548	4	AAE04737 Brugia ma
49	70.5	14.4	184	3	AAI16325 Pinus rad
50	70.5	14.4	184	4	ABE65734 Annexin-1
51	70.5	14.4	184	7	ADB94702 Programme
52	70.5	14.4	503	4	ABG16577 Novel hum
53	70	14.3	257	3	AAAG31203 Arabidops
54	70	14.3	324	3	AAAG31201 Arabidops
55	70	14.3	324	3	AAAG31201 Arabidops
56	70	14.3	758	9	ADW71760 Salmonell
57	69.5	14.2	227	3	AAAG38052 Arabidops
58	69.5	14.2	307	5	ABE49355 Listeria
59	69.5	14.2	869	8	ADW64441 Thermosta
60	69.5	14.2	1377	8	ADV81847 Streptoco
61	69.5	14.2	1387	8	ADV88434 Streptoco
62	69.5	14.2	1387	8	ADV79687 Streptoco
63	69	14.1	679	9	ADZ85056 Particla F
64	68.5	14.0	608	5	ABP73745 Candida a
65	68	13.9	484	4	AAAB92683 Human pro
66	68	13.9	414	6	ABU11747 Human MDP
67	68	13.9	614	9	ADX06837 Cyclin-de
68	68	13.9	614	9	ADY16108 PRO polyp
69	68	13.9	764	5	ABB77432 Human tnn
70	68	13.9	764	7	ADC99062 Human KRP
71	68	13.9	817	4	AAAB38657 Human pol
72	68	13.9	863	4	AAAB38656 Human pol
73	68	13.9	1135	8	ADf10706 Human the
74	68	13.9	1181	8	ADf10708 Human the
75	68	13.9	1186	8	ADf10709 Human the

ALIGNMENTS

RESULT 1	ABB78163	standard; protein; 91 AA.
ID	ABB78163	
XX	ABB78163;	
AC	05-NOV-2002	(first entry)
DT		
XX		
XX		
DE		Amino acid sequence of a YggX homologue.
XX		
KW		Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX		hydroxyl radical; DNA damage; YggX homologue.
OS		Salmonella typhimurium.
XX		
PN		US2002072118-A1.
XX		

PD 13-JUN-2002.
 XX
 XX 18-SEP-2001; 2001US-00955502.
 XX
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 XX
 XX WPI; 2002-589476/63.
 XX
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 XX cell, comprises engineering the cell to produce more YgX protein, a
 XX protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 XX The specification describes a method for reducing superoxide damage to a
 XX cell. The method comprises engineering the cell to produce more than the
 XX native amount of YgX protein (a protein identified from *Salmonella*
 XX *enterica* serovar typhimurium) or its homolog, where the cells are
 XX rendered more resistant to superoxide damage. YgX reduces the oxidation
 XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 XX clusters. The resulting decrease in free-iron levels generates fewer
 XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
 XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
 XX cell. ABB78147-78 represent YgX homologues
 XX
 XX Sequence 91 AA;
 XX
 XX

Query Match 100.0%; Score 488; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 6.2e-49;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTYLGORDAEGDFFQLYPGELGKRIYNEISKDAWAQOMHKQMTLINEKLLMMNNA 60
 DB 1 MSRTTCTYLGORDAEGDFFQLYPGELGKRIYNEISKDAWAQOMHKQMTLINEKLLMMNNA 60
 QY 61 EHRKLLBQEMVSPLEFGKDVHIEGYPTEDKK 91
 DB 61 EHRKLLBQEMVSPLEFGKDVHIEGYPTEDKK 91

RESULT 2
 ABB78161
 ID ABB78161 standard; protein; 91 AA.
 XX
 XX ABB78161;
 XX
 XX 05-NOV-2002 (first entry)
 XX
 XX Amino acid sequence of a YgX homologue.
 XX
 XX Superoxide damage; cell; YgX; *Salmonella enterica* serovar typhimurium;
 XX hydroxyl radical; DNA damage; YgX homologue.
 XX
 XX Unidentified.
 XX
 XX US2002072118-A1.
 XX
 XX 13-JUN-2002.
 XX
 XX 18-SEP-2001; 2001US-00955502.
 XX
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 XX cell, comprises engineering the cell to produce more YgX protein, a
 XX protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 XX The specification describes a method for reducing superoxide damage to a
 XX cell. The method comprises engineering the cell to produce more than the
 XX native amount of YgX protein (a protein identified from *Salmonella*
 XX *enterica* serovar typhimurium) or its homolog, where the cells are
 XX rendered more resistant to superoxide damage. YgX reduces the oxidation
 XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 XX clusters. The resulting decrease in free-iron levels generates fewer
 XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
 XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
 XX cell. ABB78147-78 represent YgX homologues
 XX
 XX Sequence 91 AA;
 XX
 XX

Query Match 97.1%; Score 474; DB 5; Length 91;
 Best Local Similarity 97.8%; Pred. No. 2.7e-47;
 Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTTCTYLGORDAEGDFFQLYPGELGKRIYNEISKDAWAQOMHKQMTLINEKLLMMNNA 60
 DB 1 MSRTTCTYLGORDAEGDFFQLYPGELGKRIYNEISKDAWAQOMHKQMTLINEKLLMMNNA 60
 QY 61 EHRKLLBQEMVSPLEFGKDVHIEGYPTEDKK 91
 DB 61 EHRKLLBQEMVSPLEFGKDVHIEGYPTEDKK 91

RESULT 3
 ABB78159
 ID ABB78159 standard; protein; 91 AA.
 XX
 XX ABB78159;
 XX
 XX 05-NOV-2002 (first entry)
 XX
 XX Amino acid sequence of a YgX homologue.
 XX
 XX Superoxide damage; cell; YgX; *Salmonella enterica* serovar typhimurium;
 XX hydroxyl radical; DNA damage; YgX homologue.
 XX
 XX Unidentified.
 XX
 XX US2002072118-A1.
 XX
 XX 13-JUN-2002.
 XX
 XX 18-SEP-2001; 2001US-00955502.
 XX
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 XX
 XX WPI; 2002-589476/63.
 XX
 XX 18-SEP-2001; 2001US-00955502.
 XX
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 XX
 XX WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 XX cell, comprises engineering the cell to produce more YgX protein, a
 XX protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 XX The specification describes a method for reducing superoxide damage to a
 XX cell. The method comprises engineering the cell to produce more than the
 XX native amount of YgX protein (a protein identified from *Salmonella*
 XX *enterica* serovar typhimurium) or its homolog, where the cells are
 XX rendered more resistant to superoxide damage. YgX reduces the oxidation
 XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 XX clusters. The resulting decrease in free-iron levels generates fewer
 XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
 XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
 XX cell. ABB78147-78 represent YgX homologues
 XX
 XX Sequence 91 AA;
 XX
 XX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-18

Perfect score: 488

Sequence: 1 MSRTIFCTYLRDAEGQDFQ.....SELPFGKDVHIEGYPTEPKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	474	97.1	91	2	conserved hypotet
2	455	93.2	91	2	hypothetical prote
3	455	93.2	91	2	hypothetical prote
4	455	93.2	91	2	hypothetical prote
5	379	77.7	90	2	conserved hypotet
6	378	77.5	90	2	hypothetical prote
7	375	76.8	90	2	conserved hypotet
8	259	53.1	93	2	hypothetical prote
9	230	47.1	105	2	conserved hypotet
10	221	45.3	90	2	conserved hypotet
11	202	41.4	88	2	conserved hypotet
12	79.5	16.3	1638	2	protein unc-73b [i
13	79.5	16.3	2488	2	guanine nucleotide
14	73.5	15.1	495	2	probable zinc-proc
15	71.5	14.7	209	2	hypothetical prote
16	71	14.5	507	2	hypothetical prote
17	71	14.5	546	2	hypothetical prote
18	71	14.5	548	2	hypothetical prote
19	70	14.3	758	2	hypothetical prote
20	70	14.3	758	2	hypothetical prote
21	70	14.3	758	2	hypothetical prote
22	70	14.3	758	2	hypothetical prote
23	69.5	14.2	859	2	hypothetical prote
24	69.5	14.2	859	2	hypothetical prote
25	69.5	14.2	859	2	hypothetical prote
26	67.5	13.8	166	2	hypothetical prote
27	67.5	13.8	287	2	hypothetical prote
28	67	13.7	618	2	hypothetical prote
29	67	13.7	1111	2	hypothetical prote

30	66.5	13.6	410	1	KHMSD	cathepsin D (EC 3.
31	66	13.5	703	2	B82148	ATP-dependent heli
32	66	13.5	1085	2	S62516	hypothetical coile
33	65.5	13.4	251	2	B90428	hypothetical prote
34	65.5	13.4	307	2	B81632	primosome componen
35	65.5	13.4	365	2	B54128	PC-binding protein
36	65	13.3	447	2	JC2076	alpha-1,3-mannosyl
37	65	13.3	507	2	A83105	probable fumarase
38	65	13.3	593	2	C64097	probable soluble 1
39	65	13.3	1230	2	S56850	SMC1 protein homol
40	64.5	13.2	327	2	AD2129	transcription regu
41	64.5	13.2	511	2	A99574	ABC transporter at
42	64.5	13.2	544	2	T40058	probable chromatin
43	64	13.1	548	2	A28209	60K filarial antig
44	63.5	13.0	156	2	F70382	conserved hypotet
45	63.5	13.0	274	2	T16581	hypothetical prote
46	63.5	13.0	379	2	S70709	type II site-speci
47	63.5	13.0	438	2	T37786	probable RNA-bind
48	63.5	13.0	2672	2	A48126	translation activa
49	63.5	13.0	2911	2	T20566	hypothetical prote
50	63	12.9	235	2	G65212	hypothetical prote
51	63	12.9	243	2	T28635	hypothetical prote
52	63	12.9	258	2	A97991	hypothetical prote
53	63	12.9	258	2	B51121	phosphoesterase, p
54	63	12.9	445	1	XDHMB	alpha-1,3-mannosyl
55	63	12.9	447	2	T16527	hypothetical prote
56	63	12.9	472	2	A64576	hypothetical prote
57	63	12.9	483	2	G64799	hypothetical prote
58	63	12.9	543	2	T16015	hypothetical prote
59	63	12.9	549	2	T16016	hypothetical prote
60	63	12.9	1166	2	H71609	hypothetical prote
61	63	12.9	1209	2	T46027	hypothetical prote
62	63	12.9	1327	2	T14594	hypothetical prote
63	62.5	12.8	165	2	A81382	guanidine nucleoti
64	62.5	12.8	214	1	KABOSB	shikimate kinase (
65	62.5	12.8	305	2	G83203	conserved hypotet
66	62.5	12.8	259	2	A75211	asparaginase (EC 3
67	62.5	12.8	339	2	A90395	conserved hypotet
68	62.5	12.8	385	2	D87723	protein R6A10.2 (
69	62.5	12.8	401	2	A81978	hypothetical prote
70	62.5	12.8	498	2	G91179	hypothetical prote
71	62.5	12.8	498	2	H86025	hypothetical prote
72	62.5	12.8	498	2	S47748	53.1K protein prec
73	62.5	12.8	906	2	G69531	alanyl-tRNA synthe
74	62.5	12.8	1141	2	T29185	hypothetical prote
75	62	12.7	226	1	G64211	formylmethionine d

ALIGNMENTS

RESULT 1
AH0879 conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C:Accession: AH0879
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
N:ature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <PAR>
A:Cross-references: UNIPARC:UP100000544C; GB:AL513382; PTDN:CAD02936.1; PTD:q16504189; C:Gene: STY3266
C:Superfamily: Fe(II) trafficking protein YggX

Query Match 97.1%; Score 474; DB 2; Length 91;
Best Local Similarity 97.8%; Pred. No. 2.4e-41;
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60
DB 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60

QY 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91
DB 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 2
A85954
hypothetical protein y9gx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C.Accession: A85954
R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A.Reference number: A85480; MUID:21074935; PMID:11206551
A.Accession: A85954
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-91 <STO>
A.Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:G12517511; F
A.Experimental source: strain O157:H7, substrain EDL933
C.Genetics:
A.Gene: y9gx
C:Superfamily: fe(II) trafficking protein Y9gx

Query Match 93.2%; Score 455; DB 2; Length 91;
Best Local Similarity 92.3%; Pred. No. 2e-39;
Matches 84; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60

QY 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91
DB 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C.Species: Escherichia coli
C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C.Accession: A65082
R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MUID:97426617; PMID:9278503
A.Accession: A65082
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-91 <BLAT>
A.Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A.Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein Y9gx

Query Match 93.2%; Score 455; DB 2; Length 91;
Best Local Similarity 92.3%; Pred. No. 2e-39;
Matches 84; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60
DB 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60

DB 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60

QY 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91
DB 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 4
F9108
hypothetical protein EC63838 [imported] - Escherichia coli (strain O157:H7, substrain RI
C.Species: Escherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C.Accession: F9108
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuwahara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A.Reference number: A96629; MUID:21156231; PMID:11258796
A.Accession: F9108
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-91 <HA>
A.Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA837261.1;
A.Experimental source: strain O157:H7, substrain RIMD 0509952
C.Genetics:
A.Gene: EC63838
C:Superfamily: fe(II) trafficking protein Y9gx

Query Match 93.2%; Score 455; DB 2; Length 91;
Best Local Similarity 92.3%; Pred. No. 2e-39;
Matches 84; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60
DB 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60

QY 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91
DB 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 5
A10116
conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain C092)
C.Species: Yersinia pestis
C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C.Accession: A10116
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhalil, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
H. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A.Reference number: AB0001; MUID:21470413; PMID:11586360
A.Accession: A10116
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-90 <YR>
A.Cross-references: UNIPARC:UPI000000CCCC4; GB:AJ590842; PIDN:CA089796.1; PID:G15979022;
C.Genetics:
A.Gene: YPO0953
C:Superfamily: fe(II) trafficking protein Y9gx

Query Match 77.7%; Score 379; DB 2; Length 90;
Best Local Similarity 78.9%; Pred. No. 1.1e-31;
Matches 71; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60
DB 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAAQWQHQTMLINEKLLMMNNA 60

QY 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 90
DB 61 EDRKLLBOEMVSLFPEGKDVHIEGYTPPSK 90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 / Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-18

Perfect score: 488

Sequence: 1 MSRTIFCTYLGRDAGQDFQ.....SFLFGKDVHIREGPTEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

1: uniprot_05.80:*

2: uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469	96.1	90	1	FERP_SALCH
2	469	96.1	90	1	FERP_SALCH
3	469	96.1	90	1	FERP_SALCH
4	469	96.1	90	1	FERP_SALCH
5	450	92.2	90	1	FERP_SALCH
6	450	92.2	90	1	FERP_SALCH
7	450	92.2	90	1	FERP_SALCH
8	446	91.4	90	1	FERP_SALCH
9	404	82.8	90	1	FERP_SALCH
10	387	79.3	90	1	FERP_SALCH
11	383	78.5	90	1	FERP_SALCH
12	379	77.7	90	1	FERP_SALCH
13	379	77.7	90	1	FERP_SALCH
14	378	77.5	90	1	FERP_SALCH
15	378	77.5	90	2	Q4QMD9_HAB18
16	376	77.0	90	1	FERP_SALCH
17	375	76.8	90	1	FERP_SALCH
18	375	76.8	90	1	FERP_SALCH
19	375	76.8	90	1	FERP_SALCH
20	369	75.6	90	1	FERP_SALCH
21	364	74.6	90	1	FERP_SALCH
22	362	74.2	90	1	FERP_SALCH
23	355	72.7	90	1	FERP_SALCH
24	328.5	67.3	90	1	FERP_SALCH
25	327.5	67.1	90	1	FERP_SALCH
26	259	53.1	77	1	FERP_SALCH
27	243	49.8	78	1	FERP_SALCH
28	242	49.6	90	1	FERP_SALCH
29	242	49.6	90	1	FERP_SALCH
30	242	49.6	90	1	FERP_SALCH
31	239	49.0	91	1	FERP_SALCH

32	232	47.5	92	1	FERP_XANOR	O5gy22 xanthomonas
33	230	47.1	90	1	FERP_XYLF	O5pc73 xyella fae
34	228.5	46.8	89	1	FERP_LEGPI	O5wvca legionella
35	228	46.7	92	1	FERP_XANCP	O5b829 xanthomonas
36	228	46.7	92	2	Q4UW14_XANCP	O4uwl4 xanthomonas
37	226	46.3	90	1	FERP_XYLF	O87066 xyella fae
38	225	46.1	78	1	FERP_WIGBR	O84dcs wigglewort
39	224.5	46.0	89	1	FERP_LEGPA	O5xix9 legionella
40	224.5	46.0	89	1	FERP_LEGPH	O5xub0 legionella
41	221	45.3	90	1	FERP_PSEAE	O9h336 pseudomonas
42	218	44.7	90	2	Q4J228_AZOV	O4j228 azobacter
43	214	43.9	90	1	FERP_COXBU	O83d06 coxiella bu
44	212	43.4	79	1	FERP_CAMP	O79v39 candidatus
45	212	43.4	90	1	FERP_NITEU	O82xf2 nitrosomonas
46	212	43.4	90	1	FERP_PSEBK	O88r49 pseudomonas
47	212	43.4	90	1	FERP_PSEBS	O87f65 pseudomonas
48	212	43.4	90	2	Q4ZLP3_PSEBS	O4zlp3 pseudomonas
49	210	43.0	90	2	O6T7F6_PSEFL	O6t7f6 pseudomonas
50	207	42.4	87	1	FERP_BUCBP	O89a44 buchnera ap
51	202	41.4	88	1	FERP_NEIGL	O5f553 neisseria g
52	202	41.4	88	1	FERP_NEIMA	O5f553 neisseria m
53	202	41.4	88	1	FERP_NEIMA	O5f553 neisseria m
54	202	41.4	91	2	Q4LS19_9BURK	O4ls19 pseudomonas
55	201.5	41.3	90	1	FERP_CHRYO	O4kt22 pseudomonas
56	199	40.8	90	2	Q4KJ22_PSEBS	O4kt22 pseudomonas
57	199	40.8	91	1	FERP_BURMA	O63j94 burkholderi
58	199	40.8	91	1	FERP_BURPS	O63j94 burkholderi
59	198	40.6	91	1	FERP_RALSO	O8y010 ralstonia s
60	191	39.1	87	1	FERP_FRATY	O5mhj8 francisella
61	188	38.5	90	1	FERP_METCA	O60aj7 methylococc
62	182.5	37.4	90	1	FERP_ACIDP	O6ff63 acinetobact
63	142	29.1	92	2	Q4WQ04_SDEL	O4wq04 anaeromyxob
64	132	27.0	96	2	Q4FV07_9GAMM	O4fv07 pseudobact
65	82.5	16.9	482	2	O5NUV1_9BURK	O5nuv1 ralstonia m
66	82.5	16.9	514	2	O6A1Z9_DSIPS	O6a1z9 desulfohal
67	79.5	16.3	1638	2	O7KPP4_CABEL	O7kpp4 caenorhabdi
68	79.5	16.3	2140	2	O6BEM2_CABEL	O6bem2 caenorhabdi
69	79.5	16.3	2488	2	O61528_CABEL	O61528 caenorhabdi
70	78.5	16.1	337	2	O81A88_BACRU	O81a88 bacillus ce
71	76.5	15.7	486	2	O7MXS1_ALCEU	O7mxs1 alcaligenes
72	75	15.4	385	2	O7J4A2_BACCI	O7j4a2 bacillus ce
73	75	15.4	508	2	O7NSFO_CHRYO	O7nsfo chromobacte
74	74.5	15.3	1589	2	O516E7_ENTHI	O516e7 entamoeba h
75	73.5	15.1	495	1	YHJ0_JALNT	O82286 salmone

ALIGNMENTS

RESULT 1
ID FERP_SALCH STANDARD, PRT, 90 AA.
AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=SC3052;
OS Salmone, Choleaeus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmone.
OX NCBI_Taxid=591;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gk1297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.,
RT "The genome sequence of Salmone enterica serovar Choleaeus, a
highly invasive and resistant zoonotic pathogen."
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-regulating processes, such as synthesis and/or

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CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE017220; AAX66958.1; -; Genomic_DNA.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; Y9GX.
CC Prodom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC FT INIT_MET 0 0 By similarity.
CC SEQUENCE 90 AA; 10768 MW; B3B6A1BE22555E3C CRC64;

Query Match 96.1%; Score 469; DB 1; Length 90;
Best Local Similarity 97.8%; Pred. No. 1.4e-41;
Matches 88; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 SRTIFCTYLQDAEGDGFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLNMMNAE 61
DB 1 SRTIFCTYLQDAEGDGFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLNMMNAE 60
QY 62 HRKLLQEMVSLFPGKDVHIEGYPTDEKK 91
DB 61 HRKLLQEMVSLFPGKDVHIEGYPTDEKK 90

RESULT 2
RETP_SALPA STANDARD; PRT; 90 AA.
ID Q5PMM1;
AC 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gx; OrderedLocustNames=SP42974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=54388;
OX [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozerky P., McCellan M.,
RA Harting C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremicki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Mink P.,
RA Delaunay K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RT Nat. Genet. 36:1268-1274(2004).
RL -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
CC SMR; Q5PMM1; 1-91.
CC HAMAP; MF_00686; -; 1.
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DR InterPro; IPR007457; Y9GX.
DR Prodom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
DR FT INIT_MET 0 0 By similarity.
DR SEQUENCE 90 AA; 10768 MW; B3B6A1BE22555E3C CRC64;

Query Match 96.1%; Score 469; DB 1; Length 90;
Best Local Similarity 97.8%; Pred. No. 1.4e-41;
Matches 88; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 SRTIFCTYLQDAEGDGFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLNMMNAE 61
DB 1 SRTIFCTYLQDAEGDGFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLNMMNAE 60
QY 62 HRKLLQEMVSLFPGKDVHIEGYPTDEKK 91
DB 61 HRKLLQEMVSLFPGKDVHIEGYPTDEKK 90

RESULT 3
RETP_SALTI STANDARD; PRT; 90 AA.
ID P67618; Q8XFW6;
AC 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gx; OrderedLocustNames=STY3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=601;
OX [1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parthill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather A., Moule T.S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RT Nature 413:848-852(2001).
RL [2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=TY2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2350-2357.2003;
RA Deng W., Ikon S.R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blatner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RT J. Bacteriol. 185:2330-2337(2003).
RL -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
CC EMBL; AE016844; AAO70576.1; -; Genomic_DNA.
CC SMR; P67618; 1-90.
CC HAMAP; MF_00686; -; 1.
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-18
Perfect score: 488
Sequence: 1 MSRTIFCTVLRDAREGQDRQ.....SFLFEKGVHIGYPTEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
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4: /cgn2_6/prodata/1/1aa/R COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB	ID
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2	369	75.6	93	2 US-09-543-681A-5443
3	221	45.3	122	2 US-09-252-991A-23355
4	187.5	38.4	92	2 US-09-328-352-5456
5	124	25.4	110	2 US-09-540-236-2859
6	71	14.5	548	2 US-09-167-299-3
7	70.5	14.0	184	2 US-09-325-932A-66
8	68.5	14.0	544	2 US-09-248-796A-18911
9	68	13.9	337	2 US-09-270-767-41746
10	68	13.9	1214	2 US-10-164-595-24
11	67.5	13.8	192	2 US-08-545-573A-9
12	66	13.5	292	2 US-09-328-352-5836
13	66	13.5	331	2 US-09-328-352-6400
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15	65	13.3	474	2 US-09-252-991A-24473
16	64	13.1	1176	2 US-09-489-039A-8879
17	63.5	13.0	546	1 US-08-533-669A-2
18	63.5	13.0	546	2 US-09-183-861-2
19	63.5	13.0	546	2 US-09-022-765-2
20	63.5	13.0	546	2 US-09-551-974A-2
21	63.5	13.0	546	2 US-09-565-501A-2
22	63.5	13.0	546	2 US-09-639-206A-2
23	63.5	13.0	546	2 US-09-874-923-2
24	63.5	13.0	546	2 US-08-798-841-2
25	63.5	13.0	982	2 US-09-551-974A-95
26	63.5	13.0	982	2 US-09-565-501A-95
27	63.5	13.0	982	2 US-09-639-206A-95

28	63.5	13.0	982	2	US-09-874-923-95	Sequence 95, Appl
29	63.5	13.0	1427	2	US-09-551-974A-97	Sequence 97, Appl
30	63.5	13.0	1427	2	US-09-565-501A-97	Sequence 97, Appl
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35	63.5	13.0	1641	2	US-09-639-206A-96	Sequence 96, Appl
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39	62.5	12.8	199	2	US-08-545-573A-42	Sequence 42, Appl
40	62.5	12.8	199	2	US-09-066-330-9	Sequence 9, Appl
41	62.5	12.8	214	2	US-08-545-573A-41	Sequence 41, Appl
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54	61.5	12.6	546	2	US-10-206-576-82	Sequence 82, Appl
55	61.5	12.6	547	2	US-09-071-035-42	Sequence 42, Appl
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57	61.5	12.6	591	2	US-09-370-368-8	Sequence 8, Appl
58	61	12.5	143	2	US-09-270-767-45872	Sequence 45872, A
59	61	12.5	184	2	US-09-270-767-61671	Sequence 61671, A
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61	61	12.5	325	2	US-09-270-767-46116	Sequence 46116, A
62	61	12.5	329	2	US-09-489-039A-10883	Sequence 10883, A
63	61	12.5	587	2	US-09-538-092-539	Sequence 539, App
64	60.5	12.4	223	2	US-09-543-681A-5667	Sequence 5667, Ap
65	60.5	12.4	337	2	US-09-248-796A-14738	Sequence 14738, A
66	60.5	12.4	525	2	US-09-540-236-2250	Sequence 2250, Ap
67	60	12.3	124	2	US-08-545-573A-15	Sequence 15, Appl
68	60	12.3	139	2	US-09-513-999C-4802	Sequence 4802, Ap
69	60	12.3	230	2	US-09-248-796A-17807	Sequence 17807, Ap
70	60	12.3	251	2	US-09-248-796A-16794	Sequence 16794, A
71	60	12.3	258	2	US-09-513-999C-4800	Sequence 4800, Ap
72	60	12.3	264	2	US-09-949-016-6012	Sequence 6012, Ap
73	60	12.3	276	2	US-09-949-016-11703	Sequence 11703, A
74	60	12.3	421	2	US-09-489-039A-7512	Sequence 7512, Ap
75	60	12.3	1326	2	US-09-252-991A-17932	Sequence 17932, A

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709 2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-11962

Query Match 88.3%; Score 431; DB 2; Length 107;
Best Local Similarity 86.8%; Pred. No. 1e-47; 5; Indels 0; Gaps 0;
Matches 79; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNA 60
DB 17 MSRTIFCTFLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNP 76

QY 61 EHRKLLQEMVSVFLPEGKDVHIEGYPTEDK 91
DB 77 EHRKLLQEMVQVFLPEGKDVHIEGYTPPEKQ 107

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 1999-04-09
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRP
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 75.6%; Score 369; DB 2; Length 93;
Best Local Similarity 75.6%; Pred. No. 8e-40;
Matches 68; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNA 60
DB 4 MSRTIFCTFLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNP 63

QY 61 EHRKLLQEMVSVFLPEGKDVHIEGYPTEDK 90
DB 64 DDRKLLQEMVRFLEFGHVDHIDGYTPPEK 93

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRP
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 45.3%; Score 221; DB 2; Length 122;
Best Local Similarity 52.3%; Pred. No. 1.3e-20;
Matches 45; Conservative 11; Mismatches 28; Indels 2; Gaps 2;

QY 1 MSRTIFCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNA 60

DB 33 MSRTIFCTYLRDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNA 92

QY 61 EHRKLLQEMVSVFLPEGKDVHIEGY 85

DB 93 EDRKFLQEMDKFL-SGEDYAKADGY 117

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRP
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 38.4%; Score 187.5; DB 2; Length 92;
Best Local Similarity 40.4%; Pred. No. 1.8e-16;
Matches 36; Conservative 15; Mismatches 37; Indels 1; Gaps 1;

QY 1 MSRTIFCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNA 60
DB 4 MSRTIFCTYLRDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNP 63

QY 61 EHRKLLQEMVSVFLPEGKDVHIEGYPTEDK 88
DB 64 EAKKFLQEMVRFLEFGHVDHIDGYTPPEK 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATI
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRP
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 25.4%; Score 124; DB 2; Length 110;
Best Local Similarity 34.6%; Pred. No. 3.5e-08;
Matches 28; Conservative 13; Mismatches 40; Indels 0; Gaps 0;

QY 5 MSRTIFCTYLQDAEGDGFOLYPGELGKRIYNEISKDAMAWOHQOTMLINEKLNMMNAEHRK 64
DB 25 VFCRRYQQLPFLPDPFNNAKGQIOTISAKANNAWLEIQTMLINEKLSMIDPOAKK 84

QY 65 LLEQEMVSVFLPEGKDVHIEGY 85
DB 85 YLNEQREKFLDNGDYKXAGY 105

RESULT 6
US-09-167-299-3
; Sequence 3, Application US/09167299

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502a-18

Perfect score: 488

Sequence: 1 MSRTFCYLYQNDAGQDFQ.....SFLFGKQVHIEGVTEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 75 summaries

Database : Published Applications AA Main:*

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- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	100.0	91	3	US-09-955-502-18
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3	474	97.1	91	3	US-09-955-502-16
4	474	97.1	91	3	US-09-955-502-17
5	458	93.9	88	3	US-09-955-502-15
6	455	93.2	91	3	US-09-955-502-11
7	455	93.2	91	3	US-09-955-502-12
8	455	93.2	91	3	US-09-955-502-13
9	386	79.1	78	3	US-09-955-502-19
10	379	77.7	90	3	US-09-955-502-20
11	378	77.5	87	3	US-09-955-502-7
12	375	76.8	90	3	US-09-955-502-10
13	370	75.8	87	3	US-09-955-502-6
14	369.5	75.7	91	3	US-09-955-502-5
15	364	74.6	87	3	US-09-955-502-8
16	326	66.8	88	3	US-09-955-502-9
17	259	53.1	86	3	US-09-955-502-21
18	242	49.6	87	3	US-09-955-502-2
19	242	49.6	86	3	US-09-955-502-3
20	241	49.4	86	3	US-09-955-502-4
21	230	47.1	89	3	US-09-955-502-22
22	221	45.3	87	3	US-09-955-502-25
23	214	43.9	88	3	US-09-955-502-33
24	212	43.4	90	3	US-09-955-502-23
25	211	43.2	87	3	US-09-955-502-24
26	202	41.4	88	3	US-09-955-502-26
27	202	41.4	88	3	US-09-955-502-27

ALIGNMENTS

RESULT 1
US-09-955-502-18
Sequence 18, Application US/09955502
Patent No. US20020071218A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
PRIORITY FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 91
TYPE: PRT
ORGANISM: Salmonella typhimurium

28	202	41.4	88	3	US-09-955-502-28	Sequence 28, Appl
29	199	40.8	87	3	US-09-955-502-29	Sequence 29, Appl
30	199	40.8	87	3	US-09-955-502-30	Sequence 30, Appl
31	190	38.9	87	3	US-09-955-502-31	Sequence 31, Appl
32	188	38.5	87	3	US-09-955-502-32	Sequence 32, Appl
33	177	15.8	167	4	US-10-437-963-158697	Sequence 158697, A
34	172	14.8	507	4	US-10-282-1222A-68134	Sequence 68134, A
35	72	14.8	1261	4	US-10-437-963-189166	Sequence 189166, A
36	71.5	14.7	184	4	US-10-393-840-52	Sequence 52, Appl
37	71	14.5	546	4	US-10-282-1222A-66021	Sequence 66021, A
38	70.5	14.4	184	4	US-10-219-220-66	Sequence 66, Appl
39	70.5	14.4	184	4	US-10-393-840-118	Sequence 118, App
40	70.5	14.4	503	5	US-10-450-763-46936	Sequence 46936, A
41	69	14.1	679	5	US-10-805-684-105	Sequence 105, App
42	68.5	14.0	449	4	US-10-424-599-279212	Sequence 279212, A
43	68.5	14.0	608	4	US-10-032-585-7582	Sequence 7582, App
44	68	13.9	764	4	US-10-416-330-37	Sequence 37, Appl
45	68	13.9	764	5	US-10-491-467-15	Sequence 15, Appl
46	68	13.9	1206	4	US-10-085-198-144	Sequence 144, App
47	68	13.9	1214	5	US-10-717-665-24	Sequence 24, Appl
48	67.5	13.8	166	5	US-10-482-706-269	Sequence 269, App
49	67.5	13.8	192	2	US-08-545-573A-9	Sequence 9, Appl1
50	67	13.7	306	4	US-10-424-599-241560	Sequence 241560, A
51	66.5	13.6	292	4	US-10-424-599-164588	Sequence 164588, A
52	66.5	13.6	561	4	US-10-437-963-169643	Sequence 169643, A
53	66.5	13.6	2910	5	US-10-732-993-3342	Sequence 3342, App
54	66	13.5	321	4	US-10-282-1222A-45018	Sequence 45018, A
55	65.5	13.4	125	2	US-08-545-573A-13	Sequence 13, Appl
56	65.5	13.4	172	5	US-10-450-763-34132	Sequence 34132, A
57	65.5	13.4	682	4	US-10-437-963-190113	Sequence 190113, A
58	65.5	13.4	728	4	US-10-437-963-190117	Sequence 190117, A
59	65	13.3	1230	4	US-10-369-493-22160	Sequence 22160, A
60	64.5	13.2	242	4	US-10-393-840-55	Sequence 55, Appl
61	64.5	13.2	447	4	US-10-106-658-4948	Sequence 4948, App
62	64.5	13.2	593	5	US-10-450-763-50306	Sequence 50306, A
63	64.5	13.2	1278	5	US-10-510-812-2	Sequence 2, Appl1
64	64	13.1	325	4	US-10-369-493-19793	Sequence 19793, A
65	64	13.1	786	5	US-10-732-993-4885	Sequence 4885, App
66	63.5	13.0	102	3	US-09-864-408A-768	Sequence 768, App
67	63.5	13.0	176	4	US-10-425-115-346175	Sequence 346175, A
68	63.5	13.0	199	5	US-10-770-712-51	Sequence 51, Appl
69	63.5	13.0	237	4	US-10-156-761-10738	Sequence 10738, A
70	63.5	13.0	239	6	US-11-097-143-6306	Sequence 6306, App
71	63.5	13.0	387	4	US-10-408-765A-1906	Sequence 1906, App
72	63.5	13.0	455	4	US-10-275-774-1983	Sequence 1983, App
73	63.5	13.0	546	5	US-10-732-993-9369	Sequence 9369, App
74	63.5	13.0	546	3	US-09-874-923-2	Sequence 2, Appl1
75	63.5	13.0	546	3	US-09-991-496-2	Sequence 2, Appl1

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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 5.07859 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502a-18
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFGKDVHIREGYTEDEK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	202	41.4	88	6	US-10-467-657-968 Sequence 968, App
2	65	13.3	593	7	US-11-194-246-317 Sequence 317, App
3	64.5	13.2	1432	6	US-10-510-386-218 Sequence 218, App
4	63	12.9	478	6	US-10-821-234-915 Sequence 915, App
5	62	12.7	251	7	US-11-054-515-1496 Sequence 1496, App
6	61	12.5	700	6	US-10-995-561-922 Sequence 922, App
7	61	12.5	700	6	US-10-995-561-922 Sequence 924, App
8	60	12.3	264	6	US-10-821-234-1555 Sequence 1555, App
9	60	12.3	834	6	US-10-453-372-658 Sequence 658, App
10	59.5	12.2	285	6	US-10-467-657-222 Sequence 222, App
11	59.5	12.2	285	6	US-10-467-657-8230 Sequence 8230, App
12	59.5	12.2	650	6	US-10-467-657-1948 Sequence 1948, App
13	59.5	12.2	1995	7	US-11-069-834-60 Sequence 60, App
14	59	12.1	257	7	US-11-054-515-1710 Sequence 1710, App
15	59	12.1	695	6	US-10-453-372-648 Sequence 648, App
16	59	12.1	697	6	US-10-485-517-202 Sequence 202, App
17	59	12.1	774	7	US-11-070-627-7 Sequence 7, App
18	59	12.1	1450	6	US-10-485-517-152 Sequence 152, App
19	58.5	12.0	177	6	US-10-467-657-1658 Sequence 1658, App
20	58.5	12.0	749	7	US-11-098-686-10505 Sequence 10505, App
21	58	11.9	336	6	US-10-453-372-640 Sequence 640, App
22	58	11.9	480	6	US-10-510-386-12 Sequence 12, App
23	58	11.9	775	6	US-10-453-372-656 Sequence 656, App
24	58	11.9	793	6	US-10-995-561-925 Sequence 925, App
25	58	11.9	804	6	US-10-453-372-650 Sequence 650, App

26	58	11.9	847	6	US-10-453-372-654 Sequence 654, App
27	58	11.9	857	6	US-10-453-372-652 Sequence 652, App
28	58	11.9	905	6	US-10-453-372-638 Sequence 638, App
29	58	11.9	905	6	US-10-453-372-662 Sequence 662, App
30	58	11.9	905	6	US-10-453-372-664 Sequence 664, App
31	58	11.9	963	6	US-10-995-561-923 Sequence 923, App
32	58	11.9	963	6	US-10-995-561-923 Sequence 960, App
33	58	11.9	1012	6	US-10-453-372-646 Sequence 646, App
34	57.5	11.8	242	7	US-11-022-562-320 Sequence 220, App
35	57.5	11.8	752	7	US-11-072-512-3003 Sequence 3003, App
36	57.5	11.8	782	6	US-10-793-626-2352 Sequence 2352, App
37	57	11.7	432	6	US-10-821-234-1463 Sequence 1463, App
38	57	11.7	504	7	US-11-072-512-3467 Sequence 3467, App
39	57	11.7	604	6	US-10-942-072-4 Sequence 4, App
40	57	11.7	1167	6	US-10-942-072-6 Sequence 6, App
41	56.5	11.6	647	7	US-11-000-463-722 Sequence 722, App
42	56.5	11.6	1254	6	US-10-528-031-47 Sequence 47, App
43	56.5	11.6	1897	6	US-10-821-234-1635 Sequence 1635, App
44	56.5	11.6	1907	7	US-11-000-463-250 Sequence 250, App
45	56	11.5	206	7	US-11-124-367A-316 Sequence 316, App
46	56	11.5	339	7	US-11-043-542-40 Sequence 40, App
47	56	11.5	373	7	US-11-024-959-442 Sequence 442, App
48	56	11.5	1501	6	US-10-793-626-2850 Sequence 2850, App
49	56	11.5	3433	6	US-10-714-781A-67 Sequence 67, App
50	55.5	11.4	136	6	US-10-793-626-580 Sequence 580, App
51	55.5	11.4	250	7	US-11-098-686-11014 Sequence 11014, App
52	55.5	11.4	279	7	US-11-098-686-10812 Sequence 10812, App
53	55.5	11.4	577	7	US-11-072-175-187 Sequence 187, App
54	55	11.3	189	7	US-11-071-262-1 Sequence 1, App
55	55	11.3	667	6	US-10-793-626-198 Sequence 198, App
56	55	11.3	692	7	US-11-038-284-33 Sequence 33, App
57	55	11.3	873	7	US-11-038-284-35 Sequence 35, App
58	55	11.3	889	7	US-11-038-284-15 Sequence 15, App
59	55	11.3	1142	7	US-11-109-156-22 Sequence 22, App
60	55	11.3	2665	7	US-11-124-368A-214 Sequence 214, App
61	55	11.3	2668	7	US-11-124-368A-215 Sequence 215, App
62	54.5	11.2	317	6	US-10-523-303A-74 Sequence 74, App
63	54.5	11.2	496	7	US-11-069-642-20 Sequence 20, App
64	54.5	11.2	774	7	US-11-175-690-520 Sequence 520, App
65	54	11.1	251	7	US-11-009-658-36 Sequence 36, App
66	54	11.1	1168	6	US-10-942-072-11 Sequence 11, App
67	54	11.1	3003	6	US-10-453-372-1080 Sequence 1080, App
68	53.5	11.0	179	6	US-10-467-657-6542 Sequence 6542, App
69	53.5	11.0	313	6	US-10-995-561-972 Sequence 972, App
70	53.5	11.0	335	6	US-10-995-561-970 Sequence 970, App
71	53.5	11.0	345	6	US-10-995-561-971 Sequence 971, App
72	53.5	11.0	384	6	US-10-467-657-2024 Sequence 2024, App
73	53.5	11.0	1404	6	US-10-878-556A-169 Sequence 169, App
74	53.5	11.0	2214	7	US-11-080-991-94 Sequence 94, App
75	53	10.9	111	6	US-10-771-257-34 Sequence 34, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 41.4%; Score 202; DB 6; Length 88;
Best Local Similarity 44.2%; Pred. No. 3.6e-16;
Matches 38; Conservative 18; Mismatches 28; Indels 2; Gaps 2;

QY 1 MSRTFTYLDADAGDPOLYGEIGKRIYNEISKDAMAOHQKQTMLINEKLNMMNA 60
DB 1 MARWFFCVKLNLEAGMKFPPLPNELGKRIFFENVSGEAMAAWTRHQTMLINEENRSLADP 60

QY 61 EHRKLEQEMVSFL-EGKDVHIEGY 85
DB 61 RAREYLAQOEQYFFGDGADA-VQGY 85

RESULT 2
US-11-194-246-317
Sequence 317, Application US/11194246
Publication No. US20050272089A1
GENERAL INFORMATION:
APPLICANT: Mott, John
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET

FILE REFERENCE: 00592.US1 (Mar 268.05920101)
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 13.3%; Score 65; DB 7; Length 593;
Best Local Similarity 24.1%; Pred. No. 9.6;
Matches 20; Conservative 10; Mismatches 23; Indels 30; Gaps 2;

QY 9 YLOR--DAEGDPOLYGEIGKRIYNE-----ISKDA 38
DB 240 FLNRFDNDNTDPOKRRDQIQLOTDNLTERRLMAIWQKTELSTWNLLSAESKSGE 299

QY 39 WAOMHQKQTMLINEKLNMMNA 61
DB 300 WRYWEAKODILKNTKKTALSKG 322

RESULT 3
US-10-510-386-218
Sequence 218, Application US/10510386
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.3

SEQ ID NO 218
LENGTH: 1432
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-510-386-218

Query Match 13.2%; Score 64.5; DB 6; Length 1432;
Best Local Similarity 22.5%; Pred. No. 31;
Matches 20; Conservative 21; Mismatches 35; Indels 13; Gaps 4;

QY 10 LQDADGDPOLYGEIGKRIYNEISKDAMAOHQKQTMLINEKLNMMNAEHRKLEQ 68
DB 977 VSKIDLDLDPFYGEGIG---YDDGTGBNMAWAFYESGNGLV---KMTLENGOERKAMIKG 1030

QY 69 EMVSFLPR-----GKDVHIEGYPTEDKX 91
DB 1031 GLFKFMDTEPPDPGDTDFAVFVYDASGK 1059

RESULT 4
US-10-821-234-915
Sequence 915, Application US/10821234
Publication No. US2005025514A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Susan
APPLICANT: Andermani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_gene version 1.0
SEQ ID NO 915
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-915

Query Match 12.9%; Score 63; DB 6; Length 478;
Best Local Similarity 25.0%; Pred. No. 12;
Matches 24; Conservative 20; Mismatches 30; Indels 22; Gaps 4;

QY 8 TYLQDADGDP--QLYPG-----ELGKRIYNEISKDAMAOHQKQTMLIN 51
DB 380 SYLQREAYDRDPLFARVYGAPQLQVEKVRTNDRKEIGEVRYQYTGDSFKAPA-KALGYMD 438

QY 52 EKLNNMAEHRKLEQEMVSFLPFEGKDVHIEGYPT 87
DB 439 DIKSGVPRAGYRGI-----VTFQFGRVHLAPPPT 469

RESULT 5
US-11-054-515-1496
Sequence 1496, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
FILE REFERENCE: PFS2393
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 / Search time 64.0524 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502a-19

Perfect score: 415

Sequence: 1 MSRRIFCTFLQREADQDFQ.....NPEHRKLEQEWVFLPFGK 78

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

A_Geneseq_21:*

- 1: Geneseqp19808:*
- 2: Geneseqp19908:*
- 3: Geneseqp20008:*
- 4: Geneseqp20018:*
- 5: Geneseqp20028:*
- 6: Geneseqp20038:*
- 7: Geneseqp20038:*
- 8: Geneseqp20048:*
- 9: Geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415	100.0	78	5	ABR78164 Amino aci
2	415	100.0	107	7	ABO65445 Klebsiell
3	395	99.2	91	5	ABR78158 Amino aci
4	395	99.2	91	5	ABR78157 Amino aci
5	395	99.2	91	5	ABR78156 Amino aci
6	386	93.0	88	5	ABR78160 Amino aci
7	386	93.0	91	5	ABR78161 Amino aci
8	386	93.0	91	5	ABR78159 Amino aci
9	386	93.0	91	5	ABR78162 Amino aci
10	386	93.0	91	5	ABR78163 Amino aci
11	350	84.3	90	5	ABR78155 Amino aci
12	347	83.6	93	7	ADFO5158 Bacteri
13	342	82.4	90	5	ABR78165 Amino aci
14	327	78.8	87	5	ABR78153 Amino aci
15	325	78.3	87	5	ABR78152 Amino aci
16	317	76.4	87	5	ABR78151 Amino aci
17	316	76.1	91	5	ABR78150 Amino aci
18	292	70.4	88	5	ABR78154 Amino aci
19	256	61.7	76	5	ABR78166 Amino aci
20	227	54.7	88	5	ABR78178 Amino aci
21	222	53.5	86	5	ABR78149 Amino aci
22	222	53.5	87	5	ABR78148 Amino aci
23	222	53.5	87	5	ABR78147 Amino aci
24	214.5	51.7	89	9	ABR41576 L. pneumo

25	214.5	51.7	95	9	ABR38294	Aeb38294 L. pneumo
26	211	50.8	87	5	ABR78170	Amb78170 Amino aci
27	211	50.8	122	7	ABO74609	AbO74609 Pseudom
28	210	50.6	88	5	ABR78171	AbB78171 Amino aci
29	210	50.6	88	5	ABR78172	AbB78172 Amino aci
30	210	50.6	88	5	ABR78173	AbB78173 Amino aci
31	210	50.6	88	6	ABR77219	AbP77219 N. gonorr
32	209.5	50.5	90	5	ABR78167	AbB78167 Amino aci
33	197.5	47.6	87	5	ABR78175	AbB78175 Amino aci
34	197.5	47.6	87	5	ABR78169	AbB78169 Amino aci
35	196	47.2	87	5	ABR78176	AbB78176 Amino aci
36	195	47.0	90	5	ABR78168	AbB78168 Amino aci
37	191.5	46.1	87	5	ABR78177	AbB78177 Amino aci
38	189	45.5	87	5	ABR78177	AbB78177 Amino aci
39	187	45.1	92	6	ADA34169	AdA34169 Acinetob
40	134	32.3	110	8	ADJ05173	AdJ05173 M. catarr
41	69.5	16.7	166	7	ADB80231	AdB80231 Mycopacte
42	68.5	16.5	167	2	AAK14362	AAK14362 E. histoly
43	68.5	16.5	507	6	ABU40210	ABU40210 Protein e
44	68.5	16.5	548	4	AAE04737	AAE04737 Brugia ma
45	67.5	16.3	641	6	ABM67978	ABM67978 Phototrab
46	67.5	16.3	2000	6	ABR52622	ABR52622 Protein B
47	67.5	16.3	2000	7	ADK62602	ADK62602 Disease t
48	66.5	16.0	102	5	ABP31411	ABP31411 Human ORF
49	66.5	16.0	193	8	ABM80636	ABM80636 Tumour-as
50	66.5	16.0	507	3	AAV74372	AAV74372 Neisseria
51	66.5	16.0	507	3	AAV74372	AAV74372 Neisseria
52	66.5	16.0	546	6	ABU38097	ABU38097 Protein e
53	65	15.7	679	9	ADZ85056	ADZ85056 Partial F
54	64.5	15.5	285	4	AAV74371	AAV74371 Neisseria
55	64	15.4	285	4	ABU92683	ABU92683 Human pro
56	64	15.4	414	6	ABU11747	ABU11747 Human MD
57	64	15.4	614	9	ADK06837	ADK06837 Cyclin-de
58	64	15.4	614	9	ADL16108	ADL16108 PRO polyP
59	64	15.4	629	8	ADN46272	ADN46272 Thermococ
60	64	15.4	764	5	ABR77432	ABR77432 Human tum
61	64	15.4	764	7	ADC9062	ADC9062 Human XPP
62	64	15.4	817	4	AAH38657	AAH38657 Human pol
63	64	15.4	863	4	AAH38656	AAH38656 Human pol
64	64	15.4	1135	8	ADL10706	ADL10706 Human the
65	64	15.4	1181	8	ADL10708	ADL10708 Human the
66	64	15.4	1186	8	ADL10709	ADL10709 Human the
67	64	15.4	1188	8	ADH45460	ADH45460 Human mol
68	64	15.4	1206	5	ADH48860	ADH48860 NOV61 pro
69	64	15.4	1214	7	ADK65785	ADK65785 Angiogene
70	63.5	15.3	105	4	ABR70079	ABR70079 Human sec
71	63.5	15.3	105	5	ABG65513	ABG65513 Human alb
72	63.5	15.3	105	8	ADL78780	ADL78780 Albumin f
73	63.5	15.3	419	4	ABG20697	ABG20697 Novel hum
74	63.5	15.3	505	3	AAV53036	AAV53036 Human sec
75	63.5	15.3	505	8	ADN03608	ADN03608 Antipsoxi

ALIGNMENTS

RESULT 1
ABR78164
ID ABR78164 standard; protein; 78 AA.
XX
AC ABR78164;
XX
DT 05-NOV-2002 (first entry)
XX
DB Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS Klebsiella pneumoniae.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
 XX 18-SEP-2001; 2001US-00955502.
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 PS
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 78 AA;

Query Match 100.0%; Score 415; DB 5; Length 78;
 Best Local Similarity 100.0%; Pred. No. 3.5e-44;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTTCTFLQREADGDPFLYPGELGKRIYNEISKEMAWQOHKQTLINCKLSMNP 60
 DB 1 MSRTTCTFLQREADGDPFLYPGELGKRIYNEISKEMAWQOHKQTLINCKLSMNP 60

OY 61 EHRKLEQEMVOFLPEGK 78
 DB 61 EHRKLEQEMVOFLPEGK 78

RESULT 2
 ABO65445
 ID ABO65445 standard; protein; 107 AA.
 XX
 AC ABO65445;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE *Klebsiella pneumoniae* polypeptide seqid 11962.
 XX
 XX Recombinant expression vector; transcription regulatory element;
 KW *Klebsiella pneumoniae* protein; antibacterial; Vaccine.
 XX
 OS *Klebsiella pneumoniae*.
 XX
 OS
 XX
 PN US610836-B1.
 XX
 PD 26-AUG-2003.
 XX
 PF 27-JAN-2000; 2000US-00489039.
 XX
 PR 29-JAN-1999; 99US-0117747P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 PI Breton GL, Osborne M;
 XX
 DR WPI; 2003-895346/82.

DR N-PSDB; ACH98996.
 XX
 XX New nucleic acid encoding a *Klebsiella pneumoniae* polypeptide, useful for
 PT preparing a vaccine composition against *Klebsiella pneumoniae*.
 XX
 XX Disclosure; SEQ ID NO 11962; 932pp; English.
 PS
 CC The invention describes a new isolated nucleic acid encoding a *Klebsiella*
 CC *pneumoniae* polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against *Klebsiella pneumoniae*. This is the amino acid sequence of a
 CC *Klebsiella pneumoniae* polypeptide of the invention
 XX
 SQ Sequence 107 AA;

Query Match 100.0%; Score 415; DB 7; Length 107;
 Best Local Similarity 100.0%; Pred. No. 5.2e-44;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTTCTFLQREADGDPFLYPGELGKRIYNEISKEMAWQOHKQTLINCKLSMNP 60
 DB 17 MSRTTCTFLQREADGDPFLYPGELGKRIYNEISKEMAWQOHKQTLINCKLSMNP 76

OY 61 EHRKLEQEMVOFLPEGK 78
 DB 77 EHRKLEQEMVOFLPEGK 94

RESULT 3
 ABB78158
 ID ABB78158 standard; protein; 91 AA.
 XX
 AC ABB78158;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.

XX
 KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.
 XX
 OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.

PS
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 8.52847 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-19

Perfect score: 415

Sequence: 1 MSRRIFCTFLQREADQDFQ.....NPEHRLLEQWVQFLRCK 78

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

1: p1r:0:0
2: p1r1:0:0
3: p1r2:0:0
4: p1r3:0:0

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	395	95.2	91	2	A85954 hypothetical prote
2	395	95.2	91	2	A65082 hypothetical prote
3	395	95.2	91	2	F91108 hypothetical prote
4	386	93.0	91	2	AH0879 conserved hypothet
5	350	84.3	90	2	C82320 conserved hypothet
6	342	82.4	90	2	AI0116 conserved hypothet
7	325	78.3	90	2	C64013 hypothetical prote
8	256	61.7	93	2	E84994 hypothetical prote
9	220	53.0	105	2	C82624 conserved hypothet
10	211	50.8	90	2	H83003 conserved hypothet
11	210	50.6	88	2	H81014 conserved hypothet
12	175	18.7	1638	2	D87749 protein unc-73b [i
13	175	18.7	2488	2	T42739 guanine nucleotide
14	172	17.3	251	2	E90428 hypothetical prote
15	172	17.3	265	2	T46013 hypothetical prote
16	169.5	16.7	94	2	F70562 probable ligand-bi
17	169.5	16.7	166	2	AH0985 hypothetical prote
18	168.5	16.5	495	2	AH0985 probable zinc-proc
19	168.5	16.5	548	2	A54510 63k antigen - nema
20	168	16.4	1111	2	T23047 hypothetical prote
21	167.5	16.3	2672	2	A48126 translation activa
22	167	16.1	544	2	T40058 probable chromatin
23	167	16.1	593	2	C64097 probable soluble 1
24	166.5	16.0	507	2	C81063 fumarate hydratase
25	166.5	16.0	511	2	A99574 ABC transporter at
26	166.5	16.0	546	2	A81807 fumarate hydratase
27	165	15.7	245	2	B43814 helix-loop-helix p
28	165	15.7	278	2	A43814 helix-loop-helix p
29	65	15.7	278	2	S16678 Lys-1 protein - mo

30	64.5	15.5	859	2	T29630 hypothetical prote
31	64	15.4	330	2	S74456 regulatory protein
32	63.5	15.3	91	2	H90521 hypothetical prote
33	63.5	15.3	197	2	T46344 hypothetical prote
34	63.5	15.3	821	2	A12417 hypothetical prote
35	63	15.2	159	2	F82675 transcription regu
36	63	15.2	401	2	AE1978 hypothetical prote
37	63	15.2	438	2	T37786 hypothetical prote
38	63	15.2	703	2	B82185 probable RNA-bind
39	63	15.2	1141	2	T29185 ATP-dependent heli
40	62.5	15.1	633	2	D75112 hypothetical prote
41	62.5	15.1	1206	2	B96507 giu-rRNA amidotran
42	62	14.9	153	2	C87301 hypothetical prote
43	62	14.9	552	2	S45886 hypothetical prote
44	62	14.9	743	2	S19437 hypothetical prote
45	62	14.9	758	2	F72363 hypothetical prote
46	61.5	14.8	485	2	A84043 hypothetical prote
47	61.5	14.8	548	2	A28209 chromosome replica
48	61.5	14.8	1011	2	T51399 DNA-directed RNA p
49	61	14.7	225	2	C88939 protein C05B4.8 [i
50	61	14.7	241	2	T27635 hypothetical prote
51	61	14.7	292	2	F84463 hypothetical prote
52	61	14.7	330	1	B64561 ketol-acid reducto
53	61	14.7	507	2	A83105 probable fumarase
54	61	14.7	561	2	T01950 hypothetical prote
55	61	14.7	859	2	S69700 hypothetical prote
56	61	14.7	946	2	T31488 hypothetical prote
57	60.5	14.6	500	2	T41385 betaine-aldehyde d
58	60.5	14.6	591	1	FOVMM hypothetical prote
59	60.5	14.6	863	1	S51789 gag polypeptide -
60	60.5	14.6	873	1	A49729 VLDL receptor prec
61	60.5	14.6	873	1	A49729 VLDL receptor prec
62	60.5	14.6	873	1	I48952 VLDL receptor prec
63	60.5	14.6	873	1	ORRBD VLDL receptor prec
64	60.5	14.6	1099	1	S31926 myosin IB heavy ch
65	60.5	14.6	1436	2	S67655 probable membrane
66	60.5	14.6	1935	2	A59286 myosin heavy chain
67	60	14.5	258	2	S58159 hypothetical prote
68	60	14.5	324	2	T05429 hypothetical prote
69	60	14.5	343	2	T02399 hypothetical prote
70	60	14.5	349	2	T30952 hypothetical prote
71	60	14.5	586	2	B84434 hypothetical prote
72	60	14.5	606	2	A72429 oligopeptide ABC t
73	60	14.5	728	2	A86453 CDS protein P9L11
74	60	14.5	755	2	T46411 hypothetical prote
75	59.5	14.3	365	2	B54128 hypothetical prote

ALIGNMENTS

RESULT 1
A85954 hypothetical protein y9gX [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954
R:Perma, N.T., Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, B.U.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Restrictions: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: y9gX
C:Superfamily: fe(II) trafficking protein y9gX
Query Match 95.2%; Score 395; DB 2; Length 91;

Best Local Similarity 94.9%; Pred. No. 7.9e-36;
Matches 74; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60
Db 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60

Qy 61 EHRKLEQEMVQPLFEKG 78
Db 61 EHRKLEQEMVQPLFEKG 78

RESULT 2
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65082
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein YggX

Query Match 95.2%; Score 395; DB 2; Length 91;
Best Local Similarity 94.9%; Pred. No. 7.9e-36;
Matches 74; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60
Db 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60

Qy 61 EHRKLEQEMVQPLFEKG 78
Db 61 EHRKLEQEMVQPLFEKG 78

RESULT 3
F91108
hypothetical protein Ecs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C:Accession: F91108
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaewara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <HAY>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA037261.1;
A:Experimental source: strain O157:H7, substrain R1MD 050952
C:Genetics:
A:Gene: Ecs3838
C:Superfamily: fe(II) trafficking protein YggX

Query Match 95.2%; Score 395; DB 2; Length 91;
Best Local Similarity 94.9%; Pred. No. 7.9e-36;
Matches 74; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60
Db 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60

Qy 61 EHRKLEQEMVQPLFEKG 78
Db 61 EHRKLEQEMVQPLFEKG 78

RESULT 4
AH0879
conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A>Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C:Accession: AH0879
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
. S.; Mole, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Farrar, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <PAR>
A:Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CA002936.1; PID:G16504189;
C:Genetics:
A:Gene: STY3266
C:Superfamily: fe(II) trafficking protein YggX

Query Match 93.0%; Score 386; DB 2; Length 91;
Best Local Similarity 91.0%; Pred. No. 7.4e-35;
Matches 71; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60
Db 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60

Qy 61 EHRKLEQEMVQPLFEKG 78
Db 61 EHRKLEQEMVQPLFEKG 78

RESULT 5
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: C82320
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82320
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <HEI>
A:Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:99654871; PIDN:
A:Experimental source: serogroup O1, strain N16961, biotype El Tor
C:Genetics:
A:Gene: VC0451
A:Map position: 1
C:Superfamily: fe(II) trafficking protein YggX

Query Match 84.3%; Score 350; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 5.8e-31;
Matches 65; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MSRTTFCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60
Db 1 MAAVTCPTLQREADGDFOLYPGELGKRIYNEISKEMAWQOHKQTMLINEKLSMNP 60

Qy 61 EHRKLEQEMVQPLFEKG 78

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 / Search time 57.4784 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-19
Perfect score: 415
Sequence: 1 MSRTFTFLQREADQDFQ.....NPEHRLLEQEWVFLPEGR 78

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: uniprot_05.80:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	390	94.0	90	1	FERP_ECO57
2	390	94.0	90	1	FERP_ECO57
3	390	94.0	90	1	FERP_ECO57
4	390	94.0	90	1	FERP_ECO57
5	381	91.8	90	1	FERP_SALCH
6	381	91.8	90	1	FERP_SALCH
7	381	91.8	90	1	FERP_SALCH
8	381	91.8	90	1	FERP_SALCH
9	362	87.2	90	1	FERP_EWVFL
10	350	84.3	90	1	FERP_EWVFL
11	350	84.3	90	1	FERP_EWVFL
12	349	84.1	90	1	FERP_EWVFL
13	348	83.9	90	1	FERP_EWVFL
14	348	83.9	90	1	FERP_EWVFL
15	345	83.1	90	1	FERP_EWVFL
16	342	82.4	90	1	FERP_EWVFL
17	337	81.2	90	1	FERP_EWVFL
18	326	78.6	94	1	FERP_EWVFL
19	326	78.6	94	1	FERP_EWVFL
20	325	78.3	90	1	FERP_EWVFL
21	325	78.3	90	1	FERP_EWVFL
22	325	78.3	90	1	FERP_EWVFL
23	317	76.4	90	1	FERP_EWVFL
24	304	73.3	90	1	FERP_EWVFL
25	292	70.4	90	1	FERP_EWVFL
26	256	61.7	77	1	FERP_EWVFL
27	240	55.8	78	1	FERP_EWVFL
28	232	55.2	91	1	FERP_EWVFL
29	229	55.2	92	1	FERP_EWVFL
30	227	54.7	90	1	FERP_EWVFL
31	223	53.7	92	1	FERP_EWVFL

32	223	53.7	92	2	Q4UW14_XANTCP
33	222	53.5	90	1	FERP_BORBR
34	222	53.5	90	1	FERP_BORBR
35	222	53.5	90	1	FERP_BORBR
36	221	53.3	78	1	FERP_WIGBR
37	220	53.0	90	1	FERP_XYFLA
38	217	52.3	90	1	FERP_XYFLA
39	214.5	51.7	89	1	FERP_LEGPA
40	214.5	51.7	89	1	FERP_LEGPA
41	214.5	51.7	89	1	FERP_LEGPA
42	211	50.8	90	1	FERP_PSEAB
43	210	50.6	88	1	FERP_NEIGI
44	210	50.6	88	1	FERP_NEIMA
45	210	50.6	88	1	FERP_NEIMA
46	205	49.4	87	1	FERP_BURMA
47	204	49.2	90	2	Q4J228_AZOVI
48	201	48.4	87	1	FERP_FRATF
49	200	48.2	79	1	FERP_CANBR
50	198	47.7	91	2	Q4LS19_9BURK
51	197.5	47.6	90	1	FERP_PSEBP
52	197.5	47.6	91	1	FERP_BURMA
53	197.5	47.6	91	1	FERP_BURMA
54	197	47.5	90	1	FERP_CHRVO
55	195.5	47.1	90	1	FERP_NITRU
56	195	47.0	90	1	FERP_PSEBM
57	195	47.0	90	2	Q4ZLP3_PSEBY
58	189	45.5	90	1	FERP_METCA
59	188.5	45.4	90	2	Q6T7F6_PSEFL
60	188.5	45.4	90	2	Q4KJ22_PSEBF
61	188.5	45.4	91	1	FERP_RALSO
62	184	44.3	90	1	FERP_ACIAO
63	156	37.6	92	2	Q4NMQ4_9BELT
64	140	33.7	96	2	Q4FVJ7_9GAMM
65	88	21.2	482	2	Q5WU11_9BORM
66	81.5	19.6	514	2	Q6A1Z9_DSPPS
67	77.5	18.7	1638	2	Q7KPP4_CABEL
68	77.5	18.7	2140	2	Q6BEM2_CABEL
69	77.5	18.7	2488	2	Q61528_CABEL
70	75.5	18.2	486	2	Q7WXS1_ALCEU
71	72.5	17.5	209	2	Q61A16_CABBR
72	72.5	17.5	508	2	Q7NSFO_CHRVO
73	72.5	17.3	265	2	Q9WV08_SULISO
74	72	17.3	265	2	Q9W207_ARATH
75	71.5	17.2	345	2	Q55821_9FLAV

ALIGNMENTS

RESULT 1
FERP_ECO57
ID FERP_ECO57 STANDARD; PRT; 90 AA.
AC POA8P4; P52065; (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+)-trafficking protein.
GN Name=yggX; OrderedLocustNames=24307; RCSB3838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perra N.T., Plunkett G., III, Burland V., Mau B., Glaesner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kitchpatrick H.A.,
Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

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RL Nature 409:529-533(2001).
RN [2]
RC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC.
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kubura S., Shiba T., Hattori M., Shingawa H.,
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL: AB005174; AAG58093.1; -; Genomic DNA.
CC EMBL: BA000007; BAB37261.1; -; Genomic DNA.
CC PIR: A85954; A85954.
CC PIR: F91108; F91108.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; Y9GX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe traffic_Y9GX; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome: Iron.
CC INIT_MET 0
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;

Query Match 94.0%; Score 390; DB 1; Length 90;
Best Local Similarity 94.8%; Pred. No. 2,8e-35;
Matches 73; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREAGDGFOLYPGELGKRIYNEISKAWAOWHOKQTMLINEKSLSNMPE 61
DB 1 SRTIFCTFLQREAGDGFOLYPGELGKRIYNEISKAWAOWHOKQTMLINEKSLSNMNAE 60
QY 62 HRKLEQEMVNFLEBKG 78
DB 61 HRKLEQEMVNFLEBKG 77

RESULT 2
FETP_ECOL6 STANDARD; PRT; 90 AA.
AC Q8FB19;
ID FETP_ECOL6 STANDARD; PRT; 90 AA.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gx; OrderedLocNames=c3550;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=06:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raeko D., Buckles B.L., Liu S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.U., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli."

```

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RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL: AB016766; AAN01998.1; -; Genomic DNA.
CC SMR: Q8FE19; 1-90.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; Y9GX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe traffic_Y9GX; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome: Iron.
CC INIT_MET 0
CC SEQUENCE 90 AA; 10805 MW; D7C66C2A35B63692 CRC64;

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Best Local Similarity 94.8%; Pred. No. 2,8e-35;
Matches 73; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREAGDGFOLYPGELGKRIYNEISKAWAOWHOKQTMLINEKSLSNMPE 61
DB 1 SRTIFCTFLQREAGDGFOLYPGELGKRIYNEISKAWAOWHOKQTMLINEKSLSNMNAE 60
QY 62 HRKLEQEMVNFLEBKG 78
DB 61 HRKLEQEMVNFLEBKG 77

RESULT 3
FETP_ECOL1 STANDARD; PRT; 90 AA.
AC P0A8F3; P52065;
ID FETP_ECOL1 STANDARD; PRT; 90 AA.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gx; OrderedLocNames=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12."
RL Electrophoresis 18:1259-1313(1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wasinger V.C., Humphrey-Smith I.;

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 / Search time 15.8132 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-19
Perfect score: 415
Sequence: 1 MSRRIFCTPLQREADQDFQ.....NPEHRKLEQEWVPLFGK 78

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/ECTUS COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	415	100.0	107	2	US-09-489-039A-11962
2	347	83.6	93	2	US-09-543-681A-5443
3	211	50.8	122	2	US-09-252-991A-23355
4	187	45.1	92	2	US-09-328-352-5456
5	134	32.3	110	2	US-09-540-236-2859
6	68.5	16.5	548	2	US-09-167-299-3
7	64	15.4	1214	2	US-10-164-595-24
8	63	15.2	325	2	US-09-134-000C-4346
9	62	14.9	331	2	US-09-328-352-6400
10	62	14.9	1741	2	US-09-902-540-11253
11	61	14.7	233	1	US-08-557-309B-40
12	61	14.7	233	2	US-08-834-306-40
13	61	14.7	233	2	US-08-993-674A-40
14	61	14.7	473	2	US-09-252-991A-24473
15	61	14.7	474	2	US-09-252-991A-24473
16	61	14.7	546	1	US-08-533-669A-2
17	61	14.7	546	2	US-09-183-861-2
18	61	14.7	546	2	US-09-022-765-2
19	61	14.7	546	2	US-09-551-974A-2
20	61	14.7	546	2	US-09-565-501A-2
21	61	14.7	546	2	US-09-639-206A-2
22	61	14.7	546	2	US-09-874-923-2
23	61	14.7	546	2	US-08-798-841-2
24	61	14.7	859	2	US-09-538-092-206
25	61	14.7	982	2	US-09-551-974A-95
26	61	14.7	982	2	US-09-565-501A-95
27	61	14.7	982	2	US-09-639-206A-95

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709 2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 100.0%; Score 415; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2.5e-48;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 60
DB 17 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 76

QY 61 EHRKLLQEQMVQFLPEGK 78
DB 77 EHRKLLQEQMVQFLPEGK 94

RESULT 2
US-09-543-681A-5443

; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 83.6%; Score 347; DB 2; Length 93;
Best Local Similarity 84.4%; Pred. No. 3.3e-39;
Matches 65; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 60
DB 4 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 63

QY 61 EHRKLLQEQMVQFLPEG 77
DB 64 DDRKLLQEQMVQFLPEG 80

RESULT 3
US-09-252-991A-23355

; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 50.8%; Score 211; DB 2; Length 122;
Best Local Similarity 54.1%; Pred. No. 1.2e-20;
Matches 40; Conservative 11; Mismatches 23; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 60

DB 33 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 92

QY 61 EHRKLLQEQMVQFL 74
DB 93 EDRKFLQEQMDKFL 106

RESULT 4
US-09-328-352-5456

; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 45.1%; Score 187; DB 2; Length 92;
Best Local Similarity 43.8%; Pred. No. 1.4e-17;
Matches 32; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 60
DB 4 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 63

QY 61 EHRKLLQEQMVQFL 73
DB 64 EHRKLLQEQMVQFL 76

RESULT 5
US-09-540-236-2859

; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 32.3%; Score 134; DB 2; Length 110;
Best Local Similarity 38.4%; Pred. No. 2.7e-10;
Matches 28; Conservative 13; Mismatches 32; Indels 0; Gaps 0;

QY 5 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 64
DB 25 MSRTIFCTFLQREADGQDFOLYPGELGKRIYNEISKEAMAOHQKOTMLINEKLSMNP 84

QY 65 LLEQEMVQFLPEG 77
DB 85 YLNEQREKFLDNG 97

RESULT 6
US-09-167-299-3
; Sequence 3, Application US/09167299

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 49.3941 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502a-19
Perfect score: 415
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	395	95.2	91	3	US-09-955-502-13
5	386	93.0	88	3	US-09-955-502-15
6	386	93.0	91	3	US-09-955-502-14
7	386	93.0	91	3	US-09-955-502-16
8	386	93.0	91	3	US-09-955-502-17
9	386	93.0	91	3	US-09-955-502-18
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11	342	82.4	90	3	US-09-955-502-20
12	327	78.8	87	3	US-09-955-502-8
13	325	78.3	87	3	US-09-955-502-7
14	316	76.4	87	3	US-09-955-502-6
15	316	76.4	91	3	US-09-955-502-5
16	292	70.4	88	3	US-09-955-502-9
17	256	61.7	76	3	US-09-955-502-21
18	227	54.7	88	3	US-09-955-502-33
19	222	53.5	86	3	US-09-955-502-4
20	222	53.5	87	3	US-09-955-502-2
21	222	53.5	87	3	US-09-955-502-3
22	220	53.0	89	3	US-09-955-502-22
23	211	50.8	87	3	US-09-955-502-25
24	210	50.6	88	3	US-09-955-502-26
25	210	50.6	88	3	US-09-955-502-27
26	210	50.6	88	3	US-09-955-502-28
27	197.5	47.6	87	3	US-09-955-502-24

28 197.5 47.6 87 3 US-09-955-502-29 Sequence 29, Appl
29 197.5 47.6 87 3 US-09-955-502-30 Sequence 30, Appl
30 196 47.2 87 3 US-09-955-502-31 Sequence 31, Appl
31 195 47.0 90 3 US-09-955-502-23 Sequence 23, Appl
32 189 45.5 87 3 US-09-955-502-32 Sequence 32, Appl
33 69.5 16.7 166 5 US-10-482-706-269 Sequence 269, Appl
34 68.5 16.5 507 4 US-10-424-599-279212 Sequence 279212, Appl
35 68.5 16.5 507 4 US-10-282-122A-68134 Sequence 68134, A
36 66.5 16.0 102 3 US-09-864-408A-768 Sequence 768, App
37 66.5 16.0 546 4 US-10-282-122A-66021 Sequence 66021, A
38 65 15.7 679 5 US-10-805-684-105 Sequence 105, App
39 64 15.4 236 4 US-10-424-599-266117 Sequence 266117, Appl
40 64 15.4 764 5 US-10-416-330-37 Sequence 37, Appl
41 64 15.4 764 5 US-10-491-467-15 Sequence 15, Appl
42 64 15.4 1206 4 US-10-085-198-144 Sequence 144, App
43 64 15.4 1214 5 US-10-717-665-24 Sequence 24, Appl
44 63.5 15.3 105 3 US-09-768-826-47 Sequence 47, Appl
45 63.5 15.3 105 3 US-09-833-245-2262 Sequence 2262, Ap
46 63.5 15.3 105 5 US-10-874-484-47 Sequence 47, Appl
47 63.5 15.3 419 5 US-10-450-763-51056 Sequence 51056, A
48 63.5 15.3 500 4 US-10-437-963-170681 Sequence 170681, A
49 63.5 15.3 505 3 US-09-938-803-20 Sequence 20, Appl
50 63.5 15.3 505 5 US-10-821-273-78 Sequence 78, Appl
51 63.5 15.3 505 5 US-10-993-986-20 Sequence 20, Appl
52 63 15.2 315 4 US-10-282-122A-57222 Sequence 57222, A
53 63 15.2 315 5 US-10-958-216-464 Sequence 464, App
54 63 15.2 315 5 US-10-958-216-464 Sequence 464, App
55 63 15.2 856 4 US-10-408-765A-2006 Sequence 2006, Ap
56 62.5 15.1 95 4 US-10-416-314-27 Sequence 27, Appl
57 62 14.9 258 4 US-10-468-091-1 Sequence 45018, A
58 62 14.9 321 4 US-10-282-122A-45018 Sequence 45018, A
59 62 14.9 1293 4 US-10-697-036-41 Sequence 41, Appl
60 61.5 14.8 204 5 US-10-756-149-5207 Sequence 5207, Ap
61 61.5 14.8 242 4 US-10-393-840-55 Sequence 55, Appl
62 61.5 14.8 511 4 US-10-282-122A-50464 Sequence 50464, A
63 61.5 14.8 1242 4 US-09-791-254-2 Sequence 2, Appl
64 61 14.7 172 5 US-10-450-763-34132 Sequence 34132, A
65 61 14.7 176 4 US-10-425-115-1346175 Sequence 1346175, A
66 61 14.7 330 3 US-09-815-245-113119 Sequence 113119, A
67 61 14.7 330 4 US-10-282-122A-58687 Sequence 58687, A
68 61 14.7 331 5 US-10-739-930-8330 Sequence 8330, Ap
69 61 14.7 487 4 US-10-425-115-358829 Sequence 358829, Ap
70 61 14.7 545 5 US-10-732-923-9369 Sequence 9369, Ap
71 61 14.7 546 3 US-09-874-923-2 Sequence 2, Appl
72 61 14.7 546 4 US-09-991-496-2 Sequence 2, Appl
73 61 14.7 546 4 US-10-098-732A-71 Sequence 71, Appl
74 61 14.7 714 5 US-10-732-923-23069 Sequence 23069, A
75 61 14.7 926 3 US-09-991-496-128 Sequence 128, App

ALIGNMENTS

RESULT 1
US-09-955-502-19
Sequence 19, Application US/09955502
Patent No. US70020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 78
TYPE: PRT
ORGANISM: Klebsiella pneumoniae

GenCore version 5.1.7
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Run on: March 1, 2006, 00:15:00 ; Search time 4.35308 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502a-19

Perfect score: 415

Sequence: 1 MSRTIFCTPLQREAGDQDFQ.....NPERKLEQEWVCFLEFGK 78

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Listing first 75 summaries

Database : Published Applications_AA_New:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	210	50.6	88	US-10-467-657-968	Sequence 968, App
2	67	16.1	593	US-11-194-246-317	Sequence 317, App
3	60.5	14.6	752	US-11-072-512-3003	Sequence 3003, App
4	59.5	14.3	834	US-10-453-372-658	Sequence 658, App
5	59.5	14.3	1088	US-11-098-686-10718	Sequence 10718, A
6	59	14.2	251	US-11-054-515-1496	Sequence 1496, App
7	58.5	14.1	508	US-11-072-512-2186	Sequence 2186, App
8	58.5	14.1	1432	US-10-510-366-218	Sequence 218, App
9	57.5	13.9	336	US-10-453-372-640	Sequence 640, App
10	57.5	13.9	695	US-10-453-372-648	Sequence 648, App
11	57.5	13.9	700	US-10-995-561-922	Sequence 922, App
12	57.5	13.9	700	US-10-995-561-924	Sequence 924, App
13	57.5	13.9	793	US-10-453-372-656	Sequence 656, App
14	57.5	13.9	793	US-10-995-561-925	Sequence 925, App
15	57.5	13.9	804	US-10-453-372-650	Sequence 650, App
16	57.5	13.9	847	US-10-453-372-654	Sequence 654, App
17	57.5	13.9	857	US-10-453-372-652	Sequence 652, App
18	57.5	13.9	905	US-10-453-372-658	Sequence 658, App
19	57.5	13.9	905	US-10-453-372-662	Sequence 662, App
20	57.5	13.9	905	US-10-453-372-664	Sequence 664, App
21	57.5	13.9	963	US-10-995-561-923	Sequence 923, App
22	57.5	13.9	963	US-10-453-372-660	Sequence 660, App
23	57.5	13.9	1012	US-10-453-372-646	Sequence 646, App
24	57	13.7	235	US-11-098-686-11270	Sequence 11270, A
25	57	13.7	395	US-11-009-658-46	Sequence 46, App1

26 56.5 13.6 397 7 US-11-022-562-223 Sequence 223, App

27 56 13.5 257 7 US-11-054-515-1710 Sequence 1710, App

28 56 13.5 341 7 US-11-055-822-1054 Sequence 1054, App

29 55.5 13.4 1995 7 US-11-069-834-60 Sequence 60, App1

30 55 13.3 264 6 US-10-821-234-1555 Sequence 1555, App

31 55 13.3 404 7 US-11-009-658-48 Sequence 48, App1

32 55 13.3 893 7 US-11-072-512-3504 Sequence 3504, App

33 54.5 13.1 524 7 US-11-118-809-4 Sequence 4, App1

34 54 13.0 103 6 US-10-467-657-4178 Sequence 4178, App

35 54 13.0 187 6 US-10-793-626-2226 Sequence 2226, App

36 54 13.0 480 6 US-10-510-386-12 Sequence 12, App1

37 53.5 12.9 166 7 US-11-175-690-104 Sequence 104, App

38 53.5 12.9 774 7 US-11-070-627-7 Sequence 7, App1

39 53.5 12.9 1299 6 US-10-821-234-1145 Sequence 1145, App

40 53.5 12.9 1404 6 US-10-878-556A-169 Sequence 169, App

41 53 12.8 189 7 US-11-071-262-1 Sequence 1, App1

42 52.5 12.7 415 7 US-11-072-512-2624 Sequence 2624, App

43 52.5 12.7 504 7 US-11-072-512-3467 Sequence 3467, App

44 52.5 12.7 1098 7 US-11-072-512-3280 Sequence 3280, App

45 52 12.5 898 7 US-11-099-691-7 Sequence 7, App1

46 52 12.5 898 7 US-11-124-367A-330 Sequence 330, App

47 52 12.5 898 7 US-11-124-367A-333 Sequence 333, App

48 51.5 12.4 285 6 US-10-467-657-222 Sequence 222, App

49 51.5 12.4 285 6 US-10-467-657-8230 Sequence 8230, App

50 51.5 12.4 336 7 US-11-165-226-135 Sequence 125, App

51 51.5 12.4 571 7 US-11-072-512-3814 Sequence 3814, App

52 51.5 12.4 635 7 US-11-098-686-10433 Sequence 10433, App

53 51.5 12.4 654 7 US-11-110-082-24 Sequence 24, App1

54 51 12.3 117 7 US-11-004-590-178 Sequence 178, App

55 51 12.3 117 7 US-11-004-590-179 Sequence 179, App

56 51 12.3 117 7 US-11-004-590-188 Sequence 188, App

57 51 12.3 117 7 US-11-004-590-210 Sequence 210, App

58 51 12.3 166 7 US-11-132-722-45 Sequence 45, App1

59 51 12.3 166 7 US-11-176-830-166 Sequence 186, App

60 51 12.3 166 7 US-11-172-409-2 Sequence 2, App1

61 51 12.3 189 7 US-11-147-492-6 Sequence 6, App1

62 51 12.3 189 7 US-11-147-492-22 Sequence 22, App1

63 51 12.3 194 7 US-11-072-512-2806 Sequence 2906, App

64 51 12.3 251 7 US-11-009-658-36 Sequence 36, App1

65 51 12.3 311 7 US-11-156-084-307 Sequence 307, App

66 51 12.3 317 7 US-11-156-084-295 Sequence 295, App

67 51 12.3 332 6 US-10-793-626-550 Sequence 550, App

68 51 12.3 456 7 US-11-069-642-8 Sequence 8, App1

69 51 12.3 488 7 US-11-169-041-197 Sequence 197, App

70 51 12.3 600 7 US-11-072-512-3845 Sequence 3845, App

71 51 12.3 618 7 US-11-110-082-25 Sequence 25, App1

72 51 12.3 1034 7 US-11-072-512-2343 Sequence 2343, App

73 51 12.3 1501 6 US-10-793-626-2850 Sequence 2850, App

74 51 12.3 2665 7 US-11-124-366A-214 Sequence 214, App

75 51 12.3 2668 7 US-11-124-366A-215 Sequence 215, App

RESULT 1

US-10-467-657-968

; Sequence 968, Application US/10467657

; Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASTIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

PRIOR FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqMan99, version 1.04

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; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match
Best Local Similarity 50.6%; Score 210; DB 6; Length 88;
Matches 38; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MSRTCTFLREADGDFOLYPGELGKRIYNEISKAWOMOHKOTMLINEKLSMNP 60
Db 1 MARWVFCVKLNKEAGMFPPLPNELGKRIFENVSGEAMAAVTRHQTMLINENRLSLDP 60

Qy 61 EHRKLLBQMNQVFLF 75
Db 61 RAREYLAQQMEQYFF 75

RESULT 2
US-11-194-246-317
; Sequence 317, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Stefan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 317
; LENGTH: 593
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match
Best Local Similarity 16.1%; Score 67; DB 7; Length 593;
Matches 12; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 35 SKEAWOMOHKOTMLINEKLSMNP 61
Db 296 SKQEWRYWEAKODILKNTKGLTRLSKE 322

RESULT 3
US-11-072-512-3003
; Sequence 3003, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
```

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; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3003
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3003

Query Match
Best Local Similarity 14.6%; Score 60.5; DB 7; Length 752;
Matches 11; Conservative 6; Mismatches 10; Indels 5; Gaps 1;

Qy 39 WAOQOHKOTMLINEKLSMNPPEHRLKEQEM 70
Db 698 WRNMQHK-----NMKSNMFDNPFVLTKEEDL 724

RESULT 4
US-10-453-372-658
; Sequence 658, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqIst version 0.1
; SEQ ID NO 658
; LENGTH: 834
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-658

Query Match
Best Local Similarity 14.3%; Score 59.5; DB 6; Length 834;
Matches 11; Conservative 5; Mismatches 10; Indels 5; Gaps 1;

Qy 39 WAOQOHKOTMLINEKLSMNPPEHRLKEOE 69
```


PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX Sequence 90 AA;
SQ

Query Match 100.0%; Score 473; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTTFTCTFLKCDARODPOLYPGEIGKRIYNEISKAMSWITKOTMLINEKLSMMNI 60
DB 1 MSRTTFTCTFLKCDARODPOLYPGEIGKRIYNEISKAMSWITKOTMLINEKLSMMNI 60

OY 61 EDRKLLBQEMVNFLEFGQDVHIAGYTPPSK 90
DB 61 EDRKLLBQEMVNFLEFGQDVHIAGYTPPSK 90

RESULT 2
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
XX ABO65445;
XX
XX 29-JUN-2004 (first entry)
XX
XX *Klebsiella pneumoniae* polypeptide seqid 11962.
XX
XX Recombinant expression vector; transcription regulatory element;
XX *Klebsiella pneumoniae* protein; antibacterial; Vaccine.
XX
XX *Klebsiella pneumoniae*.
XX
XX US610836-B1.
XX
XX 26-AUG-2003.
XX
XX 27-JAN-2000; 2000US-00489039.
XX
XX 29-JAN-1999; 99US-0117747P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton GL, Osborne M;
XX
XX WPI; 2003-895346/82.
DR

DR N-PSDB; ACH98996.
XX
XX New nucleic acid encoding a *Klebsiella pneumoniae* polypeptide, useful for
PT preparing a vaccine composition against *Klebsiella pneumoniae*.
XX
XX Disclosure; SEQ ID NO 11962; 932pp; English.
XX

XX The invention describes a new isolated nucleic acid encoding a *Klebsiella*
CC *pneumoniae* polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against *Klebsiella pneumoniae*. This is the amino acid sequence of a
CC *Klebsiella pneumoniae* polypeptide of the invention
XX

SQ Sequence 107 AA;

Query Match 84.6%; Score 400; DB 7; Length 107;
Best Local Similarity 83.3%; Pred. No. 1.5e-39;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

OY 1 MSRTTFTCTFLKCDARODPOLYPGEIGKRIYNEISKAMSWITKOTMLINEKLSMMNI 60
DB 17 MSRTTFTCTFLKCDARODPOLYPGEIGKRIYNEISKAMSWITKOTMLINEKLSMMNP 76

OY 61 EDRKLLBQEMVNFLEFGQDVHIAGYTPPSK 90
DB 77 EDRKLLBQEMVNFLEFGQDVHIAGYTPPSK 106

RESULT 3
ABB78158
ID ABB78158 standard; protein; 91 AA.
XX
XX ABB78158;
XX

XX 05-NOV-2002 (first entry)
XX

XX Amino acid sequence of a YggX homologue.
XX

XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX

XX Unidentified.
XX

XX US2002072118-A1.
XX

XX 13-JUN-2002.
XX

XX 18-SEP-2001; 2001US-00955502.
XX

XX 22-SEP-2000; 2000US-0234588P.
XX

XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX

XX Downs D, Gralnick JA;
XX

XX WPI; 2002-589476/63.
XX

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX

XX Example; Fig 1A; 16pp; English.
XX

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.84055 Seconds

(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-20

Perfect score: 473

Sequence: 1 MSRTIFCTFLKKDAERQDFQ.....VNLFEGQDVHAGYTPPSK 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

1: PIR_80:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	473	100.0	90	2 A10116	conserved hypothet
2	396	83.7	91	2 A85954	hypothetical prote
3	396	83.7	91	2 A65082	hypothetical prote
4	393	83.1	91	2 F91108	hypothetical prote
5	393	83.1	91	2 AH0879	conserved hypothet
6	374	79.1	90	2 C64013	hypothetical prote
7	366	77.4	90	2 C82320	conserved hypothet
8	256	54.1	93	2 B84994	hypothetical prote
9	221	46.7	90	2 H85003	conserved hypothet
10	203	42.9	105	2 C82624	conserved hypothet
11	198	41.9	88	2 H81014	conserved hypothet
12	81	17.1	2672	2 A48126	translation activa
13	76.5	16.2	511	2 A99574	ABC transporter at
14	74	15.6	403	2 B89808	hypothetical prote
15	71.5	15.1	1008	2 H72310	conserved hypothet
16	70	14.8	265	2 T46013	hypothetical prote
17	70	14.8	1119	2 T18491	hypothetical prote
18	69.5	14.7	996	2 A71080	hypothetical prote
19	69	14.6	1386	1 A71080	DNA-directed RNA p
20	68.5	14.5	165	2 A81382	shikimate kinase (
21	68	14.4	344	2 D70126	hypothetical prote
22	68	14.4	583	2 T48365	hypothetical prote
23	68	14.4	820	2 G88996	protein C17B7.5 (I
24	67.5	14.3	160	2 E70416	hypothetical prote
25	67.5	14.3	336	2 C64468	hypothetical prote
26	67.5	14.3	617	2 B71071	probable prollyl en
27	67.5	14.3	629	2 B83107	chemotactic transd
28	67	14.2	394	2 B70206	hypothetical prote
29	66.5	14.1	139	2 B97709	hypothetical prote

30	66.5	14.1	420	2 A25876	vitellogenin III p
31	66.5	14.1	648	2 A71647	glycine-tRNA ligas
32	66	14.0	705	2 T47949	hypothetical prote
33	66	14.0	799	2 T02656	probable salt-indu
34	65.5	13.8	91	2 H90521	hypothetical prote
35	65.5	13.8	688	2 S57131	hypothetical prote
36	65	13.7	118	2 G64302	hypothetical prote
37	65	13.7	411	2 A48946	aspartate kinase (
38	65	13.7	738	2 B69863	two-component sens
39	65	13.7	2101	2 A42184	nuclear mitotic ap
40	64.5	13.6	245	2 AG2300	hypothetical prote
41	64	13.5	158	2 AS9102	hypothetical prote
42	64	13.5	235	2 AD1735	hypothetical prote
43	64	13.5	346	2 F97871	uroporphyrinogen d
44	64	13.5	1611	1 WMTMPV	183k protein - pep
45	63.5	13.4	548	2 A54510	63k antigen - nema
46	63.5	13.4	548	2 A28209	60k filarial antiq
47	63.5	13.4	715	2 D84480	Mutator-like trans
48	63.5	13.4	884	1 RNBP73	DNA-directed RNA p
49	63.5	13.4	1010	2 F75134	hypothetical prote
50	63.5	13.4	1119	2 T15842	hypothetical prote
51	63	13.3	254	2 A64437	hypothetical prote
52	63	13.3	264	2 G89808	hypothetical prote
53	63	13.3	269	2 A81286	hypothetical prote
54	63	13.3	507	2 C81063	fumate hydratase
55	63	13.3	546	2 A81807	hypothetical prote
56	63	13.3	821	1 A39616	protein kinase RAD
57	63	13.3	974	2 A40580	iodester maternal-
58	63	13.3	1027	2 T27970	hypothetical prote
59	62.5	13.2	173	2 H86869	hypothetical prote
60	62.5	13.2	259	2 D69998	lysophospholipase
61	62.5	13.2	477	2 B61378	leukotoxin secreti
62	62.5	13.2	674	2 D97864	glycine-tRNA ligas
63	62.5	13.2	869	2 T24222	hypothetical prote
64	62.5	13.2	1939	2 T18372	repeat organellar
65	62	13.1	213	2 B83688	hypothetical prote
66	62	13.1	142	2 B71853	probable biotin ac
67	62	13.1	224	2 C64240	mobiliation prote
68	62	13.1	353	1 FOMVGR	gag polyprotein -
69	62	13.1	375	2 A36898	maapin - human
70	62	13.1	498	2 C90413	dihydropterolate sy
71	62	13.1	593	2 C64097	probable soluble I
72	62	13.1	1030	2 T37868	probable helicase
73	61.5	13.0	222	2 S62001	MR5 protein - Yea
74	61.5	13.0	287	2 P82265	conserved hypothet
75	61.5	13.0	339	2 A90395	conserved hypothet

ALIGNMENTS

RESULT 1
A10116
conserved hypothetical protein YP00953 [imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: A10116
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tiltall, R.W.; Holden, M.T.G.; Prentice, M.B.
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
H., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; PMID:21470413; PMID:11586360
A:Accession: A10116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <R>
A:Cross-references: UNIPARC:UPI00000DCC4; GB:AL590842; PIDN:CA89796.1; PID:g15979022;
C:Gene: YP00953
C:Superfamily: Fe(II) trafficking protein Y99X
Query Match 100.0%; Score 473; DB 2; Length 90;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 / Search time 66.3212 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-20

Perfect score: 473
Sequence: 1 MSRTIFCTFLKXDERQDFQ.....VNFLEGGDVHAGIYPPSK 90

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	100.0	90	1	PERP_YERPE
2	466	98.5	90	1	PERP_YERPS
3	412	87.1	90	1	PERP_ERMCT
4	391	82.7	90	1	PERP_ECO57
5	391	82.7	90	1	PERP_ECOLI
6	391	82.7	90	1	PERP_SHIFL
7	388	82.0	90	1	PERP_SALCH
8	388	82.0	90	1	PERP_SALPA
9	388	82.0	90	1	PERP_SALTY
10	388	82.0	90	1	PERP_SALTY
11	387	81.8	90	1	PERP_PHOIL
12	379	80.1	90	1	PERP_PHOIL
13	377	79.7	90	1	PERP_PHOIR
14	374	79.1	90	1	PERP_HABIN
15	374	79.1	90	2	Q4GMD3_HABE18
16	366	77.4	90	1	PERP_VIBCH
17	362	76.5	90	1	PERP_VIBPA
18	357	75.5	90	1	PERP_VIBVY
19	357	75.5	90	1	PERP_VIBVY
20	355	75.1	90	1	PERP_PASMU
21	354	74.8	90	1	PERP_MANSM
22	351	74.2	90	1	PERP_HABRU
23	330	69.8	90	1	PERP_VIBFL
24	308	65.1	90	1	PERP_SHEON
25	305	64.5	90	1	PERP_IDILO
26	256	54.1	77	1	PERP_BUCAI
27	240	50.7	78	1	PERP_WIGGR
28	237	50.1	90	1	PERP_BORRA
29	237	50.1	90	1	PERP_BORRA
30	237	50.1	90	1	PERP_BORRA
31	234	49.5	78	1	PERP_BUCAP

32	233	49.3	90	1	PERP_COXBU	Q83d06 coxiella bu
33	228	48.2	90	1	PERP_NITRU	Q82xf2 nitromona
34	222.5	47.0	89	1	PERP_LEGPL	Q5wxc4 legionella
35	221	46.7	90	1	PERP_PSEAE	Q9nu36 pseudomonas
36	220	46.5	91	1	PERP_XANAC	Q8bjh7 xanthomonas
37	218.5	46.2	89	1	PERP_LEGPA	Q53x99 legionella
38	218.5	46.2	89	1	PERP_BUCGP	Q5zu80 legionella
39	216	45.7	87	1	PERP_BUCBP	Q89a44 buchnera ap
40	216	45.7	92	1	PERP_XANOR	Q59y22 xanthomonas
41	213	45.0	90	1	PERP_CHRYO	Q78x4 xanthomace
42	210	44.4	92	1	PERP_XANCP	Q8p829 xanthomonas
43	210	44.4	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
44	208	44.0	90	2	Q4J228_AZOVI	Q4j228 azotobacter
45	208	44.0	91	1	PERP_BURMA	Q62i19 burkholderi
46	208	44.0	91	1	PERP_BURPS	Q62i19 burkholderi
47	207	43.8	90	1	PERP_XYUFT	Q87d06 xyella fas
48	206	43.6	90	1	PERP_PSEEM	Q87u15 pseudomonas
49	206	43.6	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
50	206	43.6	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
51	206	43.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
52	203	42.9	90	1	PERP_XYUFA	Q9pc73 xyella fas
53	203	42.9	91	1	PERP_RALSO	Q8y010 ralsconia s
54	199	42.1	79	1	PERP_CANBF	Q7vrg9 candidatus
55	198	41.9	88	1	PERP_NEIG1	Q5f553 neisseria g
56	198	41.9	88	1	PERP_NEIMA	Q5f553 neisseria m
57	198	41.9	88	1	PERP_NEIMB	Q5f553 neisseria m
58	197	41.6	90	1	PERP_PSERK	Q88r49 pseudomonas
59	193	40.8	90	1	PERP_METCA	Q6oa17 methylococc
60	188	39.7	90	2	Q4KJ72_PSEF5	Q4kj72 pseudomonas
61	184	38.9	87	1	PERP_FRATY	Q5nhj8 firenclisella
62	167.5	35.4	90	1	PERP_FRIAT	Q6f6f3 actinobact
63	148	31.3	96	2	Q4FV17_9GAMM	Q4fv17 psychrobact
64	138	29.2	92	2	Q4NM04_9PELT	Q4nm04 anaromyxob
65	82	17.3	1555	2	Q9U0N0_PLAF7	Q9u0n0 plasmidium
66	81	17.1	2672	1	GN1_YEAST	P33892 saccharomyc
67	78.5	16.6	502	2	Q4T616_TETNG	Q4t616 tetrarodon n
68	77.5	16.4	452	2	Q8F6U1_LEPIN	Q8f6u1 leptospira
69	77.5	16.4	464	2	Q72P14_LEPIC	Q72p14 leptospira
70	77	16.3	2248	2	Q4UBA0_THRAN	Q4uba0 theileria a
71	76.5	16.2	511	2	Q98Q71_MYCFU	Q98q71 mycoplasma
72	76	16.1	2249	2	Q4MYU4_THRPA	Q4myu4 theileria p
73	75	15.9	1032	2	Q4XV22_PLACH	Q4xv22 plasmidium
74	74	15.6	330	2	Q8XK34_CLOPE	Q8xk34 clostridium
75	74	15.6	403	2	Q5H1P0_STPAC	Q5h1p0 strephylooc

ALIGNMENTS

RESULT 1	PERP_YERPE	STANDARD	PRT	90 AA.
AC	Q82HE7			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	OrderedLocNames=YPO0953, Y3340, YP3488;			
OS	Yersinia pestis.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Yersinia.			
OX	NCBI_TaxId=632;			
RV	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=CO-92 / Biovar Orientalis;			
RX	MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;			
RA	Parikhalli J., Wren B.W., Thomson N.R., Titchell R.W., Holden M.T.G.,			
RA	Pringle J.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,			
RA	Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,			
RA	Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,			
RA	Fellwell T., Hamlin N., Holtroyd S., Jagsle K., Karlyshev A.V.,			
RA	Leather S., Mouton S., Oyston P.C.F., Quail M.A., Rutherford K.M.,			
RA	Stimmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;			

RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Liss P.,
 Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
 Perry R.D.;
 RT "Genome sequence of *Yersinia pestis* KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 RP [3]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=91001 / Biovar Mediaevalis;
 RX PubMed=1536893;
 RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
 Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
 Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
 Yang H., Wang J., Huang P., Yang R.;
 RT "Complete genome sequence of *Yersinia pestis* strain 91001, an isolate
 avirulent to humans.";
 RL DNA Res. 11:179-197(2004).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 acquisition and iron-requiring processes, such as synthesis and/or
 repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL: AJ14145; CAC89796.1; -; Genomic DNA.
 DR EMBL: AB013935; AAM6890.1; -; Genomic DNA.
 DR EMBL: AB017140; AAS63643.1; -; Genomic DNA.
 DR SMR: Q8ZHE7; 1-90.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; Y9GX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 DR ProDom: PD029191; DUF495; 1.
 DR Complete proteome; Iron.
 KW CONFLICT 16
 FT PT 16
 SQ SEQUENCE 90 AA; 10707 MW; C7374E685653F65 CRC64;
 Query Match 100.0%; Score 473; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 6.5e-41;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTIFCTFLKDAERODPOLYPGEIGKRIYNEISKEAMSWITQTMLINEKLSMMNI 60
 DB 1 MSRTIFCTFLKDAERODPOLYPGEIGKRIYNEISKEAMSWITQTMLINEKLSMMNI 60
 QY 61 EDRKLLBOEMVNFLEFGQDVHIAGYTPPSK 90
 DB 61 EDRKLLBOEMVNFLEFGQDVHIAGYTPPSK 90
 RESULT 2
 FETP_YERPS STANDARD; PRT; 90 AA.
 AC Q666M3;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 GN Ordered locus names=YPMB3225;
 OS *Yersinia pseudotuberculosis*.

CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; *Yersinia*.
 CC NCBI_TaxID=633;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=IP32953 / Serotype I;
 RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
 RA Chain P.S.G., Carniel B., Larimer F.W., Lamerdin J., Stoutland P.O.,
 Regala W.M., Georgescu A.M., Verges L.M., Land M.L., Motin V.L.,
 Brubaker R.R., Fowler J., Hinebush J., Marceau M., Medigue C.,
 Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
 Raebide A., Hauser L.J., Garcia B.;
 RA "Insights into the evolution of *Yersinia pestis* through whole-genome
 comparison with *Yersinia pseudotuberculosis*.";
 RT Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 acquisition and iron-requiring processes, such as synthesis and/or
 repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL: BX936398; CAA22463.1; -; Genomic DNA.
 DR SMR: Q666M3; 1-90.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; Y9GX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 DR ProDom: PD029191; DUF495; 1.
 DR Complete proteome; Iron.
 KW CONFLICT 90 AA; 10608 MW; C7375E7954752B64 CRC64;
 SQ SEQUENCE 90 AA; 10608 MW; C7375E7954752B64 CRC64;
 Query Match 98.5%; Score 466; DB 1; Length 90;
 Best Local Similarity 98.9%; Pred. No. 3.4e-40;
 Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSRTIFCTFLKDAERODPOLYPGEIGKRIYNEISKEAMSWITQTMLINEKLSMMNI 60
 DB 1 MSRTIFCTFLKDAERODPOLYPGEIGKRIYNEISKEAMSWITQTMLINEKLSMMNI 60
 QY 61 EDRKLLBOEMVNFLEFGQDVHIAGYTPPSK 90
 DB 61 EDRKLLBOEMVNFLEFGQDVHIAGYTPPSK 90
 RESULT 3
 FETP_ERWCT STANDARD; PRT; 90 AA.
 AC Q6D8J9;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 GN Ordered locus names=ECA0975;
 OS *Erwinia carotovora* (subsp. atroseptica) (Pectobacterium atrosepticum).
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Pectobacterium.
 CC NCBI_TaxID=29471;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 Holvea M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 Ackin R., Bacon N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 Frazer A., Hance Z., Hauser H., Jagers K., Moulé S., Nozderczak H.,
 Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 : Search time 18.246 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-20

Perfect score: 473

Sequence: 1 MSRTIFCTPLKDAERQDFQ.....VNFLPBGQDVHAGYTPPSK 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	400	84.6	107	2	US-09-489-039A-11962
2	389	82.2	93	2	US-09-543-681A-5443
3	221	46.7	122	2	US-09-252-991A-23355
4	176.5	37.3	92	2	US-09-328-352-5456
5	143	30.2	110	2	US-09-540-236-2859
6	69.5	14.7	870	2	US-09-543-681A-4768
7	69	14.6	209	2	US-09-252-991A-20905
8	67.5	14.3	701	2	US-09-252-991A-23288
9	67	14.2	415	1	US-08-602-010A-10
10	67	14.2	415	1	US-08-680-726A-10
11	67	14.2	415	2	US-09-092-409-10
12	65	13.7	1559	1	US-07-684-135A-2
13	65	13.7	1559	2	US-09-949-016-10190
14	65	13.7	2101	1	US-08-466-390-4
15	65	13.7	2101	1	US-08-470-950-4
16	65	13.7	2101	1	US-08-467-781-4
17	65	13.7	2101	1	US-08-195-487-4
18	65	13.7	2101	1	US-08-483-924-4
19	65	13.7	2101	2	US-09-452-294-1
20	65	13.7	2101	2	US-09-296-662-32
21	65	13.7	2101	4	PCT-US93-06160-4
22	65	13.7	2107	2	US-09-949-016-7646
23	65	13.7	2107	2	US-09-949-016-7647
24	65	13.7	2115	2	US-09-296-662-33
25	64.5	13.6	242	2	US-08-908-332-1
26	64	13.5	184	2	US-09-325-932A-66
27	64	13.5	534	2	US-09-312-762A-5

28	64	13.5	1176	2	US-09-489-039A-8879	Sequence 8879, Ap
29	63.5	13.4	548	2	US-09-167-299-3	Sequence 3, Appli
30	63	13.3	240	2	US-08-908-332-9	Sequence 2, Appli
31	63	13.3	242	2	US-08-908-332-2	Sequence 2, Appli
32	63	13.3	776	1	US-08-198-446B-17	Sequence 17, Appl
33	63	13.3	776	1	US-08-870-693-17	Sequence 17, Appl
34	63	13.3	821	1	US-08-198-446B-6	Sequence 6, Appli
35	63	13.3	821	1	US-08-870-693-6	Sequence 6, Appli
36	62.5	13.2	217	2	US-09-746-352A-38	Sequence 38, Appl
37	62.5	13.2	259	2	US-09-355-166-21	Sequence 21, Appl
38	62.5	13.2	514	2	US-09-746-359A-39	Sequence 39, Appl
39	62.5	13.2	546	2	US-09-746-359A-37	Sequence 37, Appl
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41	62	13.1	375	1	US-08-477-108A-2	Sequence 2, Appli
42	62	13.1	375	1	US-08-477-112-2	Sequence 2, Appli
43	62	13.1	375	1	US-09-886-319A-4	Sequence 4, Appli
44	62	13.1	375	4	PCT-US93-08322-2	Sequence 4, Appli
45	61.5	13.0	329	2	US-09-602-787A-306	Sequence 306, App
46	61.5	13.0	459	2	US-09-602-787A-302	Sequence 302, App
47	61	12.9	550	2	US-09-107-532A-7201	Sequence 7201, Ap
48	61	12.9	920	2	US-09-934-866-52	Sequence 52, Appl
49	61	12.9	920	2	US-10-701-200-52	Sequence 52, Appl
50	61	12.9	922	2	US-10-104-047-2694	Sequence 2694, Ap
51	61	12.9	1575	2	US-09-917-254-83	Sequence 83, Appl
52	61	12.9	1575	2	US-09-949-016-6743	Sequence 6743, Ap
53	60.5	12.8	302	2	US-09-830-433A-34	Sequence 34, Appl
54	60	12.7	192	2	US-08-545-573A-9	Sequence 9, Appli
55	60	12.7	306	2	US-09-538-092-262	Sequence 262, App
56	60	12.7	556	2	US-10-012-896-1005	Sequence 1005, Ap
57	60	12.7	571	2	US-10-104-047-3814	Sequence 3814, Ap
58	60	12.7	837	2	US-10-012-231A-253	Sequence 253, App
59	60	12.7	837	2	US-10-015-389A-253	Sequence 253, App
60	60	12.7	837	2	US-10-006-768A-253	Sequence 253, App
61	60	12.7	837	2	US-10-015-671A-253	Sequence 253, App
62	60	12.7	837	2	US-10-015-393A-253	Sequence 253, App
63	60	12.7	837	2	US-10-011-833A-253	Sequence 253, App
64	60	12.7	837	2	US-10-006-041A-253	Sequence 253, App
65	60	12.7	837	2	US-10-012-064A-253	Sequence 253, App
66	59.5	12.6	308	2	US-09-248-796A-14928	Sequence 14928, A
67	59.5	12.6	310	2	US-09-489-039A-13674	Sequence 13674, A
68	59.5	12.6	532	1	US-08-657-192-9	Sequence 9, Appli
69	59.5	12.6	532	2	US-08-523-373-7	Sequence 7, Appli
70	59.5	12.6	604	2	US-09-248-796A-14489	Sequence 14489, A
71	59.5	12.6	796	2	US-08-868-669A-2	Sequence 2, Appli
72	59.5	12.6	796	2	US-09-757-014-2	Sequence 7862, Ap
73	59	12.5	217	2	US-09-543-681A-7862	Sequence 5001, Ap
74	59	12.5	228	2	US-09-328-352-5001	Sequence 8397, Ap
75	59	12.5	281	2	US-09-949-016-8397	

ALIGNMENTS

RESULT 1

US-09-489-039A-11962

Sequence 11962, Application US/09489039A

Patent No. 6610636

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709 2004001

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 11962

LENGTH: 107

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11962

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Best Local Similarity 83.3%; Pred. No. 1,4e-44;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MSRTIFCTFLKKDAERODPOLYPGELIGKRIYNEISKEMASOMITKQTMLINEKLSMNNI 60
Db 17 MSRTIFCTFLGREADGDPOLYPGELIGKRIYNEISKEMAMQMKQTMLINEKLSMNNP 76
Qy 61 EDRKLLBOEMVNFLEPGODVHIAGYTPPSK 90
Db 77 EHRKLLBOEMVQFLFEGKDVHIAGYTPPEK 106

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 82.2%; Score 389; DB 2; Length 93;
Best Local Similarity 80.0%; Pred. No. 3.3e-43;
Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

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Db 4 MSRTIFCTFLNKADGDPOLYPGELIGKRIYNEISKEMAGQMAKQTMLINEKLSMNNP 63
Qy 61 EDRKLLBOEMVNFLEPGODVHIAGYTPPSK 90
Db 64 DDKRLLEOEMVRFLEFGHDVHIAGYTPPEK 93

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 46.7%; Score 221; DB 2; Length 122;
Best Local Similarity 51.1%; Pred. No. 4.8e-21;
Matches 46; Conservative 13; Mismatches 29; Indels 2; Gaps 2;

1 MSRTIFCTFLKKDAERODPOLYPGELIGKRIYNEISKEMASOMITKQTMLINEKLSMNNI 60

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Db      33 MSRTVMCRCHHELPDLDPYPGAGEDTLYNNVSRKAMDEMQRHQMTLINERLNMWNA 92
QY      61 EDRKLIEQEMVNPLEFGODVHIA-GYTPPS 89
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Db      93 EDRKFLOEQMDKFL-SGEDYAKADGYVPFS 121

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRF
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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       |||||EQLIEQEMVNPLEFGODVHIA-GYTP 87
DB      64 EAKKFLBEOGRKRFKNDESVEKAEGWKP 91

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRF
; ORGANISM: M.catarhalis
US-09-540-236-2859

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       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY      65 LLEGEMVNPLEFGODVHIAGYTP 87
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DB      85 YLNEQRKFKLDNGDYEKAPGYKP 107

RESULT 6
US-09-543-681A-4768
; Sequence 4768, Application US/09543681A

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:14:02 ; Search time 56.932 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502a-20

Perfect score: 473

Sequence: 1 MSRTIFCTPLKKAERQDFQ.....VNFLPEGQDVHAGYTPSK 90

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published_Applications_AA_Main:*

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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
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4	396	83.7	91	3	US-09-955-502-13
5	393	83.1	91	3	US-09-955-502-14
6	393	83.1	91	3	US-09-955-502-16
7	393	83.1	91	3	US-09-955-502-17
8	389	82.2	88	3	US-09-955-502-15
9	379	80.1	91	3	US-09-955-502-18
10	366	77.4	90	3	US-09-955-502-10
11	363	76.7	87	3	US-09-955-502-7
12	357	75.5	91	3	US-09-955-502-5
13	351	74.2	87	3	US-09-955-502-8
14	346	73.2	87	3	US-09-955-502-6
15	342	72.3	78	3	US-09-955-502-19
16	308	65.1	88	3	US-09-955-502-9
17	256	54.1	76	3	US-09-955-502-21
18	233	49.3	88	3	US-09-955-502-33
19	226	47.8	87	3	US-09-955-502-2
20	226	47.8	87	3	US-09-955-502-3
21	212	44.8	86	3	US-09-955-502-4
22	210	44.4	87	3	US-09-955-502-25
23	206	43.6	90	3	US-09-955-502-23
24	203	42.9	89	3	US-09-955-502-22
25	199	42.1	87	3	US-09-955-502-29
26	199	42.1	87	3	US-09-955-502-30
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33	81	17.1	102	3	US-09-864-408A-768	Sequence 768, Appl
34	74	15.6	397	4	US-10-276-774-1577	Sequence 1577, Ap
35	74	15.6	506	4	US-10-343-663A-26	Sequence 26, Appl
36	74	15.6	576	5	US-10-450-763-50273	Sequence 50273, A
37	74	15.6	589	4	US-10-297-880-1	Sequence 1, Appl
38	74	15.6	770	4	US-10-343-663A-68	Sequence 68, Appl
39	74	15.6	1116	4	US-09-790-318-2	Sequence 2, Appl
40	74	15.6	1116	4	US-10-112-944-333	Sequence 323, App
41	74	15.6	1116	4	US-10-343-663A-27	Sequence 27, Appl
42	73	15.4	397	4	US-10-112-944-780	Sequence 780, App
43	70.5	14.9	635	6	US-11-097-143-34179	Sequence 34179, A
44	70	14.8	184	4	US-10-393-840-52	Sequence 52, Appl
45	69.5	14.7	600	4	US-10-437-963-104086	Sequence 104086,
46	69.5	14.7	867	4	US-10-282-122A-69006	Sequence 69006, A
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51	69.5	14.7	1589	5	US-10-450-763-60458	Sequence 60458, A
52	68	14.4	256	4	US-10-282-122A-53103	Sequence 53103, A
53	68	14.4	344	3	US-09-820-843A-35	Sequence 35, Appl
54	67	14.2	415	4	US-10-156-275-10	Sequence 10, Appl
55	67	14.2	1261	4	US-10-437-963-19116	Sequence 18916,
56	66.5	14.1	184	5	US-10-450-763-35150	Sequence 35150, A
57	66.5	14.1	758	4	US-10-369-493-10247	Sequence 10247, A
58	66.5	14.1	1317	5	US-10-733-923-12814	Sequence 12814, A
59	66	14.0	268	4	US-10-424-559-239277	Sequence 239277,
60	66	14.0	582	5	US-10-450-763-10849	Sequence 30849, A
61	66	14.0	1006	4	US-10-437-963-171993	Sequence 14993, A
62	65	13.7	842	4	US-10-032-585-7224	Sequence 7224, Ap
63	65	13.7	1575	5	US-10-741-600-1549	Sequence 1549, Ap
64	65	13.7	1640	5	US-10-741-600-1550	Sequence 1550, Ap
65	65	13.7	2101	5	US-10-977-955-32	Sequence 32, Appl
66	65	13.7	2101	5	US-10-723-681-18	Sequence 18, Appl
67	65	13.7	2115	5	US-10-977-955-33	Sequence 33, Appl
68	64.5	13.6	553	4	US-10-756-149-5050	Sequence 5050, Ap
69	64.5	13.6	553	4	US-10-437-963-189628	Sequence 189628,
70	64.5	13.6	184	4	US-10-219-220-66	Sequence 66, Appl
71	64	13.5	184	4	US-10-393-840-118	Sequence 118, App
72	64	13.5	534	3	US-09-312-762A-5	Sequence 5, Appl
73	64	13.5	534	4	US-10-767-701-43781	Sequence 43781, A
74	64	13.5	681	4	US-11-097-143-22170	Sequence 22170, A
75	63	13.3	470	6		

RESULT 1
US-09-955-502-20
; Sequence 20, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955, 502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234, 588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Yersinia pestis

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 5.02278 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502a-20

Perfect score: 473
Sequence: 1 MSRRIFCTFLKDAERQDFQ.....VNFLEGGQDVHAGTPPSK 90

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	41.9	88	US-10-467-657-968	Sequence 968, App
2	65	13.7	2101	US-10-857-780-23	Sequence 220, App
3	64.5	13.6	242	US-11-022-562-220	Sequence 21, App
4	62.5	13.2	259	US-11-179-977-21	Sequence 5158, App
5	62.5	13.2	273	US-10-467-657-5358	Sequence 317, App
6	62	13.1	593	US-11-194-246-317	Sequence 2694, App
7	61	12.9	922	US-11-072-512-2694	Sequence 903, App
8	61	12.9	1614	US-10-821-234-903	Sequence 7704, App
9	60.5	12.8	548	US-10-467-657-7704	Sequence 3814, App
10	60	12.7	571	US-11-072-512-3814	Sequence 218, App
11	58.5	12.4	1432	US-10-510-386-218	Sequence 190, App
12	57.5	12.2	980	US-11-052-554A-17	Sequence 52, App
13	57	12.1	1504	US-10-491-096-1198	Sequence 261, App
14	57	12.1	136	US-11-019-711-98	Sequence 5, App
15	56.5	11.9	506	US-10-485-517-261	Sequence 3625, App
16	56.5	11.9	563	US-11-099-691-5	Sequence 3504, App
17	56.5	11.9	893	US-11-072-512-3625	Sequence 54, App
18	56.5	11.9	1976	US-11-069-834-52	Sequence 340, App
19	56.5	11.9	1976	US-11-069-834-54	Sequence 341, App
20	56.5	11.8	1678	US-11-124-367A-340	Sequence 178, App
21	56	11.8	1678	US-11-124-367A-341	Sequence 3313, App
22	55.5	11.7	305	US-11-156-084-178	Sequence 486, App
23	55.5	11.7	381	US-11-072-512-3313	
24	55.5	11.7	401	US-10-131-826A-486	
25	55.5	11.7			

26	55	11.6	109	7	US-11-049-536-504	Sequence 504, App
27	55	11.6	189	7	US-11-071-262-1	Sequence 1, App
28	55	11.6	251	7	US-11-054-515-1496	Sequence 1496, App
29	55	11.6	253	7	US-11-054-515-1249	Sequence 1249, App
30	55	11.6	432	6	US-10-821-234-1463	Sequence 1463, App
31	55	11.6	499	6	US-10-793-626-1484	Sequence 1484, App
32	55	11.6	1705	7	US-11-143-984A-37	Sequence 37, App
33	54.5	11.5	124	7	US-11-072-512-2018	Sequence 2018, App
34	54.5	11.5	210	6	US-10-467-657-6318	Sequence 6318, App
35	54.5	11.5	306	6	US-10-055-877-195	Sequence 195, App
36	54.5	11.5	577	7	US-11-072-175-187	Sequence 187, App
37	54.5	11.5	601	6	US-10-944-272-3	Sequence 3, App
38	54.5	11.5	601	7	US-10-944-272-3	Sequence 720, App
39	54.5	11.5	876	7	US-11-077-550-82	Sequence 82, App
40	54.5	11.5	876	7	US-11-077-550-106	Sequence 106, App
41	54.5	11.5	876	7	US-11-077-550-108	Sequence 108, App
42	54.5	11.5	1786	7	US-11-196-400-3	Sequence 3, App
43	54	11.4	248	7	US-11-024-959-401	Sequence 401, App
44	54	11.4	480	6	US-10-510-386-12	Sequence 12, App
45	54	11.4	574	6	US-10-763-712A-6	Sequence 6, App
46	54	11.4	626	6	US-10-467-657-6426	Sequence 6426, App
47	54	11.4	626	6	US-10-467-657-7618	Sequence 7618, App
48	54	11.4	1011	7	US-11-098-686-10257	Sequence 10257, App
49	53.5	11.3	177	6	US-10-467-657-1658	Sequence 1658, App
50	53.5	11.3	206	6	US-10-793-626-832	Sequence 832, App
51	53.5	11.3	233	5	US-09-978-360A-417	Sequence 417, App
52	53.5	11.3	279	7	US-11-098-686-10812	Sequence 10812, App
53	53.5	11.3	508	7	US-11-072-512-2186	Sequence 2186, App
54	53.5	11.3	690	7	US-11-052-554A-232	Sequence 232, App
55	53.5	11.3	702	6	US-10-510-386-214	Sequence 214, App
56	53.5	11.3	1813	6	US-10-495-083-10	Sequence 10, App
57	53	11.2	271	6	US-10-793-626-678	Sequence 678, App
58	52.5	11.1	235	6	US-10-821-234-1610	Sequence 1610, App
59	52.5	11.1	319	6	US-10-821-234-1555	Sequence 1555, App
60	52.5	11.1	319	6	US-10-793-626-2760	Sequence 2760, App
61	52.5	11.1	398	7	US-11-046-666-9	Sequence 9, App
62	52.5	11.1	398	7	US-11-046-666-9	Sequence 9, App
63	52.5	11.1	886	6	US-10-821-234-1329	Sequence 1329, App
64	52	11.0	241	7	US-11-072-512-2203	Sequence 2203, App
65	52	11.0	296	7	US-11-087-221-10	Sequence 10, App
66	52	11.0	384	7	US-11-219-282-19	Sequence 19, App
67	52	11.0	395	7	US-11-009-658-46	Sequence 46, App
68	52	11.0	456	7	US-11-069-642-8	Sequence 8, App
69	52	11.0	497	6	US-10-454-437-410	Sequence 410, App
70	52	11.0	588	7	US-11-052-554A-339	Sequence 339, App
71	52	11.0	599	7	US-11-109-157A-3	Sequence 3, App
72	52	11.0	600	7	US-11-072-512-3845	Sequence 3845, App
73	52	11.0	1145	6	US-10-793-626-1432	Sequence 1432, App
74	52	11.0	1613	7	US-11-108-528-84	Sequence 84, App
75	52	11.0	1613	7	US-11-108-528-86	Sequence 86, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10-467,657
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRN
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 41.9%; Score 198; DB 6; Length 88;
Best Local Similarity 44.3%; Pred. No. 1,3e-15;
Matches 39; Conservative 16; Mismatches 31; Indels 2; Gaps 2;

QY 1 MSRTFCTFLKDAERODFOLYGEIGRIYNEISKEAMSWITKQTMLINEKLSMMNI 60
DB 1 MARWVFCVXLANEAGMKFPLPDELGKRIPEVSGBAWAAWTRIQTMLINEKLSLADP 60

QY 61 EDRKLEQEMVNF-EGDVHIAGTTP 87
DB 61 RAREYLAQOMEOYFPGDGADA-VQGYVP 87

RESULT 2
US-10-857-780-23
Sequence 23, Application US/10857780
Publication No. US20050272043A1

GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEPHAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: REMELAND, RIKARD HENRY
APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
FILE REFERENCE: SEQ 4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23

LENGTH: 2101
TYPE: PRN
ORGANISM: Homo sapiens
US-10-857-780-23

Query Match 13.7%; Score 65; DB 6; Length 2101;
Best Local Similarity 36.0%; Pred. No. 44;
Matches 18; Conservative 14; Mismatches 10; Indels 8; Gaps 4;

QY 32 NEISKE---AWSQWITKQTMLINEKLSMMNIEDRKLEQEMVNFLEGO 78
DB 342 NEITREHSKATQEWLEKQAL--EKELSLA-LQDKKCLEEK--NEITLQK 386

RESULT 3
US-11-022-562-220
Sequence 220, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
FILE REFERENCE: DEN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718

PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 220
LENGTH: 242
TYPE: PRN
ORGANISM: Human Immunodeficiency Virus
US-11-022-562-220

Query Match 13.6%; Score 64.5; DB 7; Length 242;
Best Local Similarity 27.2%; Pred. No. 3.8;
Matches 25; Conservative 19; Mismatches 31; Indels 17; Gaps 4;

QY 1 MSRTFCTFLKDAERODFOLY---PGEIGRIYNEISKEAMSWITKQTMLINEKLS 56
DB 1 MAETFAUSKLEBDRPMKNSVFIIGASGETRVLKLEL---QGLFSKVTLLIGRRKLT 56

QY 57 MNNIEDRKLEQEMVNF-----LFEQDVP 80
DB 57 -FDEEAYNNVNGEYVDFEKLDDYASAPGHDV 87

RESULT 4
US-11-179-977-21
Sequence 21, Application US/11179977
Publication No. US20050249789A1

GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
FILE REFERENCE: GC511-PCT
CURRENT APPLICATION NUMBER: US/11/179,977
CURRENT FILING DATE: 2005-07-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21

LENGTH: 259
TYPE: PRN
ORGANISM: Bacillus
US-11-179-977-21

Query Match 13.2%; Score 62.5; DB 7; Length 259;
Best Local Similarity 28.8%; Pred. No. 6.9;
Matches 21; Conservative 13; Mismatches 36; Indels 3; Gaps 2;

QY 13 DAERODPOLYGEIGRIYNEISKEAMSWITKQTMLINEKLSMMNIEDRKLEQEMVN 72
DB 159 EADQND-SLYRKVSVMRYRLTLTIESAMVTEAVL--KVLPLWQAGDDCLVDKTMVI 215

QY 73 FLFEGQDVHIAGY 85
DB 216 KWFNGVASHNKAY 228

RESULT 5
US-10-467-657-5358
Sequence 5358, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMan99, version 1.04
SEQ ID NO 5358
LENGTH: 273

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 / Search time 62.41 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-21

Perfect score: 406

Sequence: 1 MNRITFCYFKKSEGDQFQ.....MFNLEHRKIKRYKMLFLFK 76

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

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2: genesepq1980s:*
3: genesepq1908s:*
4: genesepq2000s:*
5: genesepq2001s:*
6: genesepq2002s:*
7: genesepq2003as:*
8: genesepq2004s:*
9: genesepq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	406	100.0	76	5	ABB78166 Amino aci
2	265	65.3	91	5	ABB78158 Amino aci
3	265	65.3	91	5	ABB78157 Amino aci
4	265	65.3	91	5	ABB78156 Amino aci
5	259	63.8	88	5	ABB78160 Amino aci
6	259	63.8	91	5	ABB78161 Amino aci
7	259	63.8	91	5	ABB78159 Amino aci
8	259	63.8	91	5	ABB78162 Amino aci
9	259	63.8	91	5	ABB78163 Amino aci
10	256	63.1	78	5	ABB78164 Amino aci
11	256	63.1	87	5	ABB78152 Amino aci
12	256	63.1	90	5	ABB78155 Amino aci
13	256	63.1	107	7	ABB78165 Amino aci
14	248	61.1	87	5	ABB78151 Amino aci
15	247	60.8	87	5	ABB78153 Amino aci
16	246	60.6	91	5	ABB78150 Amino aci
17	236	58.1	93	7	ADFO5158 Bacterial
18	231	56.9	90	5	ABB78154 Amino aci
19	216	53.2	88	5	ABB78154 Amino aci
20	200	49.3	86	5	ABB78149 Amino aci
21	200	49.3	87	5	ABB78148 Amino aci
22	200	49.3	87	5	ABB78147 Amino aci
23	184	45.3	89	9	ABE41576 L. pneumo
24	184	45.3	95	9	ABE38294 L. pneumo

25	182	44.8	92	6	ADA34169	Ada34169 Acinetoba
26	181	44.6	87	5	ABB78175	Abb78175 Amino aci
27	175	43.1	87	5	ABB78170	Abb78170 Amino aci
28	175	43.1	87	5	ABB78174	Abb78174 Amino aci
29	175	43.1	122	7	ABO74609	AbO74609 Pseudomon
30	174.5	43.0	90	5	ABB78167	Abb78167 Amino aci
31	166	40.6	87	5	ABB78176	Abb78176 Amino aci
32	165	40.6	90	5	ABB78168	Abb78168 Amino aci
33	164	40.4	88	5	ABB78178	Abb78178 Amino aci
34	159	39.2	87	5	ABB78169	Abb78169 Amino aci
35	158	38.9	88	5	ABB78171	Abb78171 Amino aci
36	158	38.9	88	5	ABB78172	Abb78172 Amino aci
37	158	38.9	88	5	ABB78173	Abb78173 Amino aci
38	158	38.9	88	5	ABB78174	Abb78174 Amino aci
39	154	37.9	88	5	ABB78177	Abb78177 Amino aci
40	128	31.5	110	8	AD05173	Ad105173 M. catarr
41	75	18.5	903	8	ADN18395	Adn18395 Bacterial
42	73.5	18.1	319	9	AEA61809	Aea61809 Streptoco
43	73.5	18.1	321	6	ABU25343	Abu25343 Protein e
44	73	18.0	918	4	AAW79789	Aam79789 Human pro
45	73	18.0	1096	4	AAW78805	Aam78805 Human pro
46	70	17.2	817	6	ABU22957	Abu22957 Protein e
47	69.5	17.1	81	7	ADC97424	Adc97424 B. faeciu
48	69.5	17.1	523	7	ADD72115	AdD72115 Human end
49	69.5	17.1	2184	4	AAE00425	Aae00425 P. falci
50	69	17.0	341	6	ABU18904	Abu18904 Protein e
51	69	17.0	954	8	ADRI6190	Adri6190 Streptoco
52	69	17.0	2206	3	AB18254	Ab18254 Plasmodiu
53	68.5	16.9	648	7	ADFI6091	Adfi6091 Human alb
54	68.5	16.9	648	7	ADFI6086	Adfi6086 Human alb
55	68	16.7	279	3	AAO5947	Aao5947 Protein d
56	68	16.5	447	8	ADRI6238	Adri6238 Streptoco
57	67	16.5	577	4	AAU35662	Aau35662 Haemophil
58	67	16.5	577	4	ABU30623	Abu30623 Protein e
59	67	16.5	1657	2	AAW18822	Aaw18822 Human IIG
60	67	16.5	1657	7	ADJ68688	Adj68688 Human hea
61	67	16.5	1657	8	ADQ30538	Adq30538 Pancreas
62	67	16.5	1657	4	ADU04997	Adu04997 Amino aci
63	66.5	16.4	1140	4	ABB69065	Abb69065 Drosophila
64	66	16.3	251	6	ABU48870	Abu48870 Protein e
65	65.5	16.1	399	6	ABU24107	Abu24107 Protein e
66	65	16.0	240	3	AAG32199	Aag32199 Arabidops
67	65	16.0	240	5	ABG91142	Abg91142 Herpicida
68	65	16.0	320	4	AAE90768	Aae90768 C. glutami
69	64.5	15.9	109	8	ADRO8542	Adr08542 Human pro
70	64.5	15.9	205	8	ADH87009	Adh87009 Enterococ
71	64.5	15.9	358	8	ADV89039	Adv89039 Streptoco
72	64.5	15.9	358	8	ADV80292	Adv80292 Streptoco
73	64.5	15.9	358	8	ADV82414	Adv82414 Streptoco
74	64.5	15.9	767	2	AAW46272	Aaw46272 Moraxella
75	64.5	15.9	768	8	ADR51505	Adr51505 Moraxella

ALIGNMENTS

RESULT 1	ABB78166	standard; protein; 76 AA.
ID	ABB78166	
AC	ABB78166	
XX		
DT	05-NOV-2002	(first entry)
XX		
DE		Amino acid sequence of a Yggx homologue.
KW		Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
KW		hydroxyl radical; DNA damage; Yggx homologue.
XX		
OS		Unidentified.
XX		
PN	US2002072118-A1.	

PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnicks JA;
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 CC
 SQ Sequence 76 AA;

Query Match 100.0%; Score 406; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 6.3e-40;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNRIIFCTPFKKKSGODFQSYPGKLGKTIYDOISKAKEMKIEKQTILINEENIMPNL 60
 DB 1 MNRIIFCTPFKKKSGODFQSYPGKLGKTIYDOISKAKEMKIEKQTILINEENIMPNL 60

OY 61 EHRKKIEKMKLPLFK 76
 DB 61 EHRKKIEKMKLPLFK 76

RESULT 2
 ABB78158
 ID ABB78158 standard; protein; 91 AA.

AC ABB78158;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnicks JA;

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues

SQ Sequence 91 AA;

Query Match 65.3%; Score 265; DB 5; Length 91;
 Best Local Similarity 61.8%; Pred. No. 3.3e-23;
 Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

OY 1 MNRIIFCTPFKKKSGODFQSYPGKLGKTIYDOISKAKEMKIEKQTILINEENIMPNL 60
 DB 1 MSRIIFCTPFKREABGDFQSYPGKLGKTIYDOISKAKEMKIEKQTILINEENIMPNL 60

OY 61 EHRKKIEKMKLPLFK 76
 DB 61 EHRKLBQEMVNPFE 76

RESULT 3
 ABB78157
 ID ABB78157 standard; protein; 91 AA.

AC ABB78157;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnicks JA;

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 8.3098 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-21

Perfect score: 406

Sequence: 1 MNRIFCTPFKKKSGQDFQ.....MFLHKKIKIKYMLFLPK 76

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	406	100.0	93	B84994	hypothetical prote
2	265	65.3	91	A85954	hypothetical prote
3	265	65.3	91	A85082	hypothetical prote
4	265	65.3	91	P91108	hypothetical prote
5	259	63.8	91	AH0879	conserved hypothet
6	256	63.1	90	A10116	conserved hypothet
7	256	63.1	90	C64013	hypothetical prote
8	231	56.9	90	C82320	conserved hypothet
9	183	45.1	105	C82624	conserved hypothet
10	175	43.1	90	H83003	conserved hypothet
11	158	38.9	88	H81014	conserved hypothet
12	75	18.5	903	C64444	cell division cont
13	69.5	17.1	193	D97157	stage III sporulat
14	69	17.0	2206	G71611	hypothetical prote
15	68.5	16.9	128	C59096	hypothetical prote
16	68.5	16.9	323	D90527	glycerol-3-phospha
17	67	16.5	356	G72386	conserved hypothet
18	67	16.5	577	A64131	arginine-tRNA ligase
19	67	16.5	1657	A54854	Ras GTPase activat
20	66	16.3	151	D64319	probable formate d
21	66	16.3	251	B82911	exonuclease VII, 1
22	65.5	16.1	399	F97156	lactose transport
23	65.5	16.1	634	A32241	T2P11.5 protein -
24	65	16.0	240	D86395	isomerase funct (RC
25	65	16.0	604	F64081	NADH2 dehydrogenas
26	65	16.0	731	T14231	conserved hypothet
27	64.5	15.9	258	S26762	conserved hypothet
28	64.5	15.9	320	D90478	hypothetical prote
29	64.5	15.9	403	C72396	

30	64.5	15.9	510	2	A96735	hypothetical prote
31	64.5	15.9	556	1	OX8Y34	DNA endonuclease I
32	64	15.8	128	2	T28294	ORF MSV133 hypot
33	64	15.8	213	2	D69409	conserved hypothet
34	64	15.8	250	2	G64709	hypothetical prote
35	64	15.8	265	2	T46013	hypothetical prote
36	64	15.8	286	2	D90609	conserved hypothet
37	64	15.8	530	2	G64480	hypothetical prote
38	64	15.8	624	2	G82508	hypothetical prote
39	64	15.8	1024	2	T41415	probable leucine p
40	63.5	15.6	282	2	F96689	hypothetical prote
41	63.5	15.6	283	2	B84787	translin-like prot
42	63.5	15.6	529	2	T48253	myb-like protein -
43	63.5	15.6	1115	2	T41342	probable coiled-co
44	63.5	15.6	1304	2	T14073	dynamin 1b heavy ch
45	63	15.5	174	2	S73113	hypothetical prote
46	63	15.5	300	2	H72326	conserved hypothet
47	63	15.5	315	2	B59093	hypothetical prote
48	63	15.5	344	2	D70126	hypothetical prote
49	63	15.5	359	2	F84513	hypothetical prote
50	62.5	15.4	125	2	T22338	hypothetical prote
51	62.5	15.4	313	2	B90093	hypothetical prote
52	62.5	15.4	538	2	S67766	RNA-export mediato
53	62	15.3	183	2	T37599	hypothetical prote
54	62	15.3	253	2	C81393	probable transcrip
55	62	15.3	356	2	C97010	3-dehydroquinase
56	62	15.3	601	2	H81282	probable translati
57	62	15.3	889	2	AD2215	two-component hydr
58	61.5	15.1	100	2	D71632	hypothetical prote
59	61.5	15.1	137	2	A84072	hypothetical prote
60	61.5	15.1	220	2	F70223	conserved hypothet
61	61.5	15.1	233	2	T18453	hypothetical prote
62	61.5	15.1	424	2	T25803	hypothetical prote
63	61.5	15.1	490	2	G70108	hypothetical prote
64	61.5	15.1	599	2	H86227	hypothetical prote
65	61.5	15.1	1092	2	T18354	adhesin - Mycoplas
66	61.5	15.1	1549	2	T11974	glutamate synthase
67	61.5	15.1	2401	2	T28676	rhoxy protein -
68	61	15.0	103	2	T51248	ACBP/DBI - duck
69	61	15.0	215	2	C81410	hypothetical prote
70	61	15.0	227	2	B70438	hypothetical prote
71	61	15.0	351	2	D82930	SRP family of GTP-
72	61	15.0	382	2	C90407	conserved hypothet
73	61	15.0	390	2	T18202	leupin precursor -
74	61	15.0	664	2	C71106	hypothetical prote
75	61	15.0	2166	2	G70163	hypothetical prote

ALIGNMENTS

RESULT 1
B84994 hypothetical protein [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: B84994
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: AB4930; MUID:20445173; PMID:10993077
A:Accession: B84994
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-93 <STO>
A:Cross-references: UNIPARC:UPI00005B610; GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: yggX; BU553
C:Superfamily: Fe(II) trafficking protein YggX
Query Match 100.0%; Score 406; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-33;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 56.0046 Seconds
(without alignments)
957,425 Million cell updates/sec

Title: US-09-955-502a-21

Perfect score: 406
Sequence: 1 MRRIFCTFPFKKSGQDFQ.....MFLHRRKKIKKMLFLFK 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot-05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	406	100.0	77	1	FERP_BUCAL
2	300	73.9	78	1	FERP_BUCAL
3	264	65.0	90	1	FERP_YERPS
4	260	64.0	90	1	FERP_ECO57
5	260	64.0	90	1	FERP_ECO16
6	260	64.0	90	1	FERP_ECO11
7	256	63.1	90	1	FERP_HABIN
8	256	63.1	90	1	FERP_YERPE
9	256	63.1	90	2	Q4QMD9_HAE18
10	254	62.6	90	1	FERP_SALCH
11	254	62.6	90	1	FERP_SALPA
12	254	62.6	90	1	FERP_SALPA
13	254	62.6	90	1	FERP_SALTY
14	254	62.6	90	1	FERP_SALTY
15	251	61.8	91	1	FERP_MANSW
16	248	61.1	90	1	FERP_PASWU
17	247	60.8	90	1	FERP_PHORA
18	247	60.8	94	1	FERP_HABU
19	243	59.9	90	1	FERP_PHOIL
20	241	59.4	87	1	FERP_BUCBP
21	239	58.9	90	1	FERP_VIBPA
22	238	58.6	90	1	FERP_ERWCT
23	232	57.1	90	1	FERP_VIBR1
24	231	56.9	90	1	FERP_VIBR1
25	231	56.9	90	1	FERP_VIBR1
26	231	56.9	90	1	FERP_VIBR1
27	223	54.9	90	1	FERP_VIBR1
28	218	53.7	90	1	FERP_IDILO
29	216	53.2	92	1	FERP_WIGGR
30	206	50.7	79	1	FERP_SHRON
31	200	49.3	90	1	FERP_CANBP
					FERP_BORBR

32	200	49.3	90	1	FERP_BORPA	Q7w9q2 bordebella
33	200	49.3	90	1	FERP_BORPE	Q7w9q2 bordebella
34	188	46.3	90	1	FERP_XYRTP	Q87d06 xyrella fas
35	186	45.8	90	1	FERP_XYRTP	Q87d06 xyrella fas
36	185	45.6	90	1	FERP_XYRTP	Q87d06 xyrella fas
37	184	45.3	89	1	FERP_XANAC	Q87d06 xyrella fas
38	184	45.3	89	1	FERP_XANAC	Q87d06 xyrella fas
39	184	45.3	89	1	FERP_XANAC	Q87d06 xyrella fas
40	183	45.1	90	1	FERP_XYRTP	Q87d06 xyrella fas
41	182	44.8	90	1	FERP_XYRTP	Q87d06 xyrella fas
42	181	44.6	91	1	FERP_XYRTP	Q87d06 xyrella fas
43	181	44.6	91	1	FERP_XYRTP	Q87d06 xyrella fas
44	180	44.3	91	2	Q4LS19_9BURK	Q87d06 xyrella fas
45	179	44.1	92	1	FERP_XANCP	Q87d06 xyrella fas
46	179	44.1	92	1	FERP_XANCP	Q87d06 xyrella fas
47	179	44.1	92	2	Q4UW14_XANCP	Q87d06 xyrella fas
48	176	43.3	91	1	FERP_XANCP	Q87d06 xyrella fas
49	175	43.1	90	1	FERP_XANCP	Q87d06 xyrella fas
50	175	43.1	90	2	Q4J228_AZOVI	Q87d06 xyrella fas
51	170	41.9	90	2	Q677F6_PSEFL	Q87d06 xyrella fas
52	166	40.9	87	1	FERP_XANCP	Q87d06 xyrella fas
53	165	40.6	90	1	FERP_XANCP	Q87d06 xyrella fas
54	165	40.6	90	2	Q4ZLP3_PSESY	Q87d06 xyrella fas
55	164	40.4	90	1	FERP_XANCP	Q87d06 xyrella fas
56	164	40.4	90	1	FERP_XANCP	Q87d06 xyrella fas
57	159	39.2	90	1	FERP_XANCP	Q87d06 xyrella fas
58	158	38.9	88	1	FERP_XANCP	Q87d06 xyrella fas
59	158	38.9	88	1	FERP_XANCP	Q87d06 xyrella fas
60	158	38.9	88	1	FERP_XANCP	Q87d06 xyrella fas
61	158	38.9	90	2	Q4KJ22_PSEFS	Q87d06 xyrella fas
62	154	37.9	90	1	FERP_XANCP	Q87d06 xyrella fas
63	126	31.0	96	2	Q4FVJ7_9GAMM	Q87d06 xyrella fas
64	115	28.3	92	2	Q4NM04_9PELT	Q87d06 xyrella fas
65	87.5	21.6	540	2	Q736A2_BACCI	Q87d06 xyrella fas
66	85.5	21.1	540	2	Q63AA2_BACCI	Q87d06 xyrella fas
67	82	20.2	186	2	Q84EV3_MYCGA	Q87d06 xyrella fas
68	82	20.2	186	2	Q84EV3_MYCGA	Q87d06 xyrella fas
69	82	20.2	186	2	Q84EV3_MYCGA	Q87d06 xyrella fas
70	81.5	20.1	178	2	Q4XZX8_MYCGA	Q87d06 xyrella fas
71	80.5	19.8	540	2	Q4XZX8_MYCGA	Q87d06 xyrella fas
72	80.5	19.8	540	2	Q4XZX8_MYCGA	Q87d06 xyrella fas
73	80.5	19.8	540	2	Q4XZX8_MYCGA	Q87d06 xyrella fas
74	80.5	19.8	540	2	Q4XZX8_MYCGA	Q87d06 xyrella fas
75	80.5	19.7	1629	2	Q9U0K9_PLAF7	Q87d06 xyrella fas

ALIGNMENTS

RESULT 1	
FERP_BUCAL	STANDARD, PRT, 77 AA.
AC P57618;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 13-SEP-2005 (Rel. 48, Last annotation update)	
DE Ordered Re(2+) trafficking protein.	
GN OrderedOcunames=BU553;	
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum	
OC symbiotic bacterium).	
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC Enterobacteriaceae; Buchnera.	
OX NCBI_TaxID=118099;	
RM [1]	
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC STRAIN=Tokyo 1998;	
RX MEDLINE=20445173; PubMed=1093077; DOI=10.1038/35024074;	
RA Shigenobu S., Matsumoto H., Hattori M., Sakaki Y., Ishikawa H.;	
RT "Genome sequence of the endocellular bacterial symbiont of aphids	
BU Buchnera sp. Aph. "	
RL Nature 407:81-86(2000).	
CC -I- FUNCTION: Could be a mediator in iron transactions between iron	
acquistion and iron-regulating processes, such as synthesis and/or	

```

CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL, BA000003; BAB13245.1; ALT_INIT; Genomic_DNA.
CC HAMAP, MF_00686; -; 1.
CC InterPro, IPR007457; Y9GX.
CC Pfam, PF04362; DUF495; 1.
CC PIRSF, PIRSF029827; Fe_traffic_Y9GX; 1.
CC ProDom, PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC SEQUENCE 77 AA; 9511 MW; 00B049027CF480BF CRC64;

Query Match          100.0%; Score 406; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.3e-34;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRITCTFPFKKSGQDFOSYPGKLGKKIYDQISKKAMEKWIETKOTLLINEENIMNTL 60
DB 1 MNRITCTFPFKKSGQDFOSYPGKLGKKIYDQISKKAMEKWIETKOTLLINEENIMNTL 60

QY 61 EHRKKIEKMKLFLPK 76
DB 61 EHRKKIEKMKLFLPK 76

RESULT 2
PERT_BUCAP          STANDARD;          PRT;          78 AA.
ID PERT_BUCAP
AC Q8X325;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedNames=Bugs35;
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22084549; PubMed=12089438; DOI=10.1126/science.1071278;
RX Tamai I., Klaesson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RX Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL, AE014127; AAM68076.1; -; Genomic_DNA.
CC HAMAP, MF_00686; -; 1.
CC InterPro, IPR007457; Y9GX.
CC Pfam, PF04362; DUF495; 1.
CC PIRSF, PIRSF029827; Fe_traffic_Y9GX; 1.
CC ProDom, PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC SEQUENCE 78 AA; 9564 MW; ABB708696777F44 CRC64;

```

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Query Match          73.9%; Score 300; DB 1; Length 78;
Best Local Similarity 76.0%; Pred. No. 5.7e-23;
Matches 57; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNRITCTFPFKKSGQDFOSYPGKLGKKIYDQISKKAMEKWIETKOTLLINEENIMNTL 60
DB 1 MNRITCTFPFKKSGQDFOSYPGKLGKKIYDQISKKAMEKWIETKOTLLINEENIMNTL 60

QY 61 EHRKKIEKMKLFLPK 75
DB 61 NDRKKIEKMKLFLPK 75

RESULT 3
PERT_YERPS          STANDARD;          PRT;          90 AA.
ID PERT_YERPS
AC Q66M3;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedNames=YPTB3225;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=IP32953 / Serotype 1;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RX Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RX Regala W.M., Georgescu A.M., Verges L.M., Land M.L., Motin V.L.,
RX Brubaker R.R., Fowler J., Hinebusch J., Marceau M., Medigue C.,
RX Simonet M., Chenaal-Franzique V., Souza B., Dacheux D., Elliott J.M.,
RX Derdise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL, BX936398; CAH22463.1; -; Genomic_DNA.
CC SMR, Q66M3; 1-90.
CC HAMAP, MF_00686; -; 1.
CC InterPro, IPR007457; Y9GX.
CC Pfam, PF04362; DUF495; 1.
CC PIRSF, PIRSF029827; Fe_traffic_Y9GX; 1.
CC ProDom, PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC SEQUENCE 90 AA; 10608 MW; C7375E7954752B64 CRC64;

Query Match          65.0%; Score 264; DB 1; Length 90;
Best Local Similarity 61.8%; Pred. No. 3.1e-19;
Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNRITCTFPFKKSGQDFOSYPGKLGKKIYDQISKKAMEKWIETKOTLLINEENIMNTL 60
DB 1 MSRTITCTFLKQDAGQDFOLYPGBEIGRIVNEISKAMSQWITQTLINKEKLSMNMI 60

QY 61 EHRKKIEKMKLFLPK 76
DB 61 EDRKKIEKMKLFLPK 76

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 15.4077 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-21

Perfect score: 406

Sequence: 1 MRRIFCTFFKKKSGQDFQ.....MFLHRKKIKRYMLFLPK 76

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 75 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	256	63.1	107	2	US-09-489-039A-11962
2	236	58.1	93	2	US-09-543-681A-5443
3	182	44.8	92	2	US-09-328-352-5456
4	175	43.1	122	2	US-09-252-991A-23355
5	128	31.5	110	2	US-09-540-236-2859
6	69.5	17.1	81	2	US-09-107-532A-7051
7	69.5	17.1	2184	2	US-09-417-485D-6
8	68	16.7	279	2	US-09-861-451A-28
9	67	16.5	1657	1	US-08-287-959-1
10	67	16.5	1657	1	US-09-949-016-6427
11	67	16.5	1678	2	US-09-949-016-9445
12	66.5	16.4	666	2	US-09-270-767-62249
13	66.5	16.4	721	2	US-09-270-767-46645
14	66	16.3	187	2	US-09-248-796A-16267
15	65.5	16.1	515	2	US-09-605-703B-808
16	65	16.0	320	2	US-09-605-703B-810
17	65	16.0	320	2	US-09-605-703B-810
18	64.5	15.9	205	2	US-09-134-000C-4894
19	63.5	15.6	305	2	US-09-248-796A-20071
20	63	15.5	359	2	US-09-653-375B-10
21	63	15.5	539	2	US-09-252-991A-19631
22	62	15.3	826	2	US-09-830-762-5
23	62	15.3	826	2	US-09-248-796A-15075
24	61.5	15.1	148	2	US-09-134-000C-6655
25	61.5	15.1	236	2	US-09-830-230A-574
26	61.5	15.1	471	2	US-09-830-230A-573
27	61.5	15.1	490	2	US-09-830-230A-573

28	61	15.0	250	2	US-09-270-767-43235	Sequence 43235, A
29	61	15.0	374	2	US-09-270-767-57491	Sequence 57491, A
30	61	15.0	390	2	US-10-094-944-13	Sequence 13, Appl
31	60.5	14.9	76	2	US-09-583-110-2669	Sequence 2669, Ap
32	60.5	14.9	85	2	US-09-107-433-4296	Sequence 4296, Ap
33	60.5	14.9	367	2	US-09-248-796A-18155	Sequence 18155, A
34	60.5	14.9	410	1	US-08-792-283A-2	Sequence 2, Appl1
35	60.5	14.9	410	1	US-09-105-908-2	Sequence 2, Appl1
36	60.5	14.9	410	2	US-09-271-713-2	Sequence 2, Appl1
37	60.5	14.9	591	2	US-09-370-368-8	Sequence 8, Appl1
38	60.5	14.9	885	2	US-09-074-579-5	Sequence 5, Appl1
39	60.5	14.9	885	2	US-09-388-774-5	Sequence 5, Appl1
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45	59.5	14.7	202	1	US-07-804-894-1	Sequence 1, Appl1
46	59.5	14.7	202	1	US-08-419-102-1	Sequence 1, Appl1
47	59.5	14.7	226	2	US-09-949-016-11107	Sequence 11107, A
48	59.5	14.7	255	1	US-08-622-353-8	Sequence 8, Appl1
49	59.5	14.7	255	1	US-08-622-352A-10	Sequence 10, Appl
50	59.5	14.7	255	2	US-08-826-390-10	Sequence 10, Appl
51	59.5	14.7	370	2	US-09-134-001C-3769	Sequence 3769, Ap
52	59.5	14.7	387	2	US-09-270-767-59513	Sequence 59513, A
53	59.5	14.7	443	2	US-09-248-796A-16816	Sequence 16816, A
54	59.5	14.7	707	2	US-09-270-767-44096	Sequence 44096, A
55	59	14.5	110	2	US-09-774-639-112	Sequence 112, App
56	59	14.5	193	2	US-09-270-767-35785	Sequence 35785, A
57	59	14.5	193	2	US-09-270-767-51002	Sequence 51002, A
58	59	14.5	289	2	US-09-543-681A-8156	Sequence 8156, Ap
59	59	14.5	299	2	US-09-270-767-42033	Sequence 42033, A
60	59	14.5	449	2	US-09-270-767-57465	Sequence 57465, A
61	59	14.5	601	2	US-09-270-767-42194	Sequence 42194, A
62	59	14.5	1111	2	US-09-914-255-28	Sequence 28, Appl
63	58.5	14.4	690	2	US-09-328-352-5182	Sequence 5182, Ap
64	58	14.3	124	2	US-10-104-047-2018	Sequence 2018, Ap
65	58	14.3	155	2	US-09-732-210-523	Sequence 523, App
66	58	14.3	187	2	US-09-248-796A-16987	Sequence 16987, A
67	58	14.3	221	2	US-09-543-681A-8222	Sequence 8222, Ap
68	58	14.3	276	2	US-09-830-230A-724	Sequence 724, App
69	58	14.3	284	2	US-09-949-016-11051	Sequence 11051, A
70	58	14.3	304	2	US-09-830-230A-723	Sequence 723, App
71	58	14.3	363	2	US-09-248-796A-19011	Sequence 19011, A
72	58	14.3	463	2	US-08-792-295-1	Sequence 1, Appl1
73	58	14.3	463	2	US-09-076-432-1	Sequence 1, Appl1
74	58	14.3	519	2	US-09-248-796A-15238	Sequence 15238, A
75	58	14.3	701	2	US-09-538-092-303	Sequence 303, App

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Bretton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709, 2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 48.1276 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502A-21
Perfect score: 406
Sequence: 1 MNRIFCTFFKKSEGDPO.....MNLHRRKIKRYMFLFK 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	265	65.3	91	3	US-09-955-502-13
5	259	63.8	88	3	US-09-955-502-15
6	259	63.8	91	3	US-09-955-502-14
7	259	63.8	91	3	US-09-955-502-16
8	259	63.8	91	3	US-09-955-502-17
9	259	63.8	91	3	US-09-955-502-18
10	256	63.1	78	3	US-09-955-502-19
11	256	63.1	87	3	US-09-955-502-7
12	256	63.1	90	3	US-09-955-502-20
13	248	61.1	87	3	US-09-955-502-6
14	247	60.8	87	3	US-09-955-502-8
15	246	60.6	91	3	US-09-955-502-5
16	231	56.9	90	3	US-09-955-502-10
17	216	53.2	88	3	US-09-955-502-9
18	200	49.3	86	3	US-09-955-502-4
19	200	49.3	87	3	US-09-955-502-2
20	200	49.3	87	3	US-09-955-502-3
21	183	45.1	89	3	US-09-955-502-22
22	181	44.6	87	3	US-09-955-502-29
23	181	44.6	87	3	US-09-955-502-30
24	175	43.1	87	3	US-09-955-502-25
25	166	40.9	87	3	US-09-955-502-31
26	165	40.6	90	3	US-09-955-502-23
27	164	40.4	88	3	US-09-955-502-33

ALIGNMENTS

28	159	39.2	87	3	US-09-955-502-24	Sequence 24, Appl
29	158	38.9	88	3	US-09-955-502-26	Sequence 26, Appl
30	158	38.9	88	3	US-09-955-502-27	Sequence 27, Appl
31	158	38.9	88	3	US-09-955-502-28	Sequence 28, Appl
32	154	37.9	87	3	US-09-955-502-32	Sequence 32, Appl
33	78.5	19.3	2910	5	US-10-732-923-3342	Sequence 3342, Ap
34	75	18.5	903	4	US-10-369-493-1048	Sequence 1048, Ap
35	75	18.5	903	5	US-10-732-923-23186	Sequence 23186, A
36	73.5	18.1	321	4	US-10-282-122A-53267	Sequence 53267, A
37	70	17.2	817	4	US-10-282-122A-50881	Sequence 50881, A
38	69.5	17.1	2184	4	US-10-304-095-6	Sequence 6, Appl1
39	69	17.0	341	4	US-10-282-122A-46828	Sequence 46828, A
40	69	17.0	954	4	US-10-771-931-3	Sequence 3, Appl1
41	68.5	16.9	648	5	US-10-775-204-1173	Sequence 1173, Ap
42	68.5	16.9	648	5	US-10-775-204-1178	Sequence 1178, Ap
43	68	16.7	279	3	US-09-861-451A-28	Sequence 28, Appl
44	67	16.5	447	4	US-10-771-931-51	Sequence 51, Appl1
45	67	16.5	577	3	US-09-815-242-11255	Sequence 11255, A
46	67	16.5	577	4	US-10-282-122A-58547	Sequence 58547, A
47	67	16.5	1657	4	US-10-408-765A-494	Sequence 494, App
48	67	16.5	1657	5	US-10-733-969A-25	Sequence 25, Appl
49	67	16.5	1657	5	US-10-826-909-36	Sequence 36, Appl
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51	66.5	16.4	725	4	US-10-437-963-140992	Sequence 140992, A
52	66.5	16.4	943	4	US-10-437-963-140994	Sequence 140994, A
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54	66	16.3	251	4	US-10-282-122A-76794	Sequence 76794, A
55	65.5	16.1	399	4	US-10-282-122A-52031	Sequence 52031, A
56	65.5	16.1	1197	5	US-10-732-923-3337	Sequence 3337, Ap
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62	64	15.8	271	5	US-10-481-032A-318	Sequence 318, App
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69	63	15.5	344	3	US-09-820-843A-35	Sequence 35, Appl
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71	63	15.5	409	4	US-10-771-931-33	Sequence 33, Appl
72	63	15.5	556	4	US-10-029-386-32259	Sequence 32259, A
73	63	15.5	732	4	US-10-425-114-55228	Sequence 55228, A
74	63	15.5	917	6	US-11-034-275-27	Sequence 27, Appl
75	63	15.5	1043	4	US-10-310-154-449	Sequence 449, App

RESULT 1
US-09-955-502-21
Sequence 21, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 76
TYPE: PRT
ORGANISM: Buchnera sp. APS

US-09-955-502-21

Query Match	100.0%;	Score 406;	DB 3;	Length 76;
Best Local Similarity	100.0%;	Pred. No. 5.4e-38;		
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Db 1 MNRIFCTPFPPKKSEGDQFSYTGKLGKKIYDQISKAWEKMIKQTILLNBNENL 60

QY	61	EHRK	IE	KY	ML	PL	FK	76
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RESULT 2
US-09-955-502-11

; Sequence 11, Application US/09955502

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins

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; SEQ ID NO 11
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli K-12 MG1655
US-09-955-502-11

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RESULT 3
US-09-955-502-12

Sequence 12, Application US/09955502
Patent No. US20020073119A1

; GENERAL INFORMATION:
 ; APPLICANT: Downs, Diana M
 ; APPLICANT: Gralnick, Jeff

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: TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
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: TITLE OF INVENTION: Oxygen-Labile Proteins
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: FILER REFERENCE: 960296 97559

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US-09-955-502-12	
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Best Local Similarity 61.8%; Pred. No. 5e-22;
Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

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US-09-955-502-13

; Sequence 13, Application US/09955502
; Date: 11/20/2009 11:20:00 AM

APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff

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; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559

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3      / LENGTH: 91
4      /
5      / TYPE: PRT
6      /
7      / ORGANISM: Escherichia coli O157:H7
8      /
9      / US-09-955-502-13

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RESULT 5
US-09-955-502-15

; Sequence 15, Application US/09955502
Patent No. US200907319A1

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; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff

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; TITLE OF INVENTION: Method for preventing superoxide damage to cells and
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; TITLE OF INVENTION: Oxygen-Labile Proteins
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; PRT REFERENCE: 960296 97559

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Query Match	63.8%	Score 259	DB 3	Length 88
Best Local Similarity	60.5%	Pred. NO. 2.3e-21		
Matches 46	Conservative 15	Mismatches 15	Indels 0	Gaps 0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 4.24146 Seconds

(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502a-21

Perfect score: 406

Sequence: 1 MNRIFCTFFKKKSGQDFQ.....MFLNLRKKIKEXMFLFK 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	58	14.3	124	US-11-072-512-2018	Sequence 2018, App
5	58	14.3	805	US-10-927-641-77	Sequence 77, App
6	57	14.0	296	US-11-102-978-7	Sequence 7, App
7	57	14.0	552	US-11-072-512-3426	Sequence 3426, App
8	57	14.0	570	US-11-072-512-2109	Sequence 2109, App
9	57	14.0	629	US-11-072-512-3405	Sequence 3405, App
10	56.5	13.9	261	US-10-763-712a-113	Sequence 113, App
11	56.5	13.9	316	US-11-098-686-11429	Sequence 11429, App
12	56	13.8	342	US-11-156-084-25	Sequence 25, App
13	56	13.8	342	US-11-156-084-44	Sequence 44, App
14	56	13.8	369	US-11-156-084-45	Sequence 45, App
15	56	13.8	619	US-11-156-084-24	Sequence 24, App
16	55.5	13.7	296	US-11-204-187-1	Sequence 1, App
17	55.5	13.7	296	US-11-205-562-1	Sequence 1, App
18	55.5	13.7	362	US-11-098-686-11051	Sequence 11051, App
19	55	13.5	2723	US-10-895-064-388	Sequence 388, App
20	55	13.5	2723	US-11-129-741-388	Sequence 388, App
21	55	13.5	2723	US-11-129-741-3118	Sequence 3118, App
22	54	13.3	390	US-11-019-711-65	Sequence 65, App
23	54	13.3	390	US-11-219-282-12	Sequence 12, App
24	54	13.3	438	US-11-124-367a-331	Sequence 331, App
25	54	13.3	574	US-11-098-686-11000	Sequence 11000, App

26	54	13.3	898	US-11-099-691-7	Sequence 7, App
27	54	13.3	898	US-11-124-367a-330	Sequence 330, App
28	54	13.3	898	US-11-124-367a-333	Sequence 333, App
29	54	13.3	1614	US-10-821-234-903	Sequence 903, App
30	53.5	13.2	174	US-11-074-176-264	Sequence 264, App
31	53.5	13.2	360	US-10-467-657-4196	Sequence 4196, App
32	53.5	13.2	446	US-11-119-351-8	Sequence 8, App
33	53.5	13.2	626	US-10-467-657-11772	Sequence 11772, App
34	53.5	13.2	1405	US-10-995-561-529	Sequence 529, App
35	53.5	13.2	1406	US-10-995-561-530	Sequence 530, App
36	53.5	13.2	1436	US-10-995-561-531	Sequence 531, App
37	53.5	13.2	2710	US-11-051-453-41	Sequence 41, App
38	53	13.1	486	US-11-057-012-11	Sequence 11, App
39	53	13.1	581	US-10-793-628-28	Sequence 28, App
40	53	13.1	752	US-10-793-628-1036	Sequence 1036, App
41	52	12.8	208	US-10-793-628-694	Sequence 694, App
42	52	12.8	208	US-10-793-628-1326	Sequence 1326, App
43	52	12.8	471	US-11-098-686-11158	Sequence 11158, App
44	52	12.8	490	US-10-793-628-872	Sequence 872, App
45	52	12.8	550	US-11-072-512-3416	Sequence 3416, App
46	52	12.8	593	US-11-194-246-317	Sequence 317, App
47	52	12.8	634	US-11-072-512-2300	Sequence 2300, App
48	52	12.8	661	US-10-793-628-274	Sequence 274, App
49	52	12.8	1076	US-11-098-686-11338	Sequence 11338, App
50	51.5	12.7	205	US-11-054-281-12	Sequence 12, App
51	51.5	12.7	296	US-10-878-556a-190	Sequence 190, App
52	51.5	12.7	296	US-11-204-187-3	Sequence 3, App
53	51.5	12.7	296	US-11-205-562-3	Sequence 3, App
54	51.5	12.7	364	US-10-467-657-4106	Sequence 4106, App
55	51.5	12.7	364	US-11-054-281-70	Sequence 70, App
56	51.5	12.7	374	US-11-054-281-68	Sequence 68, App
57	51.5	12.7	381	US-11-072-512-3313	Sequence 3313, App
58	51.5	12.7	394	US-11-054-281-66	Sequence 66, App
59	51.5	12.7	401	US-11-054-281-67	Sequence 67, App
60	51.5	12.7	418	US-10-131-826a-486	Sequence 486, App
61	51.5	12.7	418	US-11-177-505-27	Sequence 27, App
62	51.5	12.7	418	US-11-183-205-22	Sequence 22, App
63	51.5	12.7	756	US-11-223-188-2	Sequence 2, App
64	51.5	12.7	885	US-10-793-628-1660	Sequence 1660, App
65	51.5	12.7	1145	US-10-793-628-1632	Sequence 1632, App
66	51	12.6	83	US-10-746-959c-2	Sequence 2, App
67	51	12.6	181	US-10-746-959c-10	Sequence 10, App
68	51	12.6	261	US-10-055-877-164	Sequence 164, App
69	51	12.6	261	US-10-055-877-165	Sequence 165, App
70	51	12.6	261	US-11-177-506-31	Sequence 31, App
71	51	12.6	299	US-11-156-084-47	Sequence 47, App
72	51	12.6	330	US-11-156-084-27	Sequence 27, App
73	51	12.6	342	US-11-156-084-48	Sequence 48, App
74	51	12.6	342	US-11-098-686-10943	Sequence 10943, App
75	51	12.6	724	US-11-109-156-19	Sequence 19, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581a1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 38.9%; Score 158; DB 6; Length 88;
Best Local Similarity 36.0%; Pred. No. 4,2e-11;
Matches 27; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MNRIFCTFFPKKSGQDFQSYPGKLGKKIYDQISKKAMEKWEIKQTLLINEENINMNL 60
Db 1 MARWFCVKLANEAKGKFPPLPNELGKRFENVSGEAWAATRQTMLINENRSLADP 60

Qy 61 EHRKKIEKMKLFLP 75
Db 61 RAREYLAQOMEQYFF 75

RESULT 2
US-11-219-282-13

Sequence 13, Application US/11219282
Publication No. US20060018892A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Clarke, Howard RG
APPLICANT: Dabose, Robert F
APPLICANT: Wiley, Steven R
TITLE OF INVENTION: HUMAN SERPIN POLYPEPTIDES
FILE REFERENCE: 3223-A
CURRENT APPLICATION NUMBER: US/11/219,282
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US/10/094,944
PRIOR FILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
US-11-219-282-13

Query Match 15.0%; Score 61; DB 7; Length 390;
Best Local Similarity 32.0%; Pred. No. 14;
Matches 16; Conservative 7; Mismatches 15; Indels 12; Gaps 2;

Qy 9 FPKKXSEGQDFQSYPGKLGKKIYDQISKKAMEKWEIKQTLLINEENINMF 58
Db 126 FYQTSVESTDFANAPESRRTI-----NSWVESQT---NEKIKNLF 163

RESULT 3
US-10-986-501-165

Sequence 165, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04

PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 165
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-10-986-501-165

Query Match 14.5%; Score 59; DB 6; Length 109;
Best Local Similarity 24.4%; Pred. No. 5.7;
Matches 21; Conservative 14; Mismatches 27; Indels 24; Gaps 3;

Qy 4 IIFCTFFPKKSGE-----GQDFQSYPGKLGKKIYDQISKKAMEKWEIKQTLLINEENIN- 56
Db 26 ILVTLMEKKKARHVGSEELQYFPERSTKL-----KVFEEEEKQTATSDNTKA 79

Qy 57 -----MFLNHRKKIEKTMK 71
Db 80 LVHSVYTRGAVNFLVEKELSLSEKTLK 105

RESULT 4
US-11-072-512-2018

Sequence 2018, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTAKO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2018
LENGTH: 124
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-2018

Query Match 14.3%; Score 58; DB 7; Length 124;
Best Local Similarity 35.7%; Pred. No. 8.5;
Matches 10; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 / Search time 72.9841 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-22

Perfect score: 483

Sequence: 1 MORIIFCEYEQRDEGLDFV.....LNKFLFERRVAKPEGYEPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472.5	97.8	90	5	ABB78167 Amino aci
2	246	50.9	87	5	ABB78153 Amino aci
3	238	49.3	107	7	Abd65445 K1edsteli
4	237	49.1	87	5	ABB78151 Amino aci
5	237	49.1	87	5	ABB78152 Amino aci
6	234	48.4	91	5	ABB78150 Amino aci
7	232	48.0	91	5	ABB78151 Amino aci
8	232	48.0	91	5	ABB78159 Amino aci
9	232	48.0	91	5	ABB78162 Amino aci
10	230	47.6	91	5	ABB78163 Amino aci
11	229	47.4	88	5	ABB78160 Amino aci
12	228	47.2	90	5	ABB78155 Amino aci
13	227	47.0	93	7	ADP05158 Bacterial
14	226	46.8	91	5	ABB78158 Amino aci
15	226	46.8	91	5	ABB78157 Amino aci
16	226	46.8	91	5	ABB78156 Amino aci
17	220	45.5	78	5	ABB78164 Amino aci
18	215	44.5	87	5	ABB78176 Amino aci
19	214	44.3	88	5	ABB78178 Amino aci
20	209	43.3	89	9	ABE41576 L. pneumo
21	209	43.3	95	9	ABE38294 L. pneumo
22	205	42.4	87	5	ABB78148 Amino aci
23	205	42.4	87	5	ABB78147 Amino aci
24	203.5	42.1	92	6	ADA34169 Actinotoba

25	203	42.0	90	5	ABB78165 Amino aci
26	201	41.6	87	5	ABB78177 Amino aci
27	201	41.6	88	5	ABB78171 Amino aci
28	201	41.6	88	5	ABB78172 Amino aci
29	201	41.6	88	5	ABB78173 Amino aci
30	201	41.6	88	6	ABP77219 N. gonorr
31	200	41.4	90	5	ABB78168 Amino aci
32	198	41.0	87	5	ABB78169 Amino aci
33	198	41.0	122	7	ABO74609 Pseudomon
34	197	40.8	87	5	ABB78175 Amino aci
35	196	40.6	88	5	ABB78154 Amino aci
36	195	40.4	86	5	ABB78149 Amino aci
37	192	39.8	87	5	ABB78170 Amino aci
38	191	39.5	87	5	ABB78174 Amino aci
39	183	37.9	76	5	ABB78166 Amino aci
40	150	31.1	110	8	AD05173 M. catarr
41	71	14.7	582	8	ADY10873 Plant ful
42	67.5	14.0	272	5	ABU05512 M. tuberc
43	67	13.9	87	3	AAE54259 Human pan
44	67	13.9	302	4	AAU35741 Helicobac
45	67	13.9	302	6	ABU30804 Protein e
46	67	13.9	305	7	ADM25449 Hyperther
47	66	13.7	379	4	AAI97562 Mouse Wnt
48	66	13.7	379	6	ABG71361 Mouse Wnt
49	66	13.7	379	7	ADD90585 WIF domai
50	66	13.7	379	7	ADD90566 Mouse WIF
51	66	13.7	379	7	ADD90583 WIF domai
52	66	13.7	379	7	ADD90581 WIF domai
53	66	13.7	379	7	ADD90579 WIF domai
54	66	13.7	379	8	ADP95945 Murine WI
55	64.5	13.4	327	3	AAI16535 Bacteriop
56	64	13.3	208	2	AAI41660 Triticum
57	64	13.3	365	7	ADD90570 Rat WIF-1
58	64	13.3	831	8	ADN20509 Bacterial
59	63	13.0	305	7	ADM25566 Hyperther
60	63	13.0	544	3	AAI40947 Zea mays
61	62.5	12.9	219	8	ADM57215 A thalian
62	62.5	12.9	314	6	ABU44876 Protein e
63	62.5	12.9	389	7	ADM04529 Rat Prote
64	62.5	12.9	389	7	ADM04529 Human pro
65	62.5	12.9	405	6	AAE32119 Human cyt
66	62.5	12.9	439	6	ABU50419 Protein e
67	62	12.8	174	2	AAI34740 Chlamydia
68	62	12.8	409	8	ADP58047 Plant pol
69	62	12.8	435	4	ABG08894 Novel hum
70	62	12.8	533	2	AAI39705 Chicken P
71	62	12.8	646	3	AAI57307 P. aerugi
72	62	12.8	667	5	ABE93976 Herpicida
73	62	12.8	667	8	ADN73801 Thale cre
74	62	12.8	670	3	AAI57314 P. aerugi
75	62	12.8	686	7	ABO80650 Pseudomon

ALIGNMENTS

RESULT 1	ABB78167	standard; protein; 90 AA.
ID	ABB78167	
XX	ABB78167	
AC	ABB78167	
DT	05-NOV-2002	(first entry)
XX		
DR	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX		
OS	Xylella fastidiosa.	
XX		
PH	Key	Location/Qualifiers
FT	Misc-difference 61	

FT /note= "not specified"
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from *Salmonella*
XX *enterica* serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 90 AA;
Query Match 97.8%; Score 472.5; DB 5; Length 90;
Best Local Similarity 98.9%; Pred. No. 5.7e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MORIIFCEYEQDTEGLDFVYPYGEIGQKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
DB 1 MORIIFCEYEQDTEGLDFVYPYGEIGQKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
QY 61 -SHRAFLBEELNKFLPERVAKPEGYIEPD 89
DB 61 XSHRAFLBEELNKFLPERVAKPEGYIEPD 90
RESULT 2
ABB78153
ID ABB78153 standard; protein; 87 AA.
XX
XX ABB78153;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX

PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from *Salmonella*
XX *enterica* serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;
Query Match 50.9%; Score 246; DB 5; Length 87;
Best Local Similarity 51.2%; Pred. No. 4.1e-22;
Matches 44; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 MORIIFCEYEQDTEGLDFVYPYGEIGQKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
DB 1 MARVMFCGYLKKBAAGLDFQLYPGELGRIRFNSISKQAWAMIKQOTVLVNEKKLMMNP 60
QY 61 SHRAFLBEELNKFLPERVAKPEGYI 86
DB 61 EHRQLLEAMVNFLEGRDVAIDGYV 86
RESULT 3
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
XX ABO65445;
XX
XX 29-JUL-2004 (first entry)
XX
XX *Klebsiella pneumoniae* polypeptide seqid 11962.
XX
XX Recombinant expression vector; transcription regulatory element;
XX *Klebsiella pneumoniae* protein; antibacterial; Vaccine.
XX
XX *Klebsiella pneumoniae*.
XX
XX US6610836-B1.
XX
XX 26-AUG-2003.
XX
XX 27-JAN-2000; 2000US-00489039.
XX
XX 29-JAN-1999; 99US-0117747P.
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
XX
XX Breton GL, Osborne M;
XX
XX WPI; 2003-895346/82.
XX
XX N-PSDB; ACH98996.
XX
XX New nucleic acid encoding a *Klebsiella pneumoniae* polypeptide, useful for
XX preparing a vaccine composition against *Klebsiella pneumoniae*.
XX
XX Disclosure; SEQ ID NO 11962; 932pp; English.
XX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 / Search time 9.73121 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-22

Perfect score: 483
Sequence: 1 MORLFCBYEORDTEGLDFV.....LNKPLFERRVAKPGYIIBPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	105	2	C82624 conserved hypothet
2	243	50.3	90	2	C64013 conserved hypothet
3	232	48.0	91	2	AH0879 conserved hypothet
4	228	47.2	90	2	C82320 conserved hypothet
5	226	46.8	91	2	A85954 conserved hypothet
6	226	46.8	91	2	A65082 conserved hypothet
7	226	46.8	91	2	F91108 conserved hypothet
8	203	42.0	90	2	A10116 conserved hypothet
9	201	41.6	88	2	H81014 conserved hypothet
10	198	41.0	90	2	H83003 conserved hypothet
11	185	38.3	93	2	H84994 conserved hypothet
12	67.5	14.0	272	2	H87075 conserved hypothet
13	67	13.9	302	2	B64584 conserved hypothet
14	63.5	13.1	587	2	S23312 conserved hypothet
15	63.5	13.1	1131	2	T14517 conserved hypothet
16	63	13.0	105	2	B75442 conserved hypothet
17	63	13.0	415	2	S55617 conserved hypothet
18	62.5	12.9	219	2	C96510 conserved hypothet
19	62.5	12.9	439	2	AC0491 conserved hypothet
20	62	12.8	188	2	C86508 conserved hypothet
21	62	12.8	188	2	H72114 conserved hypothet
22	62	12.8	305	1	OMP8A conserved hypothet
23	62	12.8	526	1	S26420 conserved hypothet
24	62	12.8	533	1	TVCHS conserved hypothet
25	62	12.8	863	2	C83540 conserved hypothet
26	62	12.8	863	2	S38140 conserved hypothet
27	61.5	12.7	359	2	C84983 conserved hypothet
28	61.5	12.7	445	2	T01591 conserved hypothet
29	61.5	12.7	494	2	S23315 conserved hypothet

30	61.5	12.7	729	2	G97169	protein containing
31	61.5	12.7	869	1	A47257	1-phosphatidylinos
32	61	12.6	143	2	I47053	relaxin B,C and A
33	61	12.6	301	2	G71929	GTP-binding protei
34	61	12.6	332	2	B47017	probable transcrip
35	61	12.6	332	2	AD2541	transcription init
36	61	12.6	379	2	A59180	Mnt inhibitory fac
37	60.5	12.5	440	2	AC0980	xylose isomerase (
38	60.5	12.5	1894	2	JC4980	plexin 1 precursor
39	60	12.4	243	2	AP1611	3-ketoacyl-acyl ca
40	60	12.4	318	2	C83555	hypothetical prote
41	60	12.4	360	1	F64601	conserved hypothet
42	60	12.4	878	2	G71371	probable endopepti
43	60	12.4	901	1	FAHUA3	alpha-actinin 3 -
44	60	12.4	984	2	T48216	hypothetical prote
45	59.5	12.3	761	2	AC0791	ribonucleoside-dip
46	59.5	12.3	761	2	S32629	ribonucleoside-dip
47	59.5	12.3	997	2	S33754	glutamate receptor
48	59.5	12.3	1017	2	T08553	hypothetical prote
49	59	12.2	231	2	AE0725	conserved hypothet
50	59	12.2	231	2	AP3028	hypothetical prote
51	59	12.2	231	2	B98256	hypothetical prote
52	59	12.2	283	2	D72398	conserved hypothet
53	59	12.2	290	2	AC3417	DNA polymerase, ba
54	59	12.2	360	2	E71910	hypothetical prote
55	59	12.2	486	2	P98106	glutamate-tRNA lig
56	59	12.2	496	2	D83614	conserved hypothet
57	59	12.2	3587	2	I40486	surfactin synthet
58	58.5	12.1	127	2	B72593	probable gaectrin p
59	58.5	12.1	231	2	AF1838	hypothetical prote
60	58.5	12.1	323	2	H71481	hypothetical prote
61	58.5	12.1	496	2	JC5110	hypothetical prote
62	58.5	12.1	1327	2	T21268	hypothetical prote
63	58	12.0	194	2	I39526	hypothetical prote
64	58	12.0	247	2	T27205	hypothetical prote
65	58	12.0	251	2	B90428	hypothetical prote
66	58	12.0	457	2	F64095	argininosuccinate
67	58	12.0	526	1	TYFVR	protein-tyrosine k
68	58	12.0	526	2	S15582	protein-tyrosine k
69	58	12.0	632	2	H83106	chemotactic transd
70	58	12.0	1066	2	B95037	hyaluronidase [imp
71	58	12.0	1078	2	F97907	hyaluronate lyase
72	58	12.0	1107	2	T21280	hypothetical prote
73	58	12.0	4450	2	JX0340	gramicidin S synth
74	58	12.0	4452	1	YGBS62	gramicidin S synth
75	57.5	11.9	373	2	F70781	probable cifa prot

ALIGNMENTS

RESULT 1

C82624 conserved hypothetical protein XFI908 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004

C:Accession: C82624

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: C82624

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <SIM>

A:Cross-references: UNIPARC:UPI00000C288F; GB:AE004010; GB:AE003849; NID:G9106992; PIDN:

R:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Britones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrez, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Fromm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitaajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E
A.; Authors: Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1908
C;Superfamily: fe(II) trafficking protein Y9x

Query Match 100.0%; Score 483; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-48;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORITFCYEBQDTEGLDFVYPGELGOKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
Db 16 MORITFCYEBQDTEGLDFVYPGELGOKIFACIGKVGMAAMLVHQTMLINENRLSPNP 75

Qy 61 SHRAFLBEELINKFLFERRVAKPEGYTEP 89
Db 76 SHRAFLBEELINKFLFERRVAKPEGYTEP 104

RESULT 2
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C;Accession: C64013
R;Fitschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervayage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weisman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Georgagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:9550630; PMID:7542800
A;Accession: C64013
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-90 <TRIG>
A;Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:915
C;Superfamily: fe(II) trafficking protein Y9x

Query Match 50.3%; Score 243; DB 2; Length 90;
Best Local Similarity 48.9%; Pred. No. 9.5e-21;
Matches 43; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MORITFCYEBQDTEGLDFVYPGELGOKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
Db 1 MARITFCYELKKEAGELDFQLYPSELGKRITFDSVSKQAGWIKQKQMLVNEKLMNNA 60

Qy 61 SHRAFLBEELINKFLFERRVAKPEGYTEP 88
Db 61 EHRKLLBEQWVNFLEPGKDVHIEGYTP 88

RESULT 3
AH0879
conserved hypothetical protein STY326 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typh
A;Note: This species has also been called Salmonella typh
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AH0879
R;Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AH0879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <PAR>
A;Cross-references: UNIPARC:UPI0000544C; GB:AL513382; PIDN:CAD02936.1; PID:G16504189; C
C;Genetics:
A;Gene: STY326
C;Superfamily: fe(II) trafficking protein Y9x

Query Match 48.0%; Score 232; DB 2; Length 91;
Best Local Similarity 52.8%; Pred. No. 1.8e-19;
Matches 47; Conservative 8; Mismatches 34; Indels 0; Gaps 0;

Qy 1 MORITFCYEBQDTEGLDFVYPGELGOKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
Db 1 MSRTITFCYLRDKEAGDFQLYPSELGKRITFDSVSKQAGWIKQKQMLVNEKLMNNA 60

Qy 61 SHRAFLBEELINKFLFERRVAKPEGYTEP 89
Db 61 EHRKLLBEQWVNFLEPGKDVHIEGYTP 89

RESULT 4
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: C82320
R;Heidelberg, U.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <HEI>
A;Cross-references: UNIPARC:UPI0000062CCF; GB:AE004132; GB:AE003852; NID:99654871; PIDN:..
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0451
A;Map position: 1
C;Superfamily: fe(II) trafficking protein Y9x

Query Match 47.2%; Score 228; DB 2; Length 90;
Best Local Similarity 50.0%; Pred. No. 5e-19;
Matches 44; Conservative 12; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MORITFCYEBQDTEGLDFVYPGELGOKIFACIGKVGMAAMLVHQTMLINENRLSPNP 60
Db 1 MARITFCYLRDKEAGDFQLYPSELGKRITFDSVSKQAGWIKQKQMLVNEKLMNNDP 60

Qy 61 SHRAFLBEELINKFLFERRVAKPEGYTEP 88
Db 61 EHRKLLBEQWVNFLEPGKDVHIEGYTP 88

RESULT 5
A85954
hypothetical protein Y9x [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: A85954
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, B.J.; Davis, N.W.; Jim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 65.6856 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-22

Perfect score: 483

Sequence: 1 MQRIFCEYEDRDEGLDFV.....LNKFLFERRVAKPEGYRPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	90	1	FERP_XYLFA
2	465	96.3	90	1	FERP_XYLFA
3	380	78.7	92	1	FERP_XANCP
4	380	78.7	92	2	Q4UW14_XANCP
5	367	76.0	91	1	FERP_XANAC
6	367	76.0	92	1	FERP_XANOR
7	247	51.1	90	1	FERP_IDILO
8	246	50.9	94	1	FERP_HABDU
9	244	50.5	90	1	FERP_PHOIL
10	243	50.3	90	1	FERP_HAEIN
11	243	50.3	90	1	FERP_PASNU
12	243	50.3	90	2	Q4QMD9_HAE18
13	236	48.9	91	1	FERP_MANSN
14	228	47.2	90	1	FERP_VIBCH
15	227	47.0	90	1	FERP_SALCH
16	227	47.0	90	1	FERP_SALPA
17	227	47.0	90	1	FERP_SALTI
18	227	47.0	90	1	FERP_SALTY
19	225	46.6	90	1	FERP_BRMCT
20	222	46.0	90	1	FERP_VIBPA
21	221	45.8	90	1	FERP_ECO57
22	221	45.8	90	1	FERP_ECOLI
23	221	45.8	90	1	FERP_SHIFL
24	219	45.3	90	1	FERP_PHOPR
25	217	44.9	90	1	FERP_ECOL6
26	217	44.9	90	1	FERP_VIBVU
27	217	44.9	90	1	FERP_VIBVY
28	214	44.3	90	1	FERP_COXBU
29	212	43.9	91	1	FERP_RALSO
30	211	43.7	90	1	FERP_BORBR
31	211	43.7	90	1	FERP_BORPA

32	211	43.7	90	1	FERP_BORPE	Q7WC4 bordetella
33	211	43.7	90	1	FERP_YERPS	O66M3 yersinia ps
34	209	43.3	89	1	FERP_YERPA	O5X39 yersinia
35	209	43.3	89	1	FERP_YERPH	O5Z80 legionella
36	209	43.3	90	1	FERP_VIBPL	O5E70 vibrio fisc
37	208	43.1	89	1	FERP_LEGPL	O5WC4 legionella
38	207	42.9	90	1	FERP_METCA	O60J7 methylococc
39	206	42.7	87	1	FERP_FRATY	O5N18 franciella
40	204.5	42.3	90	1	FERP_ACICD	O6Fb3 acinetobact
41	204	42.2	90	1	FERP_PSEBK	O8B49 pseudomonas
42	203	42.0	90	1	FERP_YERPE	O8ZNE yersinia pe
43	203	42.0	91	1	FERP_BURMA	O62J9 burholderi
44	203	42.0	91	1	FERP_BURPS	O62J9 burholderi
45	203	42.0	91	2	Q4LS19_9BRXK	O82Xf2 nitrosomona
46	201	41.6	88	1	FERP_NEIGL	O87Uf5 pseudomonas
47	201	41.6	88	1	FERP_NEIMA	O4Z1P3 pseudomonas
48	201	41.6	88	1	FERP_NEIMB	O9NU36 pseudomonas
49	200	41.4	90	1	FERP_CHRYO	O4J28 azotobacter
50	200	41.4	90	1	FERP_NITRU	O8EUX6 shewanella
51	200	41.4	90	1	FERP_PSRSM	O4K12 pseudomonas
52	200	41.4	90	2	Q4ZLF3_PSESY	O87Uf5 pseudomonas
53	198	41.0	90	1	FERP_PSEAP	O4Z1P3 pseudomonas
54	197	40.8	90	2	Q4U228_AZCVI	O9NU36 pseudomonas
55	196	40.6	92	1	FERP_SHEON	O4J28 azotobacter
56	194	40.2	90	2	Q4KJ72_PSEFS	O8EUX6 shewanella
57	191	39.5	78	1	FERP_BUCAP	O4K12 pseudomonas
58	190	39.3	90	2	Q67F6_PSEFL	O8K925 buchnera ap
59	185	38.3	77	1	FERP_BUCAL	O67F6 pseudomonas
60	180	37.3	78	1	FERP_WIGBR	P57618 buchnera ap
61	172	35.6	87	1	FERP_BUCBR	O8D45 wigleswort
62	168	34.8	92	2	Q4NMQ4_9BELT	O89444 buchnera ap
63	156	32.3	79	1	FERP_CANBR	O4NMQ4 anaeromyxob
64	154	31.9	96	2	Q4RVU7_9GAMM	O7VNU4 rhodospirell
65	91.5	18.9	123	2	O81221_BACCR	O4FVJ7 psychrobact
66	75.5	15.6	635	2	O6VBYO_TOXGO	O81221 bacillus ce
67	74.5	15.4	472	2	O7NVX6_CHRYO	O6BYO toxoplasma
68	73	15.1	174	2	O6B658_HELPY	O7NVX6 chromobacte
69	70.5	14.6	468	2	Q7UPU4_RHOBA	O6B658 helicobacte
70	70.5	14.6	764	2	O8LMT3_ORYSA	O7UPU4 rhodospirell
71	69.5	14.4	217	2	Q9DQBO_AHSV7	O8LMT3 oryza sativ
72	68.5	14.2	129	2	O6BJ04_DBBHA	O9DQBO african hor
73	68.5	14.2	1065	2	O9FJ16_ABBHA	O6BJ04 darbaryomyce
74	68	14.1	5141	2	O7S6D3_NEUCR	O9FJ16 arabidopsia
75	67.5	14.0	272	2	Q9ZBD7_MYCLE	O7S6D3 neurospora

ALIGNMENTS

RESULT 1			
ID	FERP_XYLFA	STANDARD;	PRT; 90 AA.
AC	Q9PC73;		
DT	10-OCT-2003 (Rel. 42, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Probable Fe(2+) trafficking protein.		
GN	OrderedlocusNames=Xt1908;		
OC	Xylella fastidiosa.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;		
OC	Xanthomonadaceae; Xylella.		
OX	NCBI_TaxID=2371;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RC	STRAIN=9ac;		
RC	MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;		
RX	Simpson A.J.G., Reinach P.C., Arruda P., Abreu F.A., Acencio M.,		
RA	Alvares R., Alves L.M.C., Araya J.E., Bata G.S., Baptista C.S.,		
RA	Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,		
RA	Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,		
RA	Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,		
RA	Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,		
RA	Facinanci A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,		

RA Praga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Gantier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitzling J.P.,
RA Krieger J.E., Kuramae E.B., Laigret F., Lamais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhat A.Jr., Nodrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pequeiro J.B.,
RA Queglio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA da Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshaho M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Melandris J., Setubal J.C.,
RT "The genome sequence of the plant pathogen *Xylella fastidiosa*,"
RL Nature 406:151-159(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE004010; AAF64714.1; ALT_INIT; Genomic_DNA.
CC HANAP; MF_00686; -, 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe traffic_YggX; 1.
CC Prodom: PD029191; DUF495; 1.
CC KW Complete proteome; Iron.
CC SQ SEQUENCE 90 AA; 10555 MW; E9BBB3BCA6D104A3 CRC64;
Query Match 100.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MORIIFCEYRDTEGLDFVYPYGGELGOKIFACIGKVGMAAWLVHQTMLINENRSLSPNP 60
QY 61 SHRAFLBEELINKFLFERRVAKDEGYIEPD 89
DB 61 SHRAFLBEELINKFLFERRVAKDEGYIEPD 89
RESULT 2
FETP_XYLFT ID FETP_XYLFT STANDARD; PRT; 90 AA.
AC Q87D06;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocNames=PD0883;
OS *Xylella fastidiosa* (strain Temecual / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; *Xylella*.
OX NCBI_TaxID=183190;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22421331; PubMed=12533478;
RX DOI=10.1128/DB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carrer H., Carriao D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harkava R., Kuramae E.B.,
RA Martino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Bata G.S., Bianco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA da Cunha A.F., Penille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira R.C., Rosa V.E. Jr., Sasaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yenal G.M., Zatz L.G.,
RA Civerolo E.L., Simpson A.U.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitzling J.P.,
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of *Xylella*
RT *fastidiosa*,"
RL J. Bacteriol. 185:1018-1026(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE012556; AAO28748.1; -, Genomic_DNA.
CC HANAP; MF_00686; -, 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe traffic_YggX; 1.
CC Prodom: PD029191; DUF495; 1.
CC KW Complete proteome; Iron.
CC SQ SEQUENCE 90 AA; 10430 MW; B5C6936496F471D CRC64;
Query Match 96.3%; Score 465; DB 1; Length 90;
Best Local Similarity 95.5%; Pred. No. 1.9e-45;
Matches 85; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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DB 1 MORIIFCEYRDTEGLDFVYPYGGELGOKIFACIGKVGMAAWLVHQTMLINENRSLSPNP 60
QY 61 SHRAFLBEELINKFLFERRVAKDEGYIEPD 89
DB 61 SHRAFLBEELINKFLFERRVAKDEGYIEPD 89
RESULT 3
FETP_XANCP ID FETP_XANCP STANDARD; PRT; 92 AA.
AC Q8P829;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocNames=XCC2419;
OS *Xanthomonas campestris* (pv. *campestris*).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; *Xanthomonas*.
OX NCBI_TaxID=340;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 35913 / NCEPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Queglio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Camargo L.E.A., Camarotte G., Cannavan F., Cardoso J., Chambergro F.,
RA Ciapina L.P., Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katayama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 18.0433 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-22

Perfect score: 483

Sequence: 1 MORITFCHEQDTEGLDFV.....LNKFLFERRVAKPEGYRPD 89

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	49.3	107	2	US-09-489-039A-11962
2	227	47.0	93	2	US-09-543-681A-5443
3	203.5	42.1	92	2	US-09-328-352-5456
4	198	41.0	122	2	US-09-252-991A-23355
5	150	31.1	110	2	US-09-540-236-2859
6	62	12.8	174	2	US-09-198-452A-158
7	62	12.8	198	2	US-09-438-185A-141
8	62	12.8	198	2	US-09-328-501-1
9	62	12.8	646	5	US-09-777-710A-1
10	62	12.8	646	5	US-10-191-289A-1
11	62	12.8	670	2	US-09-328-501-15
12	62	12.8	670	2	US-09-777-710A-15
13	62	12.8	670	5	US-10-191-289A-15
14	62	12.8	683	2	US-09-252-991A-29396
15	61	12.6	336	2	US-09-107-532A-4544
16	61	12.6	461	2	US-09-107-433-2847
17	60.5	12.5	251	2	US-09-489-039A-7987
18	60	12.4	286	2	US-09-543-681A-5269
19	59.5	12.3	626	2	US-09-248-796A-7203
20	59.5	12.3	770	2	US-09-543-681A-4291
21	59	12.2	170	2	US-09-489-039A-7536
22	59	12.2	295	2	US-08-952-089A-1
23	59	12.2	295	2	US-09-690-885-1
24	59	12.2	320	2	US-09-248-796A-15469
25	59	12.2	348	1	US-08-844-153-2
26	59	12.2	480	1	US-08-962-203-2
27	59	12.2	480	2	US-09-282-125A-2

28	59	12.2	480	2	US-09-273-142-2	Sequence 2, Appl1
29	58.5	12.1	185	2	US-09-270-767-36317	Sequence 36317, A
30	58.5	12.1	185	2	US-09-270-767-51534	Sequence 51534, A
31	58.5	12.1	496	2	US-09-695-795A-8	Sequence 8, Appl1
32	58.5	12.1	771	1	US-08-742-753-2	Sequence 2, Appl1
33	58	12.0	331	1	US-09-719-108-2	Sequence 2, Appl1
34	58	12.0	640	2	US-09-252-991A-23252	Sequence 23252, A
35	58	12.0	776	2	US-08-284-180A-3	Sequence 3, Appl1
36	58	12.0	2353	2	US-08-984-709A-50	Sequence 50, Appl1
37	57.5	11.9	278	1	US-08-258-261B-20	Sequence 20, Appl1
38	57.5	11.9	278	1	US-08-456-837-20	Sequence 20, Appl1
39	57.5	11.9	278	1	US-08-457-342-20	Sequence 20, Appl1
40	57.5	11.9	278	1	US-08-457-646A-20	Sequence 20, Appl1
41	57.5	11.9	278	1	US-08-458-076A-20	Sequence 20, Appl1
42	57.5	11.9	278	1	US-08-457-335A-20	Sequence 20, Appl1
43	57.5	11.9	278	1	US-08-729-214-20	Sequence 20, Appl1
44	57.5	11.9	278	2	US-09-028-934-20	Sequence 20, Appl1
45	57.5	11.9	647	2	US-09-252-991A-32816	Sequence 32816, A
46	57	11.8	184	2	US-09-270-767-46275	Sequence 46275, A
47	57	11.8	293	2	US-09-071-035-496	Sequence 496, App
48	57	11.8	293	2	US-10-206-576-496	Sequence 496, App
49	57	11.8	316	2	US-09-071-035-494	Sequence 494, App
50	57	11.8	316	2	US-10-206-576-494	Sequence 494, App
51	57	11.8	371	2	US-09-543-681A-6429	Sequence 6429, App
52	57	11.8	379	2	US-09-907-794A-4	Sequence 4, Appl1
53	57	11.8	379	2	US-09-905-125A-4	Sequence 4, Appl1
54	57	11.8	379	2	US-09-905-775A-4	Sequence 4, Appl1
55	57	11.8	379	2	US-09-906-700-4	Sequence 4, Appl1
56	57	11.8	379	2	US-09-903-603A-4	Sequence 4, Appl1
57	57	11.8	379	2	US-09-904-920A-4	Sequence 4, Appl1
58	57	11.8	379	2	US-09-909-064-4	Sequence 4, Appl1
59	57	11.8	379	2	US-09-905-381A-4	Sequence 4, Appl1
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61	57	11.8	379	2	US-09-906-646-4	Sequence 4, Appl1
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64	57	11.8	380	2	US-09-906-722A-4	Sequence 4, Appl1
65	57	11.8	380	2	US-09-205-858-441	Sequence 441, App
66	57	11.8	380	2	US-10-004-860-441	Sequence 441, App
67	57	11.8	484	2	US-08-913-578-2	Sequence 2, Appl1
68	57	11.8	484	2	US-08-785-427-2	Sequence 2, Appl1
69	56.5	11.7	321	2	US-09-107-532A-4975	Sequence 4975, App
70	56.5	11.7	357	2	US-09-489-039A-13955	Sequence 13955, A
71	56.5	11.7	394	1	US-08-646-590B-40	Sequence 40, Appl1
72	56.5	11.7	394	2	US-09-412-184-40	Sequence 40, Appl1
73	56.5	11.7	527	1	US-08-365-466A-26	Sequence 26, Appl1
74	56.5	11.7	527	2	US-08-880-342-26	Sequence 26, Appl1
75	56.5	11.7	1206	2	US-09-252-991A-19632	Sequence 19632, A

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,20040001
CURRENT FILING DATE: US/09/489,039A
PRIOR APPLICATION NUMBER: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match	49.3%;	Score 238;	DB 2;	Length 107;
Best Local Similarity	51.7%;	Pred. No. 1e-23;		
Matches	46;	Conservative	12;	Mismatches 31;
			Indels	0;
			Gaps	0;

Qy 1 MÖRIICEYEBORDETEGLDFVPYPGELGOKIFACIGKVGMAAMLVHQTMLINENRISPRNP 600
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Db 17 MSRTICTFLQREADGDFPOLYIGELGKRIYNELSKAANAQWÖHKOTMLINELKLSMNP 760

QY 61 SHRAFLBBLANKFLPERRVAKPEGYIBPD 89
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Db 77 EHRKLLLEGEMVQFLPEGKDVAIEGYTPPE 10

RESULT 2
US-09-543-681A-5443

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; SEQUENCE 343, APPLICATION 03/03335801
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON

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RELATING TO FOREIGN MATERIALS

1 TITLE OF INVENTION: NUCLEOTIC ACID SEQUENCES

2 TITLE OF INVENTION: NUCLEOTIC ACID SEQUENCES

3 TITLE OF INVENTION: NUCLEOTIC ACID SEQUENCES

4 TITLE OF INVENTION: NUCLEOTIC ACID SEQUENCES

5 FILE REFERENCE: 2709.1002-001

6 CURRENT APPLICATION NUMBER: US/09/543.681A

; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344

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: SEQ ID NO 3443
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: LENGTH: 93
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: TYPE: PRT
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: ORGANISM: Proteus mirabilis

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US-09-543-681A-5443	
Query Match	47.0%
Best Local Similarity	47.2%
Score	227
DB 2	Length 93
Prod No	2
544-32	

Matches 42; Conservative 14; Mismatches 1

Db 4 MSRTIPCTPLNKKGADGLDPQLYPGELGKRIFN
Qy 61 SHRAFLLEEINKPLFERRVAKPEGYIEPD 89

DB 64 DDRKLEQEMVRF,FBGHDVHIDGYTPB 92

RESULT 3
US-09-328-352-5456
; Sequence 5456, Application US/09328352
Patent No. 6672068

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; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: RIBONUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: RIBONUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

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; FILE REFERENCE: GTC99-03PA
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; CURRENT APPLICATION NUMBER: US/09/328,352
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; CURRENT FILING DATE: 1999-06-04
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; NUMBER OF SEQ. ID NOS.: 5253

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; SEQ ID NO 5456
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; LENGTH: 92
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; TYPE: PRT
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; ORIGIN: 1-92-bases forward!

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US-09-328-352-5456	Query Match	42.1%	Score 203.5	DB 2	Length 92
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Matches 40; Conservative 11; Mismatches 34; Indels 1; Gaps

QY 1 MORIFCEYEGRDTESLDVFPYPGSELGQKIFACTGKVGMAAWLVHOTMLINENRISPRNP 60

Db 4 MSRQVFCRKYQKEMEGLDPAFPGAKGQEFPE
QY 61 SHRAFLLEELNKFL-FERRVAKPEGY 85

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Db      64  EAKKFLBEEQREKFFNNDESVEKAEGW  89
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RESULT 4
US-09-252-991A-23355

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A

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/ ENVOY FILING DATE: 1998-07-27
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/ NUMBER OF SEQ ID NOS: 33142
/
/ SEQ ID NO 23355
/
/ LENGTH: 122
/

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US-09-252-991A-23355

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Best Local Similarity	42.0%;	Pred. No.
Matches	37;	Conservative
	13;	Mismatch

QY 1 MGRILFCEIEGRDIEGLDFVFIPGLSGGR
 Db 33 MSRTVMCRKTHIELPLGLDRPPYPGAKGEL

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QY      61 SHRAFLSEELNKLFERRVAKPEGIIEP  
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DB      93 EDRKFLQQEMDKFLSGEDYAKADGYVP
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RESULT 5
US-09-540-236-2859
Sequence 2859 Amplification ITS/09540236

; Patent No. 6673910
 ;
 ; GENERAL INFORMATION:
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 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: MICROPIC ACID AND AMT

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; TITLE OF INVENTION: FOR DIAGNOSTICS AND
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,233
; CURRENT FILING DATE: 2000-04-04

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; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
;
mvrr- dmt

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ORGANISM: *M. catarrhalis*
US-09-540-236-2859

Best Local Similarity 40.2%; Pred. No. Matches 33; Conservative 10; Mismatch

Db 24 MVFCRKQONTLPKLPPFPNAKGQEIQL

84 KLINEQREKFLDNGDYKPAY 105

RESULT 6
US-09-198-452A-158
; Sequence 158, Application US/09198452A

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: March 1, 2006, 00:24:18 ; Search time 56.1572 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-22

Perfect score: 483

Sequence: 1 MORIIFCEYRQRTGDLFV.....LNKFLFERRVAKPGYIEPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_A1_Main:*

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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US12_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	100.0	89	3	US-09-955-502-22
2	246	50.9	87	3	US-09-955-502-8
3	237	49.1	87	3	US-09-955-502-6
4	237	49.1	87	3	US-09-955-502-7
5	234	48.4	91	3	US-09-955-502-5
6	232	48.0	91	3	US-09-955-502-14
7	232	48.0	91	3	US-09-955-502-16
8	232	48.0	91	3	US-09-955-502-17
9	230	47.6	91	3	US-09-955-502-18
10	229	47.4	88	3	US-09-955-502-15
11	228	47.2	90	3	US-09-955-502-10
12	226	46.8	91	3	US-09-955-502-11
13	226	46.8	91	3	US-09-955-502-12
14	226	46.8	91	3	US-09-955-502-13
15	220	45.5	78	3	US-09-955-502-19
16	215	44.5	87	3	US-09-955-502-31
17	214	44.3	88	3	US-09-955-502-33
18	205	42.4	87	3	US-09-955-502-2
19	205	42.4	87	3	US-09-955-502-3
20	203	42.0	90	3	US-09-955-502-20
21	201	41.6	88	3	US-09-955-502-32
22	201	41.6	88	3	US-09-955-502-26
23	201	41.6	88	3	US-09-955-502-27
24	201	41.6	88	3	US-09-955-502-28
25	200	41.4	90	3	US-09-955-502-23
26	198	41.0	87	3	US-09-955-502-24
27	197	40.8	87	3	US-09-955-502-29

28	197	40.8	87	3	US-09-955-502-30	Sequence 30, Appl
29	196	40.6	88	3	US-09-955-502-9	Sequence 9, Appl
30	195	40.4	86	3	US-09-955-502-4	Sequence 4, Appl
31	192	39.8	87	3	US-09-955-502-25	Sequence 25, Appl
32	183	37.9	76	3	US-09-955-502-21	Sequence 21, Appl
33	71	14.7	580	4	US-10-425-115-224020	Sequence 224020,
34	71	14.7	582	4	US-10-425-114-66688	Sequence 66688, A
35	70.5	14.6	764	4	US-10-437-963-104787	Sequence 104787,
36	67.5	14.0	272	4	US-10-080-170-163	Sequence 163, App
37	67.5	14.0	272	4	US-10-080-170-163	Sequence 163, App
38	67.5	14.0	272	4	US-10-468-356-163	Sequence 163, App
39	67	13.9	87	3	US-09-925-297-711	Sequence 711, App
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43	66	13.7	379	4	US-10-013-310-7	Sequence 7, Appl
44	66	13.7	379	4	US-10-682-230-7	Sequence 7, Appl
45	66	13.7	379	5	US-10-745-110-2	Sequence 2, Appl
46	66	13.7	379	5	US-10-507-343-2	Sequence 15, Appl
47	66	13.7	379	5	US-10-507-343-15	Sequence 17, Appl
48	66	13.7	379	5	US-10-507-343-17	Sequence 19, Appl
49	66	13.7	379	5	US-10-507-343-19	Sequence 21, Appl
50	66	13.7	379	5	US-10-507-343-21	Sequence 21, Appl
51	66	13.7	593	4	US-10-424-559-213920	Sequence 213920,
52	65	13.5	87	4	US-10-425-115-362001	Sequence 362001,
53	65	13.5	578	4	US-10-437-963-107904	Sequence 107904,
54	64.5	13.4	73	4	US-10-424-559-262025	Sequence 262025,
55	64.5	13.4	287	4	US-10-437-963-188594	Sequence 188594,
56	64.5	13.4	327	3	US-09-727-892-81	Sequence 81, Appl
57	64	13.3	112	4	US-10-437-963-111206	Sequence 111206,
58	64	13.3	368	5	US-10-156-761-14350	Sequence 14350, A
59	64	13.3	658	4	US-10-335-977-6532	Sequence 6532, Ap
60	64	13.3	831	4	US-10-335-977-6532	Sequence 6532, Ap
61	63.5	13.1	154	4	US-10-335-977-6531	Sequence 6531, Ap
62	63.5	13.1	155	4	US-10-335-977-6531	Sequence 6531, Ap
63	63.5	13.1	288	4	US-10-437-963-163689	Sequence 163689,
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65	63.5	13.1	446	5	US-10-732-923-11149	Sequence 11149, A
66	62.5	12.9	314	4	US-10-282-122A-78343	Sequence 78343, A
67	62.5	12.9	375	5	US-10-732-923-11589	Sequence 11589, A
68	62.5	12.9	389	4	US-10-108-260A-3014	Sequence 3014, Ap
69	62.5	12.9	405	4	US-10-473-574-17	Sequence 17, Appl
70	62.5	12.9	439	4	US-10-282-122A-78343	Sequence 78343, A
71	62	12.8	174	4	US-10-282-762-158	Sequence 158, App
72	62	12.8	409	5	US-10-732-923-13651	Sequence 8124, Ap
73	62	12.8	435	5	US-10-450-763-39253	Sequence 39253, A
74	62	12.8	453	5	US-10-732-923-13651	Sequence 13651, A
75	62	12.8	478	4	US-10-424-559-260720	Sequence 260720,

ALIGNMENTS

RESULT 1
US-09-955-502-22
Sequence 22, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296 97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 89
TYPE: PRT
ORGANISM: Xylella fastidiosa

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: March 1, 2006, 00:25:12 ; Search time 4.8656 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502a-22

Perfect score: 483

Sequence: 1 MQRIFCEYEQRTGDLFV.....LNKFLFERRVAKPEGYIEPD 89

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Published Applications_AA_New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/PC7_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	64	13.3	379	7	US-11-136-619-23
4	61	12.6	335	7	US-11-136-619-30
5	61	12.6	379	7	US-11-136-619-2
6	58	12.0	351	7	US-11-136-619-14
7	58	12.0	376	6	US-10-925-970-3
8	57	11.8	378	7	US-11-129-143-49
9	57	11.8	379	6	US-10-131-826A-308
10	56	11.6	372	7	US-11-143-980-37
11	56	11.6	533	7	US-11-230-995-3
12	56	11.6	430	6	US-10-821-231C-1
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18	55	11.4	774	7	US-11-242-730-7
19	54.5	11.3	124	7	US-11-072-512-3487
20	54.5	11.3	636	6	US-10-516-587-2
21	54	11.2	205	7	US-11-054-281-12
22	54	11.2	364	7	US-11-054-281-70
23	54	11.2	374	7	US-11-054-281-68
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25	54	11.2	394	7	US-11-054-281-67

26	54	11.2	418	7	US-11-244-219-2	Sequence 2, Appl1
27	54	11.2	1425	7	US-11-102-476-2	Sequence 2, Appl1
28	54	11.2	1224	7	US-11-102-476-4	Sequence 4, Appl1
29	54	11.2	1889	7	US-11-102-476-46	Sequence 46, Appl1
30	53.5	11.1	774	7	US-11-077-886-34	Sequence 34, Appl1
31	53.5	11.1	774	7	US-11-242-730-6	Sequence 6, Appl1
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33	53.5	11.1	2504	6	US-10-647-956A-8	Sequence 8, App
34	53	11.0	378	7	US-11-072-512-3698	Sequence 3698, Ap
35	53	11.0	471	7	US-11-098-686-11229	Sequence 11229, A
36	53	11.0	1207	6	US-10-755-092-7	Sequence 7, Appl1
37	52.5	10.9	148	7	US-11-072-512-3547	Sequence 3547, Ap
38	52.5	10.9	200	7	US-11-176-830-710	Sequence 710, App
39	52.5	10.9	296	6	US-10-467-657-3198	Sequence 3198, Ap
40	52.5	10.9	498	6	US-10-510-947-9	Sequence 9, Appl1
41	52.5	10.9	528	6	US-10-511-538-255	Sequence 255, App
42	52.5	10.9	685	7	US-11-098-686-10574	Sequence 10574, A
43	52	10.8	181	7	US-11-000-463-890	Sequence 890, App
44	52	10.8	182	7	US-11-000-463-418	Sequence 418, App
45	52	10.8	235	7	US-11-098-686-11270	Sequence 11270, A
46	52	10.8	271	6	US-10-857-780-19	Sequence 19, Appl1
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54	51.5	10.7	1508	7	US-11-043-889-47	Sequence 47, Appl1
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61	51	10.6	1344	7	US-11-091-663-20	Sequence 20, Appl1
62	51	10.6	1822	7	US-11-169-041-193	Sequence 193, App
63	51	10.6	5712	7	US-11-143-980-47	Sequence 47, Appl1
64	50.5	10.5	200	7	US-11-176-830-722	Sequence 722, App
65	50.5	10.5	290	6	US-10-793-626-1892	Sequence 1892, Ap
66	50.5	10.5	303	6	US-10-793-626-1140	Sequence 1140, Ap
67	50.5	10.5	304	6	US-10-055-877-173	Sequence 173, App
68	50.5	10.5	359	6	US-10-793-626-2742	Sequence 2742, Ap
69	50.5	10.5	525	6	US-10-763-712A-108	Sequence 108, App
70	50.5	10.5	554	6	US-10-467-657-8240	Sequence 8240, Ap
71	50	10.4	193	6	US-10-467-657-2700	Sequence 2700, Ap
72	50	10.4	200	7	US-11-176-830-726	Sequence 726, App
73	50	10.4	270	6	US-10-988-476-2	Sequence 2, Appl1
74	50	10.4	500	7	US-11-098-686-10274	Sequence 10274, A
75	49.5	10.2	184	7	US-11-177-860-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwln99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 41.6%; Score 201; DB 6; Length 88;
Best Local Similarity 41.9%; Pred. No. 1,7e-18;
Matches 36; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MORIIFCEYBQRDEGLDFVYPGELGQIFACIGKVGMAAMLVHOTMLINENRLSPRP 60
Db 1 MARWIFCYKLNABGKMPPLPNELGKRIFENVSQBAWAATRTQTMLINENRLSLADP 60

Qy 61 SHRAFLBBLNKLFLFERRVAKPEGYI 86
Db 61 RAREYLAQOMBQYFPGDGADAVQGYV 86

RESULT 2

US-11-136-619-22
Sequence 22, Application US/11136619
Publication No. US20050288226A1

GENERAL INFORMATION:
APPLICANT: You, Liang
APPLICANT: He, Biao
APPLICANT: Xu, Zhihong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: METHODS FOR TREATING AND DIAGNOSING CANCER WITH WNT INHIBITORY
FILE REFERENCE: 023070-148711US
CURRENT APPLICATION NUMBER: US/11/136,619
PRIOR FILING DATE: 2005-05-23
PRIOR APPLICATION NUMBER: US 60/664,241
PRIOR FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: US 60/573,197
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 379
TYPE: PRT
ORGANISM: Mus musculus
US-11-136-619-22

Query Match 13.7%; Score 66; DB 7; Length 379;
Best Local Similarity 28.6%; Pred. No. 1.1;
Matches 24; Conservative 13; Mismatches 35; Indels 12; Gaps 3;

Qy 17 LDFVYPBELGQKIFACIGKV-GMAAMLVHOTMLINENRLSPRPSHRAFLBEE----- 68
Db 124 LGTVPHKASVVOVGPPCLGKQDGVAAFEVDVIVNNSBGNITLRTQNAIFPRTCOQACBP 183

Qy 69 ---BLNKFLFERRVAK-PEGYIEP 88
Db 184 GGCRRNGFCNERRVCECPDGFYGP 207

RESULT 3

US-11-136-619-23
Sequence 23, Application US/11136619
Publication No. US20050288226A1

GENERAL INFORMATION:
APPLICANT: You, Liang
APPLICANT: He, Biao
APPLICANT: Xu, Zhihong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: METHODS FOR TREATING AND DIAGNOSING CANCER WITH WNT INHIBITORY
FILE REFERENCE: 023070-148711US
CURRENT APPLICATION NUMBER: US/11/136,619
PRIOR FILING DATE: 2005-05-23
PRIOR APPLICATION NUMBER: US 60/664,241

PRIOR FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: US 60/573,197
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23
LENGTH: 379
TYPE: PRT
ORGANISM: Rattus rattus
US-11-136-619-23

Query Match 13.3%; Score 64; DB 7; Length 379;
Best Local Similarity 28.6%; Pred. No. 2;
Matches 24; Conservative 13; Mismatches 35; Indels 12; Gaps 3;

Qy 17 LDFVYPBELGQKIFACIGKV-GMAAMLVHOTMLINENRLSPRPSHRAFLBEE----- 68
Db 124 LGTVPHKASVVOVGPPCLGKQDGVAAFEVDVIVNNSBGNITLRTQNAIFPRTCOQACBP 183

Qy 69 ---BLNKFLFERRVAK-PEGYIEP 88
Db 184 GGCRRNGFCNERRVCECPDGFYGP 207

RESULT 4

US-11-136-619-30
Sequence 30, Application US/11136619
Publication No. US20050288226A1

GENERAL INFORMATION:
APPLICANT: You, Liang
APPLICANT: He, Biao
APPLICANT: Xu, Zhihong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: METHODS FOR TREATING AND DIAGNOSING CANCER WITH WNT INHIBITORY
FILE REFERENCE: 023070-148711US
CURRENT APPLICATION NUMBER: US/11/136,619
PRIOR FILING DATE: 2005-05-23
PRIOR APPLICATION NUMBER: US 60/664,241
PRIOR FILING DATE: 2005-03-21
PRIOR APPLICATION NUMBER: US 60/573,197
PRIOR FILING DATE: 2004-05-21
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 30
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
US-11-136-619-30

Query Match 12.6%; Score 61; DB 7; Length 335;
Best Local Similarity 27.4%; Pred. No. 4;
Matches 23; Conservative 14; Mismatches 35; Indels 12; Gaps 3;

Qy 17 LDFVYPBELGQKIFACIGKV-GMAAMLVHOTMLINENRLSPRPSHRAFLBEE--- 72
Db 96 LGTVPHKASVVOVGPPCLGKQDGVAAFEVDVIVNNSBGNITLQTPQNAIFPRTCOQACBP 155

Qy 73 -----FLFERRVAK-PEGYIEP 88
Db 156 GGCRRNGFCNERRVCECPDGFYGP 179

RESULT 5

US-11-136-619-2
Sequence 2, Application US/11136619
Publication No. US20050288226A1

GENERAL INFORMATION:
APPLICANT: You, Liang
APPLICANT: He, Biao
APPLICANT: Xu, Zhihong
APPLICANT: Jablons, David M.
TITLE OF INVENTION: METHODS FOR TREATING AND DIAGNOSING CANCER WITH WNT INHIBITORY

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 69.2055 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-11

Perfect score: 486
Sequence: 1 MSRTIFCTFLGRBAEGDFO.....NFLFGKKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_AA_Main:

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	91	3	US-09-955-502-11
2	486	100.0	91	3	US-09-955-502-12
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4	469	96.5	91	3	US-09-955-502-14
5	469	96.5	91	3	US-09-955-502-15
6	469	96.5	91	3	US-09-955-502-16
7	455	93.6	91	3	US-09-955-502-17
8	455	93.6	91	3	US-09-955-502-18
9	402	82.7	90	3	US-09-955-502-19
10	396	81.5	90	3	US-09-955-502-20
11	395	81.3	78	3	US-09-955-502-21
12	388	79.8	91	3	US-09-955-502-22
13	387	79.6	87	3	US-09-955-502-23
14	379	78.0	87	3	US-09-955-502-24
15	373	76.7	87	3	US-09-955-502-25
16	332	68.3	88	3	US-09-955-502-26
17	265	54.5	76	3	US-09-955-502-27
18	255	52.5	87	3	US-09-955-502-28
19	255	52.5	87	3	US-09-955-502-29
20	241	49.6	86	3	US-09-955-502-30
21	231	47.5	87	3	US-09-955-502-31
22	227	46.7	88	3	US-09-955-502-32
23	227	46.7	89	3	US-09-955-502-33
24	226	46.5	89	3	US-09-955-502-34
25	225	46.3	87	3	US-09-955-502-35
26	213	43.8	88	3	US-09-955-502-36
27	213	43.8	88	3	US-09-955-502-37

28	213	43.8	88	3	US-09-955-502-28	Sequence 28, Appl
29	206	42.4	87	3	US-09-955-502-29	Sequence 29, Appl
30	206	42.4	87	3	US-09-955-502-30	Sequence 30, Appl
31	200	41.2	87	3	US-09-955-502-31	Sequence 31, Appl
32	200	41.2	87	3	US-09-955-502-32	Sequence 32, Appl
33	83	17.1	1647	5	US-10-450-763-41109	Sequence 41109, A
34	81	16.7	507	4	US-10-282-122A-68134	Sequence 68134, A
35	78	16.0	546	4	US-10-282-122A-66021	Sequence 66021, A
36	74.5	15.3	632	4	US-10-369-493-18744	Sequence 18744, A
37	71.5	14.7	679	5	US-10-805-684-105	Sequence 105, App
38	70.5	14.5	764	4	US-10-416-330-37	Sequence 37, Appl
39	70.5	14.5	764	5	US-10-491-467-15	Sequence 15, Appl
40	70.5	14.5	786	5	US-10-732-923-4885	Sequence 4885, Ap
41	70.5	14.5	1206	4	US-10-085-189-144	Sequence 144, Appl
42	70.5	14.5	1214	5	US-10-717-665-24	Sequence 24, Appl
43	69.5	14.3	481	3	US-09-934-455-466	Sequence 466, App
44	69.5	14.3	481	4	US-10-225-066A-180	Sequence 180, App
45	69.5	14.3	481	4	US-10-225-067-64	Sequence 64, Appl
46	69.5	14.3	481	5	US-10-374-780A-396	Sequence 396, App
47	69.5	14.3	481	5	US-10-225-066A-180	Sequence 180, App
48	69.5	14.3	561	4	US-10-437-963-169643	Sequence 169643, A
49	69.5	14.3	660	6	US-11-097-143-24705	Sequence 24705, A
50	69.5	14.3	1261	4	US-10-437-963-189166	Sequence 189166, A
51	69	14.2	258	4	US-10-415-478A-36	Sequence 36, Appl
52	69	14.2	258	5	US-10-472-928-2088	Sequence 2088, Ap
53	68.5	14.1	184	4	US-10-393-840-52	Sequence 52, Appl
54	68	14.0	102	3	US-09-864-408A-768	Sequence 768, App
55	67.5	13.9	184	4	US-10-219-220-66	Sequence 66, Appl
56	67.5	13.9	184	4	US-10-393-840-118	Sequence 118, App
57	67.5	13.9	545	5	US-10-732-923-9369	Sequence 9369, Ap
58	67.5	13.9	546	3	US-09-874-923-2	Sequence 2, Appl
59	67.5	13.9	546	3	US-09-991-496-2	Sequence 2, Appl
60	67.5	13.9	546	4	US-10-098-732A-11	Sequence 71, Appl
61	67.5	13.9	925	3	US-09-991-496-128	Sequence 128, App
62	67.5	13.9	935	3	US-09-991-496-127	Sequence 127, App
63	67.5	13.9	982	3	US-09-874-923-95	Sequence 95, Appl
64	67.5	13.9	982	3	US-09-991-496-95	Sequence 95, Appl
65	67.5	13.9	1427	3	US-09-874-923-97	Sequence 97, Appl
66	67.5	13.9	1427	3	US-09-991-496-97	Sequence 97, Appl
67	67.5	13.9	1641	3	US-09-874-923-96	Sequence 96, Appl
68	67.5	13.9	1641	3	US-09-991-496-96	Sequence 96, Appl
69	66.5	13.7	279	4	US-10-425-114-44570	Sequence 44570, A
70	66.5	13.7	675	4	US-10-424-599-229257	Sequence 229257, A
71	66.5	13.7	1026	4	US-10-437-963-195890	Sequence 195890, A
72	66.5	13.7	1374	4	US-10-437-963-189670	Sequence 189670, A
73	66.5	13.7	1588	4	US-10-437-963-189741	Sequence 189741, A
74	66	13.6	507	4	US-10-282-122A-47787	Sequence 47787, A
75	66	13.6	511	4	US-10-282-122A-50464	Sequence 50464, A

ALIGNMENTS

RESULT 1
US-09-955-502-11
Sequence 11, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 91
TYPE: PRT
ORGANISM: Escherichia coli K-12 MG1655

GenCore version 5.1.7
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Run on: March 1, 2006, 00:02:41 ; Search time 6.1975 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502A-11

Perfect score: 486
Sequence: 1 MSRTFTCTFLQREARGDFO.....NFLPGEKVEHTEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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- 3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
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- 8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	66	13.6	593	7	US-11-194-246-317
3	65.5	13.5	395	7	US-11-009-658-46
4	65	13.4	478	6	US-10-821-234-915
5	62	12.8	1501	6	US-10-793-626-2850
6	61.5	12.7	179	6	US-10-467-657-6542
7	60.5	12.4	264	6	US-10-821-234-1555
8	60.5	12.4	404	7	US-11-009-658-48
9	60.5	12.4	834	6	US-10-453-372-658
10	60	12.3	448	6	US-10-618-320A-25
11	60	12.3	480	6	US-10-510-386-12
12	60	12.3	677	6	US-10-793-626-198
13	59.5	12.2	177	6	US-10-467-657-1658
14	59	12.1	266	6	US-09-995-561-922
15	59	12.1	604	6	US-10-942-072-4
16	59	12.1	1142	7	US-11-109-156-22
17	59	12.1	1167	6	US-10-942-072-6
18	58.5	12.0	336	6	US-10-453-372-640
19	58.5	12.0	349	6	US-10-821-234-1387
20	58.5	12.0	577	7	US-11-072-512-187
21	58.5	12.0	695	6	US-10-453-372-648
22	58.5	12.0	700	6	US-10-995-561-922
23	58.5	12.0	700	6	US-10-995-561-924
24	58.5	12.0	775	6	US-10-453-372-656
25	58.5	12.0	793	6	US-10-995-561-925

26 58.5 12.0 804 6 US-10-453-372-650 Sequence 650, App

27 58.5 12.0 847 6 US-10-453-372-654 Sequence 652, App

28 58.5 12.0 857 6 US-10-453-372-652 Sequence 654, App

29 58.5 12.0 905 6 US-10-453-372-638 Sequence 638, App

30 58.5 12.0 905 6 US-10-453-372-662 Sequence 662, App

31 58.5 12.0 905 6 US-10-453-372-664 Sequence 664, App

32 58.5 12.0 963 6 US-10-995-561-923 Sequence 923, App

33 58.5 12.0 963 6 US-10-453-372-660 Sequence 660, App

34 58.5 12.0 1012 6 US-10-453-372-660 Sequence 660, App

35 58.5 12.0 1299 6 US-10-821-234-1145 Sequence 1145, App

36 58.5 12.0 3803 6 US-10-995-561-773 Sequence 773, App

37 58.5 12.0 3960 6 US-10-995-561-771 Sequence 771, App

38 58.5 12.0 5335 6 US-10-995-561-777 Sequence 777, App

39 58.5 12.0 5406 6 US-10-995-561-774 Sequence 774, App

40 58.5 12.0 5415 6 US-10-995-561-779 Sequence 779, App

41 58.5 12.0 5464 6 US-10-995-561-775 Sequence 775, App

42 58.5 12.0 5935 6 US-10-995-561-776 Sequence 776, App

43 58 11.9 251 7 US-11-054-515-1496 Sequence 1496, App

44 58 11.9 1995 7 US-11-069-834-60 Sequence 60, App

45 57.5 11.8 752 7 US-11-072-512-3003 Sequence 3003, App

46 57 11.7 194 7 US-11-072-512-2906 Sequence 2906, App

47 57 11.7 279 7 US-11-098-686-10812 Sequence 10812, App

48 57 11.7 504 7 US-11-072-512-3467 Sequence 3467, App

49 56 11.5 296 7 US-11-087-227-10 Sequence 10, App

50 56 11.5 372 7 US-11-143-986-5 Sequence 5, App

51 56 11.5 386 7 US-11-143-986-6 Sequence 6, App

52 56 11.5 386 7 US-11-143-986-2 Sequence 2, App

53 56 11.5 386 7 US-11-143-986-3 Sequence 3, App

54 56 11.5 397 7 US-11-022-562-223 Sequence 223, App

55 56 11.5 426 7 US-11-098-686-10340 Sequence 10340, App

56 56 11.5 481 7 US-11-186-284-91 Sequence 91, App

57 56 11.5 527 6 US-10-793-626-28 Sequence 28, App

58 56 11.5 697 6 US-10-485-517-202 Sequence 202, App

59 56 11.5 752 6 US-10-793-626-1036 Sequence 1036, App

60 56 11.5 1168 6 US-10-942-072-11 Sequence 11, App

61 56 11.5 1188 7 US-11-115-639-42 Sequence 42, App

62 56 11.5 1188 7 US-11-115-639-43 Sequence 43, App

63 56 11.5 1404 6 US-10-878-556A-169 Sequence 169, App

64 55.5 11.4 207 7 US-11-124-367A-438 Sequence 438, App

65 55.5 11.4 317 7 US-11-124-367A-437 Sequence 437, App

66 55.5 11.4 328 7 US-11-124-367A-436 Sequence 436, App

67 55.5 11.4 440 7 US-11-072-512-3856 Sequence 3856, App

68 55.5 11.4 623 7 US-11-072-512-2547 Sequence 2547, App

69 55.5 11.4 2101 6 US-10-857-780-23 Sequence 23, App

70 55 11.3 257 6 US-10-667-295-61 Sequence 61, App

71 55 11.3 257 7 US-11-054-515-1710 Sequence 1710, App

72 55 11.3 286 6 US-10-667-295-60 Sequence 60, App

73 55 11.3 327 6 US-10-667-295-59 Sequence 59, App

74 55 11.3 359 7 US-11-087-227-8 Sequence 8, App

75 55 11.3 359 7 US-11-192-450-6 Sequence 6, App

ALIGNMENTS

RESULT 1

US-10-467-657-968

Sequence 968, App

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: CONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWinn9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 43.8%; Score 213; DB 6; Length 88;
Best Local Similarity 44.3%; Pred. No. 7.3e-17;
Matches 39; Conservative 16; Mismatches 33; Indels 0; Gaps 0;

QY 1 MSRTFTCTFLQREAGGDFQLYPGELGKRIYNEISKEAMQOHKOTMLINEKLMNNA 60
DB 1 MARWFCVYLNKEAGMGKPPPLPNEIGKRIFFENVSQEMAAWTRHQTMLINENRLSLDP 60

QY 61 EHRKLLBOEMVNFLEFGKEVHIIEGYTPE 88
DB 61 RAREYLAQOMEOYFFGCGADAVQGYVPQ 88

RESULT 2

US-11-194-246-317
Sequence 317, Application US/11194246
Publication No. US20050272089A1

GENERAL INFORMATION:
APPLICANT: Mott, John
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
FILE REFERENCE: 00592.US1 (Mar 268,05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 13.6%; Score 66; DB 7; Length 593;
Best Local Similarity 44.4%; Pred. No. 9.9;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 35 SKEAMQOHKOTMLINEKLMNNAE 61
DB 296 SKQEWRYWEAKQDILKNTKLTALSGE 322

RESULT 3

US-11-009-658-46
Sequence 46, Application US/11009658
Publication No. US20060003430A1

GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
FILE REFERENCE: BB1332
CURRENT APPLICATION NUMBER: US/11/009,658
CURRENT FILING DATE: 2004-12-10
PRIOR APPLICATION NUMBER: US/09/914,098
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/121,119
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Microsoft Office 97
SEQ ID NO 46
LENGTH: 395
TYPE: PRT
ORGANISM: Zea mays

US-11-009-658-46

Query Match 13.5%; Score 65.5; DB 7; Length 395;
Best Local Similarity 21.9%; Pred. No. 6.9;
Matches 28; Conservative 19; Mismatches 36; Indels 45; Gaps 4;

QY 1 MSRTFTCTFLQREAGGDFQLYPGELGKRIYNEISKEAMQOHKOTMLINE----- 52
DB 224 ISKLGICIFVQRESTPDPFGVSGAVSERIH-----RAHQQKNAPMMLLPFGGTTNGDY 278

QY 53 -----KKLN-----MNAHRKLLBOEMVNFLEFGKEVHI 83
DB 279 LLPFTGFLAKAPQVILRYPYRFRFNAWDSMGARHVFLLCOFVNYL---EVRILP 335

QY 84 GYTPEDKK 91
DB 336 VYFPEQOR 343

RESULT 4

US-10-821-234-915
Sequence 915, Application US/10821234
Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes version 1.0
SEQ ID NO 915
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-915

Query Match 13.4%; Score 65; DB 6; Length 478;
Best Local Similarity 25.7%; Pred. No. 9.9;
Matches 27; Conservative 18; Mismatches 26; Indels 34; Gaps 5;

QY 8 TFLQREAGGDF--QLYP-----GELGKRIYNEISKEAMQOHKOTM 48
DB 380 SYLQREAYDRDPLFARVYGAPQLQVEKVRTNDRKELGEVRVQYTGDSFKFA---KALG 435

QY 49 LINEKLMNNAEHRKLLBOEMVNFLEFGKEVHI-----EGYTP 87
DB 436 VMDLKSQVPRAGYRGI-----VTFQFRGRVHLAPPPTWEGYDP 475

RESULT 5

US-10-793-626-2850
Sequence 2850, Application US/10793626
Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2850
LENGTH: 1501
TYPE: PRT
ORGANISM: Artificial Sequence

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502a-12

Perfect score: 486

Sequence: 1 MSRTIFCTFLQREAREGQDFQ.....NFLFGKVEHVRGYTPEDKK 91

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 75 summaries

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8: geneseqp20048.*
9: geneseqp20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	486	100.0	91	5	ABR78156
4	469	96.5	91	5	ABR78161
5	469	96.5	91	5	ABR78159
6	469	96.5	91	5	ABR78162
7	455	93.6	91	5	ABR78163
8	453	93.2	88	5	ABR78160
9	450	92.6	107	7	ABO65445
10	402	82.7	90	5	ABR78165
11	396	81.5	90	5	ABR78164
12	395	81.3	78	5	ABR78165
13	388	79.8	93	7	ADP05158
14	388	79.8	91	5	ABR78150
15	387	79.6	87	5	ABR78152
16	379	78.0	87	5	ABR78151
17	373	76.7	87	5	ABR78153
18	332	68.3	88	5	ABR78154
19	265	54.5	88	5	ABR78156
20	255	52.5	87	5	ABR78148
21	255	52.5	86	5	ABR78147
22	241	49.6	86	5	ABR78149
23	231.5	47.6	89	9	ABR41576
24	231.5	47.6	95	9	ABR38294

25	231	47.5	87	5	ABR78170	Abb78170	Amino aci
26	231	47.5	122	7	ABO74609	Abb74609	Pseudomon
27	227	46.7	88	5	ABR78178	Abb78178	Amino aci
28	227	46.7	90	5	ABR78168	Abb78168	Amino aci
29	225	46.3	87	5	ABR78169	Abb78169	Amino aci
30	216.5	44.5	90	5	ABR78167	Abb78167	Amino aci
31	213	43.8	88	5	ABR78171	Abb78171	Amino aci
32	213	43.8	88	5	ABR78172	Abb78172	Amino aci
33	213	43.8	88	5	ABR78173	Abb78173	Amino aci
34	213	43.8	88	6	ABR78129	Abb78129	N. gonorr
35	206	42.4	87	5	ABR78175	Abb78175	Amino aci
36	200	41.2	87	5	ABR78177	Abb78177	Amino aci
37	200	41.2	87	5	ABR78174	Abb78174	Amino aci
38	200	41.2	87	5	ABR78176	Abb78176	Amino aci
39	199.5	41.0	92	6	ADA34169	Ad34169	Actinoba
40	131	27.0	110	8	ADU05173	AdU05173	M. catarr
41	83	17.1	506	3	AA74371	Aa74371	Neisseria
42	83	17.1	1647	4	ABG10750	Abg10750	Novel hum
43	81	16.7	507	6	ABU40210	Abu40210	Protein e
44	78	16.0	507	3	AA74372	Aa74372	Neisseria
45	78	16.0	507	3	AA74373	Aa74373	Neisseria
46	78	16.0	546	6	ABJ38097	Abj38097	Protein e
47	76	15.6	548	6	AAE04737	Aae04737	Brugia ma
48	75	15.4	309	8	ADN46828	Adn46828	Thermococ
49	74.5	15.3	632	8	ADS29711	Ads29711	Bacterial
50	72	14.8	474	7	ABO75727	AbO75727	Pseudomon
51	71.5	14.7	679	9	ADZ85056	Adz85056	Pertial P
52	71	14.6	311	7	ADM26256	Adm26256	Hyperther
53	70.5	14.5	285	4	AA892683	Aa892683	Human pro
54	70.5	14.5	414	6	ABU11747	Abu11747	Human MDP
55	70.5	14.5	614	9	ADX06837	Adx06837	Cyclin-de
56	70.5	14.5	614	9	ADY16108	Ady16108	PRO polyp
57	70.5	14.5	764	5	ABR77432	Abb77432	Human tun
58	70.5	14.5	764	7	ADC99062	Adc99062	Human KPP
59	70.5	14.5	817	4	AA38657	Aa38657	Human pol
60	70.5	14.5	863	4	AA38656	Aa38656	Human pol
61	70.5	14.5	1135	8	ADS10706	AdS10706	Human the
62	70.5	14.5	1181	8	ADS10708	AdS10708	Human the
63	70.5	14.5	1186	8	ADS10709	AdS10709	Human the
64	70.5	14.5	1188	8	ADH45460	Adh45460	Human mol
65	70.5	14.5	1206	5	ADH48860	Adh48860	NOV61 pro
66	70.5	14.5	1214	7	ADK65785	Adk65785	Angiogene
67	69.5	14.3	374	4	AA396682	Aa396682	Human pol
68	69.5	14.3	389	4	AA441468	Aa441468	Human pol
69	69.5	14.3	481	5	AAU933169	Aau933169	Arabidops
70	69.5	14.3	481	7	ADD30148	Add30148	Plant yle
71	69.5	14.3	481	7	ADG31497	Adg31497	Plant yle
72	69.5	14.3	481	8	ADI41933	Adi41933	Plant tra
73	69.5	14.3	485	5	ABB08477	Abb08477	Human lat
74	69.5	14.3	488	4	AA894458	Aa894458	Human pro
75	69.5	14.3	488	4	AA667252	Aa667252	Amino aci

ALIGNMENTS

RESULT 1
ID ABR78158 standard; protein; 91 AA.
XX ABR78158;
AC 05-NOV-2002 (first entry)
DT Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX US2002072118-A1.
XX

PD 13-JUN-2002.
 XX 18-SEP-2001; 2001US-00955502.
 XX 22-SEP-2000; 2000US-0234588P.
 PR
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX
 SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3,1e-48;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEMAAQOMQKOTMLINEKLNMMNA 60
 DB 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEMAAQOMQKOTMLINEKLNMMNA 60
 QY 61 EHRKLLBQEMVNFLEFGKEVHIIEGYTPEDKK 91
 DB 61 EHRKLLBQEMVNFLEFGKEVHIIEGYTPEDKK 91

RESULT 2
 ABB78157
 ID ABB78157 standard; protein; 91 AA.
 XX
 AC ABB78157;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgxB homologue.
 XX
 KW Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YgxB homologue.
 XX
 OS Unidentified.
 XX
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX
 SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3,1e-48;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEMAAQOMQKOTMLINEKLNMMNA 60
 DB 1 MSRTTCTFLQREAGDGFOLYPGELGKRIYNEISKEMAAQOMQKOTMLINEKLNMMNA 60
 QY 61 EHRKLLBQEMVNFLEFGKEVHIIEGYTPEDKK 91
 DB 61 EHRKLLBQEMVNFLEFGKEVHIIEGYTPEDKK 91

RESULT 3
 ABB78156
 ID ABB78156 standard; protein; 91 AA.
 XX
 AC ABB78156;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgxB homologue.
 XX
 KW Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YgxB homologue.
 XX
 OS *Escherichia coli*.
 XX
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds

(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-12

Perfect score: 486
Sequence: 1 MSRTFCTFLQREAGQDFQ.....NFLPFGKWHVHGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	91	2 A85954	hypothetical prote
2	486	100.0	91	2 A65082	hypothetical prote
3	486	100.0	91	2 F91108	hypothetical prote
4	469	96.5	91	2 AH0879	conserved hypotet
5	402	82.7	90	2 C82320	conserved hypotet
6	396	81.5	90	2 A10116	conserved hypotet
7	387	79.6	90	2 C64013	hypothetical prote
8	265	54.5	93	2 B84994	hypothetical prote
9	231	47.5	90	2 H83003	conserved hypotet
10	226	46.5	105	2 C82624	conserved hypotet
11	213	43.8	88	2 H81014	conserved hypotet
12	78	16.0	507	2 C81063	conserved hypotet
13	78	16.0	546	2 A81807	conserved hypotet
14	76	15.6	548	2 A54510	conserved hypotet
15	75.5	15.5	1638	2 D87749	conserved hypotet
16	75.5	15.5	2488	2 T42739	conserved hypotet
17	74.5	15.3	683	2 AC2256	conserved hypotet
18	72	14.8	265	2 T46013	hypothetical prote
19	72	14.8	447	2 T16527	hypothetical prote
20	72	14.8	507	2 A83105	hypothetical prote
21	72	14.8	511	2 A95974	hypothetical prote
22	69	14.2	258	2 A97991	hypothetical prote
23	69	14.2	258	2 B95121	hypothetical prote
24	69	14.2	258	2 A28209	hypothetical prote
25	69	14.2	1119	2 T15842	hypothetical prote
26	68	14.0	2672	2 A48126	hypothetical prote
27	67.5	13.9	209	2 T64172	hypothetical prote
28	67	13.8	235	2 G65212	hypothetical prote
29	67	13.8	324	2 T05429	hypothetical prote

30	67	13.8	433	2 A70465	probable GTP bindi
31	67	13.8	447	2 JC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2 T40058	probable chromatin
33	66.5	13.7	1260	2 T04440	hypothetical prote
34	66	13.6	593	2 C64097	probable soluble 1
35	66	13.6	689	2 F83902	beta-galactosidase
36	65.5	13.5	173	2 H86869	hypothetical prote
37	65.5	13.5	305	2 A75211	asparaginase (EC 3
38	65.5	13.5	323	2 A90536	lipoprotein (import
39	65.5	13.5	365	2 B54128	Fe-binding protein
40	65.5	13.5	821	2 A12417	hypothetical prote
41	65	13.4	251	2 B90428	hypothetical prote
42	65	13.4	330	2 S74456	regulatory protein
43	65	13.4	445	1 X0R0MB	alpha-1,3-mannosyl
44	65	13.4	456	2 G71152	hypothetical prote
45	65	13.4	1008	2 H85055	probable transposo
46	65	13.4	1141	2 T29185	hypothetical prote
47	65	13.4	1230	2 S56850	SMC1 protein homol
48	64.5	13.3	245	2 AG2300	hypothetical prote
49	64.5	13.3	305	2 A71247	probable L-asparag
50	64.5	13.3	495	2 AH0985	probable zinc-prot
51	64.5	13.3	859	2 T29630	hypothetical prote
52	64	13.2	220	2 S62410	hypothetical prote
53	64	13.2	438	2 T37786	probable RNA-bindi
54	64	13.2	447	1 A38561	alpha-1,3-mannosyl
55	64	13.2	583	2 T48365	hypothetical prote
56	64	13.2	604	2 S66993	hypothetical prote
57	64	13.2	990	2 T43445	hypothetical prote
58	64	13.2	1051	2 S27002	phospholipase C (B
59	64	13.2	1234	2 S52099	phospholipase C (B
60	64	13.2	1234	2 I38994	phospholipase C (B
61	63.5	13.1	91	2 H90521	hypothetical prote
62	63.5	13.1	243	2 T29635	hypothetical prote
63	63.5	13.1	460	2 T00639	hypothetical prote
64	63.5	13.1	591	1 F0M7MM	gag polypeptide -
65	63	13.0	880	2 AE0179	probable ATPase ch
66	63	13.0	1251	2 A56677	neuronal cell cycl
67	63	13.0	1327	2 T14594	guanine nucleoti
68	63	13.0	1611	1 NM7MPV	183k protein - pep
69	62.5	12.9	581	1 SYBSET	glutamate-tRNA lig
70	62.5	12.9	551	2 B84106	hypothetical prote
71	62.5	12.9	555	2 C96667	unknown protein, 7
72	62.5	12.9	617	2 B71071	probable prolyl en
73	62.5	12.9	964	1 T04325	probable ATP-depen
74	62.5	12.9	1417	2 T00661	hypothetical prote
75	62	12.8	169	2 PNO560	phytochrome - long

ALIGNMENTS

RESULT 1
A85954
hypothetical protein Y9GX [imported] - Escherichia coli (strain O157:H7, substrain EDJ933
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954
R:Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Pochanovs, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE005174; NID:912517511; F
A:Experimental source: strain O157:H7, substrain EDJ933
C:Genetics:
A:Gene: Y9GX
C:Superfamily: fe(II) trafficking protein Y9GX
Query Match 100.0%; Score 486; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRTTCTFLQREABEGDQFLYPGELGKRIYNEISKEAQAQOHKQTMLINEKLMNNA 60
Db 1 MSRTTCTFLQREABEGDQFLYPGELGKRIYNEISKEAQAQOHKQTMLINEKLMNNA 60

Qy 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91
Db 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 2

hypoetical protein b2962 - Escherichia coli (strain K-12)

C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: A65082

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A:Experimental source: strain K-12, substrain M6155

C:Superfamily: fe(ii) trafficking protein Y9X

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRTTCTFLQREABEGDQFLYPGELGKRIYNEISKEAQAQOHKQTMLINEKLMNNA 60
Db 1 MSRTTCTFLQREABEGDQFLYPGELGKRIYNEISKEAQAQOHKQTMLINEKLMNNA 60

Qy 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91
Db 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 3

hypoetical protein EC63838 [imported] - Escherichia coli (strain O157:H7, substrain RI

C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: F91108

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-91 <HAY>

A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA037261.1;
A:Experimental source: strain O157:H7, substrain RIMD 0509952

C:Genetics:
A:Gene: EC63838

C:Superfamily: fe(ii) trafficking protein Y9X

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91
Db 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 4

conserved hypothetical protein STY326 [imported] - Salmonella enterica subsp. enterica

C:Species: Salmonella enterica subsp. enterica serovar Typh
A>Note: this species has also been called Salmonella typh
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004

C:Accession: AH0879

R:Fairhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Comerion, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AH0879

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-91 <PAR>

A:Cross-references: UNIPARC:UPI000005444C; GB:AL513382; PIDN:CAD02936.1; PID:G16504189;
A:Genetics:
A:Gene: STY326

C:Superfamily: fe(ii) trafficking protein Y9X

Query Match 96.5%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 7.9e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRTTCTFLQREABEGDQFLYPGELGKRIYNEISKEAQAQOHKQTMLINEKLMNNA 60
Db 1 MSRTTCTFLQREABEGDQFLYPGELGKRIYNEISKEAQAQOHKQTMLINEKLMNNA 60

Qy 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91
Db 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 91

RESULT 5

conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serog

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004

C:Accession: C82320

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.,
Chadson, D.; Emolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, F

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: C82320

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-90 <HEI>

A:Cross-references: UNIPARC:UPI0000002CCF; GB:AE004132; GB:AE003852; NID:G9654871; PIDN
A:Experimental source: serogroup O1, strain N16961; Biotype El Tor

C:Genetics:
A:Gene: VC0451

C:Superfamily: 1
C:Superfamily: fe(ii) trafficking protein Y9X

Query Match 82.7%; Score 402; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 3.6e-33;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MSRTTCTFLQREABEGDQFLYPGELGKRIYNEISKEAQAQOHKQTMLINEKLMNNA 60
Db 1 MSRTTCTFLQREABEGDQFLYPGELGKRIYNEISKEAQAQOHKQTMLINEKLMNNA 60

Qy 61 EHRKLLQEMVNFLEPGKEVHIIEGYTPEDKK 90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-12
Perfect score: 486
Sequence: 1 MSRTIFCTPLQREAEQDFQ.....NFLFEKGVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniProt_sprot:*
2: uniProt_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481	99.0	90	1	PERP_ECO57
2	481	99.0	90	1	PERP_ECOLI
3	481	99.0	90	1	PERP_SHIFL
4	477	98.1	90	1	PERP_ECOL6
5	464	95.5	90	1	PERP_SALCH
6	464	95.5	90	1	PERP_SALPA
7	464	95.5	90	1	PERP_SALTI
8	464	95.5	90	1	PERP_SALTY
9	411	84.6	90	1	PERP_ERWCT
10	404	83.1	90	1	PERP_YERPS
11	402	82.7	90	1	PERP_VIBCH
12	402	82.7	90	1	PERP_VIBVU
13	402	82.7	90	1	PERP_VIBVY
14	399	82.1	90	1	PERP_VIBPA
15	396	81.5	90	1	PERP_YERPE
16	389	80.0	91	1	PERP_MANSN
17	387	79.6	90	1	PERP_HABIN
18	387	79.6	90	2	Q4QMD9_HAB18
19	382	78.6	90	1	PERP_PHOPR
20	381	78.4	90	1	PERP_PHOHL
21	379	78.0	90	1	PERP_PASMT
22	373	76.7	94	1	PERP_HABDU
23	366	75.3	90	1	PERP_VIBF1
24	335	68.9	90	1	PERP_IDILO
25	332	68.3	92	1	PERP_SHEON
26	265	54.5	77	1	PERP_BICAT
27	255	52.5	90	1	PERP_BORBR
28	255	52.5	90	1	PERP_BORPA
29	255	52.5	90	1	PERP_BORPE
30	247	50.8	78	1	PERP_BUCAP
31	235	48.4	78	1	PERP_WIGBR

32	231.5	47.6	89	1	PERP_LEGPA	05x3x9 legionella
33	231.5	47.6	89	1	PERP_LEGPH	05x80 legionella
34	231	47.5	90	1	PERP_PSEBA	09nu3 pseudomonas
35	231	47.5	91	1	PERP_XANAC	08p1h7 xanthomonas
36	228.5	47.0	89	1	PERP_LEGPL	05wvc4 legionella
37	227	46.7	90	1	PERP_COXBU	083d06 coxiella bu
38	227	46.7	90	1	PERP_PSESM	087u05 pseudomonas
39	227	46.7	90	2	Q4ZLP3_PSESY	04zlp3 pseudomonas
40	226	46.5	90	1	PERP_XLIPA	09pc73 xylolla fas
41	225	46.3	90	1	PERP_PSEBP	088r49 pseudomonas
42	225	46.3	92	1	PERP_XANOR	05g22 xanthomonas
43	223	45.9	90	2	Q4J228_AZOV1	04j228 azotobacter
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46	222	45.7	92	2	Q4UW14_XANCP	04uw14 xanthomonas
47	220	45.3	90	1	PERP_NITEU	082x2 nitrosomona
48	215	44.2	90	2	Q6T7F6_PSEPL	06t7f6 pseudomonas
49	214	44.0	87	1	PERP_BUCBP	089444 buchnera ap
50	213	43.8	88	1	PERP_NEIG1	05f553 neisseria g
51	213	43.8	88	1	PERP_NEIMA	067615 neisseria m
52	213	43.8	88	1	PERP_NEIMB	067616 neisseria m
53	212	43.6	79	1	PERP_CANBP	07vrg9 candidatus
54	212	43.6	90	2	Q4KJ2_PSEF5	04kj2 pseudomonas
55	211	43.4	90	1	PERP_CHRVO	07n8r4 chromobacte
56	207	42.6	91	2	Q4LS19_9BURK	04ls19 burholderi
57	206	42.4	91	1	PERP_BURMA	0621u9 burholderi
58	206	42.4	91	1	PERP_BURPS	0631f4 burholderi
59	206	42.4	91	1	PERP_RALSO	08y010 ralstonia s
60	200	41.2	90	1	PERP_METCA	060a17 methylococ
61	199	40.9	87	1	PERP_FRATP	05njh8 francisella
62	194.5	40.0	90	1	PERP_AC1AD	06f6f3 acinetobact
63	144	29.6	96	2	Q4FVJ7_9GAMM	04fvj7 psychrobact
64	142	29.2	92	2	Q4NM04_9DELT	04nm04 anaeromyxob
65	90.5	18.6	482	2	Q5NUY1_9BURK	05nuy1 ralstonia m
66	85.5	17.6	514	2	Q6A1Z9_DESPS	06a1z9 desulfofale
67	81	16.7	507	2	Q88PF3_PSEBP	088pf3 pseudomonas
68	81	16.7	508	2	Q7NSF0_CHRVO	07nsf0 chromobacte
69	80	16.5	486	2	Q7WXS1_ALCEU	07wxs1 alcaligenes
70	78.5	16.2	760	2	Q4YVR2_PLABE	04yvr2 plasmodium
71	78	16.0	507	2	Q9UYE9_NEIMB	09uye9 neisseria m
72	78	16.0	546	2	Q9UTB3_NEIMA	09utb3 neisseria m
73	77.5	15.9	337	2	Q4UB40_THERAN	04ub40 thelaxia a
74	77.5	15.9	337	2	Q81AR8_BACCR	081ar8 bacillus ce
75	77.5	15.9	1123	2	Q7RJL0_PLAYVO	07rjl0 plasmodium

ALIGNMENTS

RESULT 1
ID PERP_ECO57 STANDARD; PRT; 90 AA.
AC P0A8B4; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; Ordered locus names=z4307, ECg3838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RC MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfist G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Apodoca E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

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RL Nature 409:529-533(2001).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=0157:H7 / Sakai / RIMD 0509552 / EHEC.
RX MEDLINE=21156231; PubMed=1158796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kubura S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, AE005174; AAG58093.1; -; Genomic DNA.
CC EMBL, BA000007; BAB37261.1; -; Genomic DNA.
CC PIR, A85954; A85954.
CC PIR, P91108; P91108.
CC HAMAP, MF_00686; -; 1.
CC InterPro, IPR007457; Y9gX.
CC Pfam, PF04362; DUF495; 1.
CC PIRSF, PIRSF029827; Fe traffic_Y9gX; 1.
CC ProDom, PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC INIT MET 0 0 By similarity.
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;
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Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
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AC FETP_ECOLI
ID POA8B3; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DT Probable Fe(2+) trafficking protein.
GN Name=y9gX; Ordered locus Names=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RT Science 277:1453-1474(1997).

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RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298666;
RA Link A.U., Rodison K., Church G.W.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12."
RT Electrophoresis 18:1259-1313(1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wessinger V.C., Humphrey-Smith I.;
RT "Small genes/gene-products in Escherichia coli K-12."
RL FEWS Microbiol. Lett. 169:375-382(1998).
RN [4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RT hydroxyapatite chromatography."
RL Electrophoresis 20:2181-2195(1999).
RN [5]
RP INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.U., Koutsolioutou A., Carrasco D., Demple B.;
RT "SoxRS-regulated expression and genetic analysis of the Y9gX gene of
RT Escherichia coli."
RL J. Bacteriol. 185:6624-6632(2003).
RN [6]
RP STRUCTURE BY NMR, AND FUNCTION.
RX PubMed=15883188; DOI=10.1110/ps.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.U., Gehring K.;
RT "The solution structure of the oxidative stress-related protein Y9gX
RT from Escherichia coli."
RL Protein Sci. 14:1673-1678(2005).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes. Necessary to
CC maintain high levels of aconitase under oxidative stress.
CC -I- SUBUNIT: Monomer (Probable).
CC -I- INDUCTION: By oxidative stress and soxS.
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, U28377; AAA69129.1; -; Genomic DNA.
CC EMBL, U00096; AAC75999.1; -; Genomic DNA.
CC PIR, A65082; A65082.
CC PDB: 1YHD; NMR; A=1-90.
CC SWISS-2DPAGE; POA8B3; COLI.
CC ECHOBASE; BR2809; -.
CC EcoGene; EG12984; Y9gX.
CC HAMAP, MF_00686; -; 1.
CC InterPro, IPR007457; Y9gX.
CC Pfam, PF04362; DUF495; 1.
CC PIRSF, PIRSF029827; Fe traffic_Y9gX; 1.
CC ProDom, PD029191; DUF495; 1.
CC 3D-structure; Complete proteome; Direct protein sequencing; Iron.
CC INIT MET 0 0
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;
SQ
Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTTCTFLQRAEGQDPFLYPGLGKRIYNEISKAWAQWQHKQTMLINEKKNMNAE 61

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 / Search time 18.4487 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-12
Perfect score: 486
Sequence: 1 MSRTFTCTFLQREAGQDFQ.....NFLFGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents, AA:
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4: /cgn2_6/ptodata/1/1aa/CTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	450 92.6	107 2	US-09-489-039A-11962 Sequence 11962, A
2	389 80.0	93 2	US-09-543-681A-5443 Sequence 5443, Ap
3	231 47.5	122 2	US-09-252-991A-23355 Sequence 23355, A
4	199.5 41.0	92 2	US-09-328-352-5456 Sequence 5456, Ap
5	131 27.0	110 2	US-09-540-236-2859 Sequence 2859, Ap
6	76 15.6	548 2	US-09-167-299-3 Sequence 3, Appl1
7	72 14.8	474 2	US-09-252-991A-24473 Sequence 24473, A
8	70.5 14.5	1214 2	US-10-164-595-24 Sequence 24, Appl1
9	67.5 13.9	184 2	US-09-325-932A-66 Sequence 66, Appl1
10	67.5 13.9	546 1	US-08-533-668A-2 Sequence 2, Appl1
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28	67.5 13.9	1641 2	US-09-639-206A-96 Sequence 96, Appl1
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55	61 12.6	444 2	US-09-861-451A-16 Sequence 16, Appl1
56	61 12.6	430 2	US-09-438-185A-934 Sequence 934, App
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63	60.5 12.4	640 2	US-10-243-735-2 Sequence 2, Appl1
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66	60 12.3	98 2	US-09-270-767-56301 Sequence 56301, A
67	60 12.3	184 2	US-09-270-767-61671, A Sequence 61671, A
68	60 12.3	271 2	US-09-248-796A-19265 Sequence 19265, A
69	60 12.3	279 2	US-09-198-452A-221 Sequence 221, App
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74	60 12.3	410 2	US-09-949-016-8705 Sequence 8705, Ap
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ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match	92.6%	Score 450;	DB 2;	Length 107;
Best Local Similarity	91.2%	Pred. No. 1e-48;		
Matches	83;	Conservative	5;	Mismatches 3;
			Indels	0;
			Gaps	0;

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RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A

APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

;; CURRENT FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: US 60/128,706
;; PRIOR FILING DATE: 1999-04-09

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; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis

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Query Match	80.0%;	Score 389;	DB 2;	Length 93;
Best Local Similarity	80.0%;	Pred. No. 3.8e-41;		
Matches 72; Conservative	7;	Mismatches 11;	Indels 0;	Gaps 0;

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0y      1 MSRTTCTCTFLQREABGQDFQLYPGEIGRIYNEISKEAQAQWQHQTMLINEKJLMMNA 60
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Db      4 MSRTTCTCTPLNKEADGDLFQLYPGEIGRIYNEISKEAQAQWQHQTMLINEKJLMMNP 63

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QY      61 EHRKLLQEEMVNFLLPEGKVHIEGYTPEDK 90
        : ||||| | | | | : | | | | : |
Db      64 DDKRLLEQEMVRFLFEGHDVHIIDGYTPPEK 93
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RESULT 3
US-09-252-991A-23355
! Sequence 23355, Application US/09252991A

: : : : : Rubenfield et al.
 : APPLICANT: Marc J. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 : : : : :
 : TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 : TITLE OF INVENTION:

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;          SEQ ID NO 23355
;          NUMBER OF SEQ ID NOS: 33142
;          LENGTH: 122

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ORGANISM: <i>Escherichia coli</i>	47.5%	Score 231:	DB 2:	Length 122:
S-09-252-991A-23355				
Query Match				

Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 1 MSRTICTFLQREAGODPOLYRGELGRIYNEISKAAVQMOHQOTMLINEKKLNMNA 60

Db 33 MSRTVMCRKTHBELPGLDRPYPFGANGGEDIYNNVSRKAMDWQKOTMLINERLLNNNA 92

Qy 61 EHRRLLEQBMVNFLEGGKVIHIGYTP 87

Dh 93 EDRRFLQDEMDFLGGEDIYAKADGYVP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352

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; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

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; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456

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! ORGANISM: *Acinetobacter baumannii*
US-09-328-352-5456

Best Local Similarity 42.7%; Pred. No. 2.2e-17;
Matches 38; Conservative 15; Mismatches 35; Indels 1; Gaps

Db 4 MSRQVFCRKYQKEMEGILDPAFPFGAKQGFEE
QY 61 EHRKLLQEMVNFLEFGKEVH-IEGYTPE 88

RESULT 5

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; Patent No. 6673910
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; GENERAL INFORMATION:
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; APPLICANT: Gary L. Breton et al.

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FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04

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; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.cattarrhalis
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Query Match	27.0%	Score 131	DB 2	Length 110
Best Local Similarity	34.9%	Pred. No. 1.1e-08		
Matches 29	Conservative 13	Mismatches 41	Indels 0	Gaps 0

25 VFCKRYQÖNLPEKLPNPPFPNAKGQEIÇ

Db 85 YLINEQREKFLDNGDYEKYPAGYKP 107

RESULT 6
US-09-167-299-3
; Sequence 3, Application US/09167299

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 / Search time 57.6264 Seconds
(without alignments)
659,810 Million cell updates/sec

Title: US-09-955-502A-12

Perfect score: 486

Sequence: 1 MSRTIFCTFLGREGAGDFQ.....NFLPGEKVEHIGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database: Published Applications_AA_Main:*

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2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*

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6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	486	100.0	91	3	US-09-955-502-12
3	486	100.0	91	3	US-09-955-502-13
4	469	96.5	91	3	US-09-955-502-14
5	469	96.5	91	3	US-09-955-502-15
6	469	96.5	91	3	US-09-955-502-16
7	455	93.6	91	3	US-09-955-502-17
8	455	93.6	91	3	US-09-955-502-18
9	402	82.7	90	3	US-09-955-502-19
10	396	81.5	90	3	US-09-955-502-20
11	395	81.3	78	3	US-09-955-502-21
12	388	79.8	91	3	US-09-955-502-22
13	387	79.6	87	3	US-09-955-502-23
14	379	78.0	87	3	US-09-955-502-24
15	373	76.7	88	3	US-09-955-502-25
16	332	66.3	88	3	US-09-955-502-26
17	265	54.5	76	3	US-09-955-502-27
18	255	52.5	87	3	US-09-955-502-28
19	255	52.5	87	3	US-09-955-502-29
20	241	49.6	86	3	US-09-955-502-30
21	231	47.5	87	3	US-09-955-502-31
22	227	46.7	88	3	US-09-955-502-32
23	227	46.7	90	3	US-09-955-502-33
24	226	46.5	89	3	US-09-955-502-34
25	225	46.3	87	3	US-09-955-502-35
26	213	43.8	88	3	US-09-955-502-36
27	213	43.8	88	3	US-09-955-502-37

ALIGNMENTS

28	213	43.8	88	3	US-09-955-502-28	Sequence 28, Appl
29	206	42.4	87	3	US-09-955-502-29	Sequence 29, Appl
30	206	42.4	87	3	US-09-955-502-30	Sequence 30, Appl
31	200	41.2	87	3	US-09-955-502-31	Sequence 31, Appl
32	200	41.2	87	3	US-09-955-502-32	Sequence 32, Appl
33	83	17.1	1647	5	US-10-450-763-41109	Sequence 41109, A
34	81	16.7	507	4	US-10-282-122A-66134	Sequence 66134, A
35	78	16.0	546	4	US-10-282-122A-66021	Sequence 66021, A
36	74.5	15.3	632	4	US-10-369-493-18744	Sequence 18744, A
37	71.5	14.7	679	5	US-10-805-684-105	Sequence 105, App
38	70.5	14.5	764	4	US-10-416-330-37	Sequence 37, Appl
39	70.5	14.5	764	5	US-10-491-467-15	Sequence 15, Appl
40	70.5	14.5	786	5	US-10-732-923-4885	Sequence 4885, Ap
41	70.5	14.5	1206	4	US-10-085-198-144	Sequence 144, Appl
42	70.5	14.5	1214	5	US-10-717-665-24	Sequence 24, Appl
43	69.5	14.3	481	3	US-09-934-455-465	Sequence 465, App
44	69.5	14.3	481	3	US-10-225-066A-180	Sequence 180, App
45	69.5	14.3	481	4	US-10-225-067-64	Sequence 64, Appl
46	69.5	14.3	481	4	US-10-374-780A-396	Sequence 396, App
47	69.5	14.3	481	5	US-10-225-066A-180	Sequence 180, App
48	69.5	14.3	561	4	US-10-437-963-169643	Sequence 169643, A
49	69.5	14.3	660	6	US-11-097-143-24705	Sequence 24705, A
50	69.5	14.3	1261	4	US-10-437-963-189166	Sequence 189166, A
51	69	14.2	258	4	US-10-415-478A-36	Sequence 36, Appl
52	69	14.2	258	5	US-10-472-928-2088	Sequence 2088, Ap
53	68.5	14.1	184	4	US-10-393-840-52	Sequence 52, Appl
54	68	14.0	102	3	US-09-864-408A-768	Sequence 768, App
55	67.5	13.9	184	4	US-10-219-220-66	Sequence 66, Appl
56	67.5	13.9	184	4	US-10-393-840-118	Sequence 118, App
57	67.5	13.9	545	5	US-10-732-923-9369	Sequence 9369, Ap
58	67.5	13.9	546	3	US-09-874-923-2	Sequence 2, Appl
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60	67.5	13.9	546	4	US-10-098-732A-71	Sequence 71, Appl
61	67.5	13.9	926	3	US-09-991-496-128	Sequence 128, App
62	67.5	13.9	926	3	US-09-991-496-128	Sequence 127, App
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66	67.5	13.9	1427	3	US-09-874-923-97	Sequence 97, Appl
67	67.5	13.9	1641	3	US-09-874-923-96	Sequence 96, Appl
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69	66.5	13.7	279	4	US-10-425-114-44570	Sequence 44570, A
70	66.5	13.7	675	4	US-10-424-599-229257	Sequence 229257, A
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RESULT 1
US-09-955-502-11
Sequence 11, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIORITY FILING DATE: 2000-09-22
PRIORITY FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 11
LENGTH: 91
TYPE: PRF
ORGANISM: Escherichia coli K-12 MG1655

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 5.07859 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502a-12

Perfect score: 486

Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLPFGKVEHLRGYPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	65	13.4	478	6	US-10-821-234-915
5	62	12.8	1501	6	US-10-793-626-2850
6	61.5	12.7	179	6	US-10-467-657-6542
7	60.5	12.4	264	6	US-10-821-234-1585
8	60.5	12.4	404	7	US-11-009-658-48
9	60.5	12.4	834	6	US-10-453-372-658
10	60	12.3	448	6	US-10-618-320A-25
11	60	12.3	480	6	US-10-510-386-12
12	60	12.3	677	6	US-10-793-626-198
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14	59	12.1	266	5	US-09-995-493-6
15	59	12.1	604	6	US-10-942-072-4
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18	58.5	12.0	336	6	US-10-453-372-640
19	58.5	12.0	349	6	US-10-821-234-1387
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21	58.5	12.0	695	6	US-10-453-372-648
22	58.5	12.0	700	6	US-10-995-561-922
23	58.5	12.0	700	6	US-10-995-561-924
24	58.5	12.0	775	6	US-10-453-372-656
25	58.5	12.0	793	6	US-10-995-561-925

26 58.5 12.0 804 6 US-10-453-372-650 Sequence 650, App

27 58.5 12.0 847 6 US-10-453-372-654 Sequence 654, App

28 58.5 12.0 857 6 US-10-453-372-652 Sequence 652, App

29 58.5 12.0 905 6 US-10-453-372-638 Sequence 638, App

30 58.5 12.0 905 6 US-10-453-372-662 Sequence 662, App

31 58.5 12.0 905 6 US-10-453-372-664 Sequence 664, App

32 58.5 12.0 963 6 US-10-995-561-923 Sequence 923, App

33 58.5 12.0 963 6 US-10-453-372-660 Sequence 660, App

34 58.5 12.0 1012 6 US-10-453-372-646 Sequence 646, App

35 58.5 12.0 1299 6 US-10-821-234-1145 Sequence 1145, App

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39 58.5 12.0 5406 6 US-10-995-561-774 Sequence 774, App

40 58.5 12.0 5415 6 US-10-995-561-779 Sequence 779, App

41 58.5 12.0 5464 6 US-10-995-561-775 Sequence 775, App

42 58.5 12.0 5935 6 US-10-995-561-776 Sequence 776, App

43 58 11.9 251 7 US-11-054-515-1496 Sequence 1496, App

44 58 11.9 1995 7 US-11-069-834-60 Sequence 60, App

45 57.5 11.8 752 7 US-11-072-512-3003 Sequence 3003, App

46 57 11.7 194 7 US-11-072-512-2906 Sequence 2906, App

47 57 11.7 279 7 US-11-098-686-10812 Sequence 10812, App

48 57 11.7 504 7 US-11-072-512-3467 Sequence 3467, App

49 56 11.5 296 7 US-11-087-227-10 Sequence 10, App

50 56 11.5 372 7 US-11-143-986-5 Sequence 5, App

51 56 11.5 372 7 US-11-143-986-6 Sequence 6, App

52 56 11.5 386 7 US-11-143-986-2 Sequence 2, App

53 56 11.5 397 7 US-11-143-986-3 Sequence 3, App

54 56 11.5 397 7 US-11-022-562-223 Sequence 223, App

55 56 11.5 426 7 US-11-098-686-10340 Sequence 10340, App

56 56 11.5 427 7 US-11-186-284-91 Sequence 91, App

57 56 11.5 581 6 US-10-793-626-28 Sequence 28, App

58 56 11.5 697 6 US-10-485-517-202 Sequence 202, App

59 56 11.5 752 6 US-10-793-626-1036 Sequence 1036, App

60 56 11.5 1168 6 US-10-942-072-11 Sequence 11, App

61 56 11.5 1188 7 US-11-115-639-42 Sequence 42, App

62 56 11.5 1188 7 US-11-115-639-43 Sequence 43, App

63 56 11.5 1404 6 US-10-878-556A-169 Sequence 169, App

64 55.5 11.4 207 7 US-11-124-367A-437 Sequence 437, App

65 55.5 11.4 317 7 US-11-124-367A-436 Sequence 436, App

66 55.5 11.4 328 7 US-11-124-367A-436 Sequence 436, App

67 55.5 11.4 440 7 US-11-072-512-3856 Sequence 3856, App

68 55.5 11.4 623 7 US-11-072-512-2547 Sequence 2547, App

69 55.5 11.4 2101 6 US-10-857-780-23 Sequence 23, App

70 55 11.3 257 6 US-10-667-295-61 Sequence 61, App

71 55 11.3 257 7 US-11-054-515-1710 Sequence 1710, App

72 55 11.3 286 6 US-10-667-295-60 Sequence 60, App

73 55 11.3 327 6 US-10-667-295-59 Sequence 59, App

74 55 11.3 359 7 US-11-087-227-8 Sequence 8, App

75 55 11.3 359 7 US-11-192-450-6 Sequence 6, App

ALIGNMENTS

RESULT 1

US-10-467-657-968

Sequence 968, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: PONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASTIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 43.8%; Score 213; DB 6; Length 88;
Best Local Similarity 44.3%; Pred. No. 7.3e-17;
Matches 39; Conservative 16; Mismatches 33; Indels 0; Gaps 0;

QY 1 MSRTFTCTFLQREAGQDFPOLYPGELGKRIYNEISKEAMQWQHOKTMLINEKLIAMNNA 60
DB 1 MARWFCVKLNEAGCKMFPPLPNEIKRIFENVSQEAAMATRTQMLINENRLSLDP 60

QY 61 EHRKLLBQEMVNFLEFGKEVHIIEGYTPE 88
DB 61 RAREYLAQOMEQYFFGDXADAVQGYVPQ 88

RESULT 2
US-11-194-246-317
Sequence 317, Application US/11194246
Publication No. US20050272089A1

GENERAL INFORMATION:
APPLICANT: Mott, John
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
FILE REFERENCE: 00592, US1 (Mar 268, 05920101)
CURRENT FILING DATE: 2005-08-01
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/345,438
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 13.6%; Score 66; DB 7; Length 593;
Best Local Similarity 44.4%; Pred. No. 9.9;
Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 35 SKAWAOWHOKOTMLINEKLIAMNNAE 61
DB 296 SKQENRYWEAKODILKNTKLTALSKS 322

RESULT 3
US-11-009-658-46
Sequence 46, Application US/11009658
Publication No. US20060003430A1
GENERAL INFORMATION:
APPLICANT: E. I. du Pont de Nemours and Company
TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
FILE REFERENCE: B01332
CURRENT APPLICATION NUMBER: US/11/009,658
PRIOR FILING DATE: 2004-12-10
PRIOR APPLICATION NUMBER: US/09/914,098
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/121,119
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Microsoft Office 97
SEQ ID NO 46
LENGTH: 395
TYPE: PRT
ORGANISM: Zea mays

US-11-009-658-46

Query Match 13.5%; Score 65.5; DB 7; Length 395;
Best Local Similarity 21.9%; Pred. No. 6.9;
Matches 28; Conservative 19; Mismatches 36; Indels 45; Gaps 4;

QY 1 MSRTFTCTFLQREAGQDFPOLYPGELGKRIYNEISKEAMQWQHOKTMLINE----- 52
DB 224 ISKLCIGCFIVQREKSTPDPFGKGVSGAVSERIH-----RAHQQKNAPMMLFPEGTTNGDY 278

QY 53 -----KKLN-----MNAHRKLLBQEMVNFLEFGKEVHI 83
DB 279 LLPFTGFLAKAPQVILRYPRKFNAMDSGASHVELLCQFVNYL---EVRILP 335

QY 84 GYTPEDKK 91
DB 336 VYFSEQR 343

RESULT 4
US-10-821-234-915
Sequence 915, Application US/10821234
Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Staehle-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: PC_SEQ_genes Version 1.0
SEQ ID NO 915
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-915

Query Match 13.4%; Score 65; DB 6; Length 478;
Best Local Similarity 25.7%; Pred. No. 9.9;
Matches 27; Conservative 18; Mismatches 26; Indels 34; Gaps 5;

QY 8 TYLQREAGQDF-QLYP-----GELGKRIYNEISKEAMQWQHOKTM 48
DB 380 SYLQREAYDRDPLAVYGAPQLQVEKVRTNDRKELGAVVQYTGDRSFRFA-----KALG 435

QY 49 LINEKLIAMNNAEHRKLLBQEMVNFLEFGKEVHI-----EGYTP 87
DB 436 VMDDKSGVPRAGYRGI-----VTFQFRGRVHLAPPFTWEGYDP 475

RESULT 5
US-10-793-626-2850
Sequence 2850, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMBERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
PRIOR FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2850
LENGTH: 1501
TYPE: PRT
ORGANISM: Artificial Sequence

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 / Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502a-13

Perfect score: 486

Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLPEKVEHIEGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

A_Geneseq_21:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*
- 9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	91	5	ABB78158 Amino aci
2	486	100.0	91	5	ABB78157 Amino aci
3	486	100.0	91	5	ABB78156 Amino aci
4	469	96.5	91	5	ABB78161 Amino aci
5	469	96.5	91	5	ABB78159 Amino aci
6	469	96.5	91	5	ABB78162 Amino aci
7	455	93.6	91	5	ABB78163 Amino aci
8	453	93.2	88	5	ABB78160 Amino aci
9	450	92.6	107	7	ABO65445 Kiebsiell
10	402	82.7	90	5	ABB78155 Amino aci
11	396	81.5	90	5	ABB78165 Amino aci
12	395	81.3	78	5	ABB78164 Amino aci
13	389	80.0	93	7	ADP05158 Bacteri
14	388	79.8	91	5	ABB78150 Amino aci
15	387	79.6	87	5	ABB78152 Amino aci
16	379	78.0	87	5	ABB78151 Amino aci
17	373	76.7	87	5	ABB78153 Amino aci
18	332	68.3	88	5	ABB78154 Amino aci
19	265	54.5	76	5	ABB78166 Amino aci
20	255	52.5	87	5	ABB78148 Amino aci
21	255	52.5	87	5	ABB78147 Amino aci
22	241	49.6	86	5	ABB78149 Amino aci
23	231.5	47.6	89	9	ABE41576 L. pneumo
24	231.5	47.6	95	9	ABE38294 L. pneumo

ALIGNMENTS

25	231	47.5	87	5	ABB78170 Amino aci
26	231	47.5	122	7	ABO74609 Pseudomon
27	227	46.7	88	5	ABB78178 Amino aci
28	227	46.7	90	5	ABB78168 Amino aci
29	225	46.3	87	5	ABB78169 Amino aci
30	216.5	44.5	90	5	ABB78167 Amino aci
31	213	43.8	88	5	ABB78171 Amino aci
32	213	43.8	88	5	ABB78172 Amino aci
33	213	43.8	88	5	ABB78173 Amino aci
34	213	43.8	88	5	ABB78174 Amino aci
35	206	42.4	87	5	ABB78175 Amino aci
36	200	41.2	87	5	ABB78177 Amino aci
37	200	41.2	87	5	ABB78174 Amino aci
38	200	41.2	87	5	ABB78176 Amino aci
39	199.5	41.0	87	5	ADA34169 Acinetoba
40	131	27.0	110	8	ADP05173 M. catarr
41	83	17.1	506	3	AA74371 Neisseria
42	83	17.1	1647	4	ABG10750 Novel hum
43	81	16.7	507	6	ABU40210 Protein e
44	78	16.0	507	3	AA74372 Neisseria
45	78	16.0	507	3	AA74373 Neisseria
46	78	16.0	546	6	ABU38097 Protein e
47	76	15.6	548	6	ABO4737 Brugia ma
48	75	15.4	309	8	ADN46828 Thermococ
49	74.5	15.3	632	8	ADS29711 Bacteri
50	72	14.8	474	7	ABO75727 Pseudomon
51	71.5	14.7	679	9	ADZ85056 Partial F
52	71	14.6	311	7	ADM26256 Hyperther
53	70.5	14.5	285	4	ABE92683 Human pro
54	70.5	14.5	414	6	ABU11747 Human MDD
55	70.5	14.5	614	9	ADX06837 Cyclin-de
56	70.5	14.5	614	9	ADY16108 PRO polyp
57	70.5	14.5	764	5	ABB77432 Human tum
58	70.5	14.5	764	5	ADC99062 Human KRP
59	70.5	14.5	817	4	AAH38657 Human pol
60	70.5	14.5	863	4	AAH38656 Human pol
61	70.5	14.5	1135	8	ADS10706 Human the
62	70.5	14.5	1181	8	ADS10709 Human the
63	70.5	14.5	1186	8	ADH45460 Human mol
64	70.5	14.5	1188	8	ADH45460 Human mol
65	70.5	14.5	1206	5	ADH48860 NOV61 pro
66	70.5	14.5	1214	7	ADK65785 Angiogene
67	69.5	14.3	374	4	AAH39682 Human pol
68	69.5	14.3	389	4	AAH41468 Human pol
69	69.5	14.3	481	5	AAU93169 Arabidops
70	69.5	14.3	481	7	ADD30148 Plant yle
71	69.5	14.3	481	7	ADD31497 Plant yle
72	69.5	14.3	481	8	ADL1933 Plant tra
73	69.5	14.3	485	5	ABO8477 Human lat
74	69.5	14.3	488	4	ABE94458 Human pro
75	69.5	14.3	488	4	AAE67252 Amino aci

RESULT 1
ABB78158 standard; protein; 91 AA.

ABB78158; 05-NOV-2002 (first entry)

Amino acid sequence of a YggX homologue.

Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.

Unidentified.

US2002072118-A1.

PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.
 PA
 PI Downs D, Gralnick JA;
 XX
 DR WPI, 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 PS
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3.1e-48;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTTCTFLQREAGQDFOLYPGELGKRIYNEISKAWAQMOMKOTMLINEKLMNNA 60
 DB 1 MSRTTCTFLQREAGQDFOLYPGELGKRIYNEISKAWAQMOMKOTMLINEKLMNNA 60
 OY 61 EHRKLLQEMVNFLEPGKEVHIIGYTPEDKK 91
 DB 61 EHRKLLQEMVNFLEPGKEVHIIGYTPEDKK 91

RESULT 2

ABB78157
 ID ABB78157 standard; protein; 91 AA.

AC ABB78157;
 XX

DT 05-NOV-2002 (first entry)
 XX

DE Amino acid sequence of a YggX homologue.
 XX

KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.
 XX

OS Unidentified.
 XX

PN US2002072118-A1.
 XX

PD 13-JUN-2002.
 XX

PF 18-SEP-2001; 2001US-00955502.
 XX

PR 22-SEP-2000; 2000US-0234588P.
 XX

PA (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;
 XX

DR WPI, 2002-589476/63.
 XX

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 PS

XX Example; Fig 1A; 16pp; English.
 XX

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3.1e-48;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTTCTFLQREAGQDFOLYPGELGKRIYNEISKAWAQMOMKOTMLINEKLMNNA 60
 DB 1 MSRTTCTFLQREAGQDFOLYPGELGKRIYNEISKAWAQMOMKOTMLINEKLMNNA 60
 OY 61 EHRKLLQEMVNFLEPGKEVHIIGYTPEDKK 91
 DB 61 EHRKLLQEMVNFLEPGKEVHIIGYTPEDKK 91

RESULT 3
 ABB78156
 ID ABB78156 standard; protein; 91 AA.

AC ABB78156;
 XX

DT 05-NOV-2002 (first entry)
 XX

DE Amino acid sequence of a YggX homologue.
 XX

KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.
 XX

OS Escherichia coli.
 XX

PN US2002072118-A1.
 XX

PD 13-JUN-2002.
 XX

PF 18-SEP-2001; 2001US-00955502.
 XX

PR 22-SEP-2000; 2000US-0234588P.
 XX

PA (DOWN/) DOWNS D.
 XX (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;
 XX

DR WPI, 2002-589476/63.
 XX

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 PS

XX Example; Fig 1A; 16pp; English.
 XX

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:13:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-13

Perfect score: 486
Sequence: 1 MSRTTFCITFLQREASQDFQ.....NFLFEKVEVHIGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	91	2	A85954
2	486	100.0	91	2	A65082
3	486	100.0	91	2	P91108
4	469	96.5	91	2	AH0879
5	402	82.7	90	2	C82320
6	396	81.5	90	2	A10116
7	387	79.6	90	2	C64013
8	265	54.5	93	2	E84994
9	231	47.5	90	2	H83003
10	226	46.5	105	2	C82624
11	213	43.8	88	2	H81014
12	78	16.0	507	2	C81063
13	78	16.0	546	2	A81807
14	76	15.6	548	2	A54510
15	75.5	15.5	1638	2	D87749
16	75.5	15.5	2488	2	T42739
17	74.5	15.3	683	2	AC2256
18	72	14.8	265	2	T46013
19	72	14.8	447	2	T16527
20	72	14.8	507	2	A83105
21	72	14.8	511	2	A89574
22	69	14.2	258	2	A97991
23	69	14.2	258	2	E95121
24	69	14.2	548	2	A28209
25	69	14.2	1119	2	T15842
26	68	14.0	2672	2	A48126
27	67.5	13.9	209	2	T64172
28	67	13.8	235	2	G65212
29	67	13.8	324	2	T05429

30	67	13.8	433	2	A70465	probable GTP bindi
31	67	13.8	447	2	JC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2	T40058	probable chromatin
33	66.5	13.7	1260	2	T04440	hypothetical prote
34	66	13.6	593	2	C64097	probable soluble 1
35	66	13.6	689	2	P83902	delta-galactosidase
36	65.5	13.5	173	2	H86869	hypothetical prote
37	65.5	13.5	305	2	A75211	asparaginase (EC 3
38	65.5	13.5	323	2	A90536	lipoprotein (impor
39	65.5	13.5	365	2	B54128	Fe-binding protein
40	65.5	13.5	821	2	A12417	hypothetical prote
41	65	13.4	251	2	E90428	regulatory protein
42	65	13.4	330	2	S74456	alpha-1,3-mannosyl
43	65	13.4	445	1	XUHM8	hypothetical prote
44	65	13.4	456	2	G71152	probable transposo
45	65	13.4	1008	2	H85055	hypothetical prote
46	65	13.4	1141	2	T29185	probable transposo
47	65	13.4	1230	2	S56850	hypothetical prote
48	64.5	13.3	345	2	AG2300	SMC1 protein homol
49	64.5	13.3	305	2	A71247	probable L-asparag
50	64.5	13.3	495	2	AH0985	probable zinc-prot
51	64.5	13.3	859	2	T29630	hypothetical prote
52	64	13.2	220	2	S62410	hypothetical prote
53	64	13.2	438	2	T37786	probable RNA-bind1
54	64	13.2	447	1	A38561	alpha-1,3-mannosyl
55	64	13.2	583	2	T48365	hypothetical prote
56	64	13.2	604	2	S66993	hypothetical prote
57	64	13.2	990	2	T43445	hypothetical prote
58	64	13.2	1051	2	S27002	phospholipase C (B
59	64	13.2	1234	2	S52099	phospholipase C be
60	64	13.2	1389	2	I38994	hypothetical prote
61	63.5	13.1	91	2	H90521	hypothetical prote
62	63.5	13.1	243	2	T29635	hypothetical prote
63	63.5	13.1	460	2	T00639	hypothetical prote
64	63.5	13.1	591	1	FOWM8	gag polyprotein -
65	63	13.0	880	2	AE0179	neuroal ATPase ch
66	63	13.0	1251	2	A56677	neutonal cell cycl
67	63	13.0	1327	2	T14594	guanine nucleoti
68	63	13.0	1611	1	MMTMPV	183k protein - pep
69	62.5	12.9	483	1	SVASST	glutamate-cRNA lig
70	62.5	12.9	551	2	E84106	hypothetical prote
71	62.5	12.9	555	2	C96667	unknown protein, 7
72	62.5	12.9	617	2	B71071	probable prolyl en
73	62.5	12.9	964	1	T04325	probable ATP-depen
74	62.5	12.9	1417	2	T00661	hypothetical prote
75	62	12.8	169	2	PN0560	phytochrome - long

ALIGNMENTS

RESULT 1
A85954
hypothetical protein y9gx [imported] - Escherichia coli (strain O157:H7, substrain EDL9:
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #seqname_revision 16-Feb-2001 #ext_change 05-Oct-2004
C:Accession: A85954
R:Perera, N.T.; Plunkett II, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoustis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE005174; MUD:912517511;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: y9gx
C:Superfamily: fe(II) trafficking protein Y9gx
Query Match 100.0%; Score 486; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTFCTFLQREAGQDFQLYPGELKRIYNELSKEAQAQWQHQTMLINEKLNMMNA 60

Db 1 MSRTFCTFLQREAGQDFQLYPGELKRIYNELSKEAQAQWQHQTMLINEKLNMMNA 60

[illegible]

RESULT 2
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)

Query Match	100.0%	Score 486;	DB 2;	length 91;
Best Local Similarity	100.0%	Pred. No. 1.6e-41;		
Match 91; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

Oy 1 MSRTICTFLQREAEAGDFFOLYGEIGKRIYNEISKEAQAOMOHOTMLINEKKLNMMNA 600
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MSRTICTFLQREAEAGDFFOLYGEIGKRIYNEISKEAQAOMOHOTMLINEKKLNMMNA 600

Qy	61	EHRKLTQEMVNFLEGGKEVHI	EGYTPDEKK	91
Db	61	EHRKLTQEMVNFLEGGKEVHI <td>EGYTPDEKK</td> <td>91</td>	EGYTPDEKK	91

```

RESULT 3
P01106
hypothetical protein ECG3838 [imported] - Escherichia coli (strain O157:H7, substrain R)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C:Accession: F91108
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G.
G:Gisawa, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and
R:Reference number: A99629; MUID:21156231; PMID:11258756

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Query Match	100.0%;	Score 486;	DB 2;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 1.6e-41;		
Matches 91; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 MSRTICTFLQREAGODFQLYPELGRKLYNEISKEAMQWQHKTMLINEKLNMMNA 600

Db 1 MSRTICTFLQREAGODFQLYPELGRKLYNEISKEAMQWQHKTMLINEKLNMMNA 600

QY		61 EHRKLLGEQWVNFLEFGKEVHIIEGYTPEDKK 91
DB		61 EHRKLLGEQWVNFLEFGKEVHIIEGYTPEDKK 91

RESULT 4
AH0879
conserved hypothetical protein STY3266 [imported] - *Salmonella enterica* subsp. *enterica*
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A:Note: this species has also been called *Salmonella typhi*
i:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004

Query Match	96.5%	Score 469	DB 2	Length 91
Best Local Similarly	94.5%	Pred. NO.	7.9e-40	
Matches 86	Conservative	5	Mismatches 0	Indels 0
			Gaps	0

Oy

1 MSRTTCTFLORAEAGODPOLYPGELKRIYNEISKMAQWQHKTMLINEKLINMNA 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Dd

1 MSRTTFCTYLORDAEGODPOLYPGELKRIYNEISKMAQWQHKTMLINEKLINMNA 60

```
QY      61 EHRKLLQEMVNFLEGEKGVHIEGYTPEDKK 91
      |||||:||||:|||||
Db      61 EHRKLLQEMVNFLEGEKGVHIEGYTPEDKK 91
```

RESULT 5
C82320
conserved hypothetical protein VC0451 [imported] - *Vibrio cholerae* (strain N16961 serog
C) [species: *Vibrio cholerae*
C] [date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C] [accession: C82320
R.Heldelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.
Charadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Base, S.; Qin, H.; Dragoi, I.; Sellers, J.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Frazer, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301

Query Match	82.7%	Score 402; DB 2;	length 90;
Best Local Similarity	83.3%	Pred. No. 3.6e-33;	
Matches	75; Conservative	7; Mismatches	8; Indels 0; Gaps 0.

QY 61 EHRKLLLEQEMVNFLEFGSKRVHIEGYTPEDRK 90

61 EHRKLEQEMVNFLEGEKVEHIEGYTPEDK 90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-13
Perfect score: 486
Sequence: 1 MSRTFFCTFLQREAGQDFQ.....NFLFEKGVHIGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481	99.0	90	1	POA8P4 escherichia
2	481	99.0	90	1	POA8P3 escherichia
3	481	99.0	90	1	POA8P5 shigella fl
4	477	98.1	90	1	POA8P1 escherichia
5	464	95.5	90	1	POA8P2 escherichia
6	464	95.5	90	1	POA8P4 escherichia
7	464	95.5	90	1	POA8P3 escherichia
8	464	95.5	90	1	POA8P5 shigella fl
9	411	84.6	90	1	POA8P1 escherichia
10	404	83.1	90	1	POA8P2 escherichia
11	402	82.7	90	1	POA8P4 escherichia
12	402	82.7	90	1	POA8P3 escherichia
13	402	82.7	90	1	POA8P5 shigella fl
14	399	82.1	90	1	POA8P1 escherichia
15	396	81.5	90	1	POA8P2 escherichia
16	389	80.0	90	1	POA8P4 escherichia
17	387	79.6	90	1	POA8P3 escherichia
18	387	79.6	90	1	POA8P5 shigella fl
19	382	78.6	90	1	POA8P1 escherichia
20	381	78.4	90	1	POA8P2 escherichia
21	379	78.0	90	1	POA8P4 escherichia
22	373	76.7	90	1	POA8P3 escherichia
23	366	75.3	90	1	POA8P5 shigella fl
24	335	68.9	90	1	POA8P1 escherichia
25	332	68.3	90	1	POA8P2 escherichia
26	265	54.5	90	1	POA8P4 escherichia
27	255	52.5	90	1	POA8P3 escherichia
28	255	52.5	90	1	POA8P5 shigella fl
29	247	50.8	90	1	POA8P1 escherichia
30	247	50.8	90	1	POA8P2 escherichia
31	235	48.4	90	1	POA8P4 escherichia

32	231.5	47.6	89	1	FETP_LEGPA	Q5X3X9 legionella
33	231.5	47.6	89	1	FETP_LEGPH	Q5Z8U0 legionella
34	231	47.5	90	1	FETP_PSEAE	Q9H3U6 pseudomonas
35	231	47.5	91	1	FETP_XANAC	Q8PH77 xanthomonas
36	228.5	47.0	89	1	FETP_LEGPA	Q5X3X9 legionella
37	227	46.7	90	1	FETP_COXBU	Q83D06 coxiella bu
38	227	46.7	90	1	FETP_PSESM	Q87UJ5 pseudomonas
39	227	46.7	90	2	Q4ZLP3 PSEBSY	Q4ZLP3 pseudomonas
40	226	46.5	90	1	FETP_XLTPA	Q9PC73 xylolla fas
41	225	46.3	90	1	FETP_PSEBK	Q88F49 pseudomonas
42	225	46.3	92	1	FETP_XANOR	Q59722 xanthomonas
43	223	45.9	90	2	Q4J228 AZOVI	Q4J228 azotobacter
44	222	45.7	90	1	FETP_XLTPA	Q87UJ5 pseudomonas
45	222	45.7	92	1	FETP_XANCP	Q88289 xanthomonas
46	222	45.7	92	2	Q4UM14 XANCP	Q4UM14 xanthomonas
47	220	45.3	90	1	FETP_NITRU	Q82X52 nitrosomonas
48	215	44.2	90	2	Q6TVF6_PSEFL	Q6TVF6 pseudomonas
49	214	44.0	87	1	FETP_BUCBP	Q89444 buchnera ap
50	213	43.8	88	1	FETP_NEIG1	Q5F553 neisseria g
51	213	43.8	88	1	FETP_NEIMA	Q67615 neisseria m
52	212	43.6	79	1	FETP_CANBP	Q7V799 candidatus
53	212	43.6	90	2	Q4KJ22_PSEFS	Q4KJ22 pseudomonas
54	212	43.4	90	1	FETP_CHRVO	Q7N874 chromobacte
55	207	42.6	91	2	Q4LS19_9BURK	Q4LS19 burholderi
56	206	42.4	91	1	FETP_BURMA	Q621U9 burholderi
57	206	42.4	91	1	FETP_BURPS	Q63JF4 burholderi
58	206	42.4	91	1	FETP_RALSO	Q8Y010 ralstonia s
59	206	42.4	91	1	FETP_METCA	Q60A17 methylococ
60	200	40.9	87	1	FETP_PRAAT	Q50N18 francisella
61	199	40.9	90	1	FETP_AC1AD	Q6FE23 acinetobact
62	194.5	40.0	90	1	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
63	144	29.6	96	2	Q4NM04_9DELT	Q4NM04 anaeromyxob
64	142	29.2	92	2	Q5NUY1_9BURK	Q5NUY1 ralstonia m
65	90.5	18.6	482	2	Q6A1Z9_DESPS	Q6A1Z9 desulfotale
66	85.5	17.6	514	2	Q88PF3_PSEBK	Q88PF3 pseudomonas
67	81	16.7	507	2	Q7NSP0_CHRVO	Q7NSP0 chromobacte
68	81	16.7	508	2	Q7WXS1_ALCEBU	Q7WXS1 alcaligenes
69	80	16.5	486	2	Q4VVR2_PLABE	Q4VVR2 plasmidum
70	78.5	16.2	760	2	Q9JYB9_NEIMB	Q9JYB9 neisseria m
71	78	16.0	507	2	Q9JYB9_NEIMB	Q9JYB9 neisseria m
72	78	16.0	546	2	Q9JYB9_NEIMA	Q9JYB9 neisseria m
73	77.5	15.9	337	2	Q4UB40_THEIA	Q4UB40 thelaxia a
74	77.5	15.9	337	2	Q81AR8_BACCR	Q81AR8 bacillus ce
75	77.5	15.9	1123	2	Q7RJ10_PLAYAO	Q7RJ10 plasmidum

ALIGNMENTS

RESULT 1
ID FETP_ECOS7 STANDARD; PRT; 90 AA.
AC POA8P4; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS Name=yggX; OrderedLocustNames=24307; EC=3838;
GN Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_Taxid=83334;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RC MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick J.D.,
RA Posfai G., Hackett J., Link S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamowski K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

```

RL Nature 409:529-533 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC.
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
R Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kubara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22 (2001).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
CC -1- SUBUNIT: Monomer (by similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE005174; AAG58093.1; -; Genomic DNA.
CC EMBL; BA000007; BAB37261.1; -; Genomic DNA.
CC PIR; A85954; A85954.
CC PIR; F91108; F91108.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; Y9gX.
CC Pfam; PF04362; DUF495; 1.
CC PIRSF; PIRSF029827; Fe_traffic_Y9gX; 1.
CC ProDom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC INIT MET 0
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREAEQDDPOLYPGELGKRLYNEISKEAWQWQHKQTMLINEKKNMNAE 61
DB 1 SRTIFCTFLQREAEQDDPOLYPGELGKRLYNEISKEAWQWQHKQTMLINEKKNMNAE 60

QY 62 HKLLAEQWVNTFLFSGKEVHIGTYPEDYK 91
DB 61 HKLLAEQWVNTFLFSGKEVHIGTYPEDYK 90

RESULT 2
FETP_ECOLI STANDARD; PRT; 90 AA.
ID FETP_ECOLI
AC POA8P3; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gX; Ordered locus names=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Berna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirtpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RT Science 277:1453-1474 (1997).

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RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Rodison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12."
RT Electrophoresis 18:1259-1313 (1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9668784;
RA Wasinger V.C., Humphrey-Smith I.;
RT "Small genes/gene-products in Escherichia coli K-12."
RL FEWS Microbiol. Lett. 169:375-382 (1998).
RN [4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RT hydroxyapatite chromatography."
RL Electrophoresis 20:2181-2195 (1999).
RN [5]
RP INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.J., Koutsolioutou A., Carraeco D., Demple B.;
RT "SoxRS-regulated expression and genetic analysis of the Y9gX gene of
RT Escherichia coli."
RL J. Bacteriol. 185:6624-6632 (2003).
RN [6]
RP STRUCTURE BY NMR, AND FUNCTION.
RX PubMed=15883188; DOI=10.1110/ps.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;
RT "The solution structure of the oxidative stress-related protein Y9gX
RT from Escherichia coli."
RL Protein Sci. 14:1673-1678 (2005).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes. Necessary to
CC maintain high levels of aconitase under oxidative stress.
CC -1- SUBUNIT: Monomer (Probable).
CC -1- INDUCTION: By oxidative stress and soxS.
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U28377; AAA69129.1; -; Genomic DNA.
CC EMBL; U00096; AAC75999.1; -; Genomic DNA.
CC PIR; A65082; A65082.
CC PDB: 1YHD; NMR; A=1-90.
CC SWISS-2DPAGE; POA8P3; COLI.
CC Echobase; EB2809; -.
CC Ecogene; EG12984; Y9gX.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; Y9gX.
CC Pfam; PF04362; DUF495; 1.
CC PIRSF; PIRSF029827; Fe_traffic_Y9gX; 1.
CC ProDom; PD029191; DUF495; 1.
CC 3D-structure; Complete proteome; Direct protein sequencing; Iron.
CC INIT MET 0
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREAEQDDPOLYPGELGKRLYNEISKEAWQWQHKQTMLINEKKNMNAE 61

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Query Match 92.6%; Score 450; DB 2; Length 107;
Best Local Similarity 91.2%; Pred. No. 1e-48; Indels 0; Gaps 0;
Matches 83; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGDGFQLYPGELGKRIYNEISKAWAOMQHQTMLINEKKNMNA 60
DB 17 MSRTTCTFLQREAGDGFQLYPGELGKRIYNEISKAWAOMQHQTMLINEKKNMNA 76

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPPEK 91
DB 77 EHRKLEQEMVNFLEPGKEVHIEGYTPPEK 107

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 80.0%; Score 389; DB 2; Length 93;
Best Local Similarity 80.0%; Pred. No. 3.8e-41; Indels 0; Gaps 0;
Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGDGFQLYPGELGKRIYNEISKAWAOMQHQTMLINEKKNMNA 60
DB 4 MSRTTCTFLQREAGDGFQLYPGELGKRIYNEISKAWAOMQHQTMLINEKKNMNA 63

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTPPEK 90
DB 64 EHRKLEQEMVNFLEPGKEVHIEGYTPPEK 93

RESULT 3
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; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 47.5%; Score 231; DB 2; Length 122;
Best Local Similarity 51.7%; Pred. No. 3.6e-21; Indels 0; Gaps 0;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

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DB 33 MSRTTCTFLQREAGDGFQLYPGELGKRIYNEISKAWAOMQHQTMLINEKKNMNA 92

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTP 87
DB 93 EHRKLEQEMVNFLEPGKEVHIEGYTP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 41.0%; Score 199.5; DB 2; Length 92;
Best Local Similarity 42.7%; Pred. No. 2.2e-17; Indels 1; Gaps 1;
Matches 38; Conservative 15; Mismatches 35; Indels 1; Gaps 1;

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DB 4 MSRTTCTFLQREAGDGFQLYPGELGKRIYNEISKAWAOMQHQTMLINEKKNMNA 63

QY 61 EHRKLEQEMVNFLEPGKEVHIEGYTP 88
DB 64 EHRKLEQEMVNFLEPGKEVHIEGYTP 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 27.0%; Score 131; DB 2; Length 110;
Best Local Similarity 34.9%; Pred. No. 1.1e-08; Indels 0; Gaps 0;
Matches 29; Conservative 13; Mismatches 41; Indels 0; Gaps 0;

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QY 65 EHRKLEQEMVNFLEPGKEVHIEGYTP 87
DB 85 EHRKLEQEMVNFLEPGKEVHIEGYTP 107

RESULT 6
US-09-167-299-3
; Sequence 3, Application US/09167299

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
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Title: US-09-955-502a-13

Perfect score: 486
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	469	96.5	91	3	US-09-955-502-15
6	469	96.5	91	3	US-09-955-502-16
7	469	96.5	91	3	US-09-955-502-17
8	453	93.2	91	3	US-09-955-502-18
9	402	82.7	90	3	US-09-955-502-19
10	396	81.5	90	3	US-09-955-502-20
11	395	81.3	78	3	US-09-955-502-21
12	388	79.8	91	3	US-09-955-502-22
13	387	79.6	87	3	US-09-955-502-23
14	379	78.0	87	3	US-09-955-502-24
15	373	76.7	87	3	US-09-955-502-25
16	332	68.3	88	3	US-09-955-502-26
17	265	54.5	76	3	US-09-955-502-27
18	255	52.5	87	3	US-09-955-502-28
19	255	52.5	87	3	US-09-955-502-29
20	241	49.6	86	3	US-09-955-502-30
21	231	47.5	87	3	US-09-955-502-31
22	227	46.7	88	3	US-09-955-502-32
23	227	46.7	90	3	US-09-955-502-33
24	226	46.5	89	3	US-09-955-502-34
25	225	46.3	87	3	US-09-955-502-35
26	213	43.8	88	3	US-09-955-502-36
27	213	43.8	88	3	US-09-955-502-37

28	213	43.8	88	3	US-09-955-502-38	Sequence 28, Appl
29	206	42.4	87	3	US-09-955-502-39	Sequence 29, Appl
30	206	42.4	87	3	US-09-955-502-40	Sequence 30, Appl
31	200	41.2	87	3	US-09-955-502-41	Sequence 31, Appl
32	200	41.2	87	3	US-09-955-502-42	Sequence 32, Appl
33	83	17.1	1647	5	US-10-450-763-41109	Sequence 41109, A
34	81	16.7	507	4	US-10-282-122A-68134	Sequence 68134, A
35	74.5	15.3	546	4	US-10-369-493-18744	Sequence 18744, A
36	71.5	14.7	679	5	US-10-805-684-105	Sequence 105, Appl
37	70.5	14.5	764	4	US-10-416-330-37	Sequence 37, Appl
38	70.5	14.5	764	4	US-10-491-467-15	Sequence 15, Appl
39	70.5	14.5	786	5	US-10-732-923-4885	Sequence 4885, Ap
40	70.5	14.5	1206	4	US-10-085-198-144	Sequence 144, Appl
41	70.5	14.5	1214	5	US-10-717-665-24	Sequence 24, Appl
42	69.5	14.3	481	3	US-09-934-455-466	Sequence 466, Appl
43	69.5	14.3	481	4	US-10-225-066A-180	Sequence 180, Appl
44	69.5	14.3	481	4	US-10-225-067-64	Sequence 64, Appl
45	69.5	14.3	481	4	US-10-374-780A-396	Sequence 396, Appl
46	69.5	14.3	481	5	US-10-225-066A-180	Sequence 180, Appl
47	69.5	14.3	561	4	US-10-437-963-169643	Sequence 169643, A
48	69.5	14.3	660	6	US-11-097-143-24705	Sequence 24705, A
49	69.5	14.3	1261	4	US-10-437-963-189166	Sequence 189166, A
50	69.5	14.3	1261	4	US-10-415-478A-36	Sequence 36, Appl
51	69	14.2	258	4	US-10-472-928-2088	Sequence 2088, Ap
52	69	14.2	258	5	US-10-393-840-52	Sequence 52, Appl
53	68.5	14.1	184	4	US-09-864-408A-768	Sequence 768, Appl
54	68	14.0	102	3	US-10-219-220-66	Sequence 66, Appl
55	67.5	13.9	184	4	US-10-393-840-118	Sequence 118, Appl
56	67.5	13.9	545	5	US-10-732-923-9369	Sequence 9369, Ap
57	67.5	13.9	546	3	US-09-874-923-2	Sequence 2, Appl
58	67.5	13.9	546	3	US-09-874-923-2	Sequence 2, Appl
59	67.5	13.9	546	3	US-09-991-496-2	Sequence 2, Appl
60	67.5	13.9	546	4	US-10-098-732A-71	Sequence 71, Appl
61	67.5	13.9	926	3	US-09-991-496-128	Sequence 128, Appl
62	67.5	13.9	955	3	US-09-991-496-127	Sequence 127, Appl
63	67.5	13.9	982	3	US-09-874-923-95	Sequence 95, Appl
64	67.5	13.9	982	3	US-09-991-496-95	Sequence 95, Appl
65	67.5	13.9	1427	3	US-09-874-923-97	Sequence 97, Appl
66	67.5	13.9	1427	3	US-09-991-496-97	Sequence 97, Appl
67	67.5	13.9	1641	3	US-09-874-923-96	Sequence 96, Appl
68	67.5	13.9	1641	3	US-09-991-496-96	Sequence 96, Appl
69	66.5	13.7	279	4	US-10-425-114-44570	Sequence 44570, A
70	66.5	13.7	675	4	US-10-424-599-229257	Sequence 229257, A
71	66.5	13.7	1026	4	US-10-437-963-195890	Sequence 195890, A
72	66.5	13.7	1374	4	US-10-437-963-189670	Sequence 189670, A
73	66.5	13.7	1588	4	US-10-437-963-189741	Sequence 189741, A
74	66	13.6	507	4	US-10-282-122A-47787	Sequence 47787, A
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ALIGNMENTS

RESULT 1
US-09-955-502-11
Sequence 11, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIORITY FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIORITY FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 91
TYPE: PRT
ORGANISM: Escherichia coli K-12 MG1655

US-09-955-502-11

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Db 1 MSRTICTFLOREAGODFOLYFEGELKRIYNEISKEANAQWQHKTMLINEKLNMMNA 600

QY 61 EHRKLLQEMVNFLEGEKVHIGYTPEDKK 91
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RESULT 2
US-09-955-502-12

1 APPLICANT: Downs, Diana M.
2 APPLICANT: Gralnick, Jeff A.
3 TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
4 TITLE OF INVENTION: Oxygen-labile Proteins
5 FILE REFERENCE: 960296.97559
6 CURRENT APPLICATION NUMBER: US/09/955,502
7 CURRENT FILING DATE: 2001-09-18
8 PRIOR APPLICATION NUMBER: 60/234,588
9 PRIOR FILING DATE: 2000-09-22
10 NUMBER OF SEQ ID NOS: 33
11 SOFTWARE: PatentIn Ver. 2.1

ORGANISM: Escherichia coli O157:H7EDL933
US-09-955-502-12

Query Match	100.0%;	Score 486;	DB 3;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 7.2e-47;		
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DB 61 EHKLLIQEAMVNFLEGGKVNIEGYTPEDKK 91

RESULT 3
US-09-955-502-13

? APPLICANT: Downs, Diana M.
 ? APPLICANT: Gralnick, Jeff A.
 ? TITLE OR INVENTION: Method for Preventing Superoxide Damage to Cells and
 ? TITLE OR INVENTION: Oxygen-Labile Proteins
 ? FILE REFERENCE: 960296.9753
 ? CURRENT APPLICATION NUMBER: US/09/955,502
 ? CURRENT FILING DATE: 2001-09-18
 ? PRIOR APPLICATION NUMBER: 60/234,588
 ? PRIOR FILING DATE: 2000-09-22
 ? NUMBER OF SEQ ID NOS: 33
 ? SOFTWARE: PatentIn Ver. 2.1

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QY 61 EHRKLLQEMVNFLEGEKVHIEGYTPEDKK 91
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RESULT 4
US-09-955-502-14

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296, 97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella paratyphi
US-09-955-502-14

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/ APPLICANT: Downs, Diana M.
/
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
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/ TITLE OF INVENTION: Oxygen-Labile Proteins
/ FILE REFERENCE: 960296.97559
/
/ CURRENT APPLICATION NUMBER: US/09/955,502
/
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ PRIOR FILING DATE: 2000-09-22
/
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
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/ LENGTH: 91
/ TYPE: PRT
/ ORGANISM: Salmonella dublin
US-09-955-502-16

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Query Match	96.5%	Score 469;	DB 3;	Length 91;
Best Local Similarity	94.5%;	Pred. No. 5.9e-45;		
Matches	86;	Conservative	5;	Mismatches 0;
				Indels 0;
				Gaps 0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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Title: US-09-955-502a-13

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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7	60.5	12.4	264	US-10-821-234-1555
8	60.5	12.4	404	US-11-009-658-48
9	60.5	12.4	834	US-10-453-372-658
10	60	12.3	448	US-10-618-320A-25
11	60	12.3	480	US-10-510-386-12
12	60	12.3	677	US-10-793-626-198
13	59.5	12.2	177	US-10-467-657-1658
14	59	12.1	266	US-09-995-493-6
15	59	12.1	604	US-10-942-072-4
16	59	12.1	1142	US-11-109-156-22
17	59	12.1	1167	US-10-942-072-6
18	58.5	12.0	336	US-10-453-372-640
19	58.5	12.0	349	US-10-821-234-1387
20	58.5	12.0	577	US-11-072-512-187
21	58.5	12.0	695	US-10-453-372-648
22	58.5	12.0	700	US-10-995-561-922
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25	58.5	12.0	793	US-10-995-561-925

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48 57 11.7 504 7 US-11-072-512-3467 Sequence 3467, App
49 56 11.5 296 7 US-11-087-227-10 Sequence 10, App
50 56 11.5 372 7 US-11-143-986-5 Sequence 5, App
51 56 11.5 372 7 US-11-143-986-2 Sequence 2, App
52 56 11.5 386 7 US-11-143-986-2 Sequence 2, App
53 56 11.5 386 7 US-11-143-986-3 Sequence 3, App
54 56 11.5 397 7 US-11-022-562-223 Sequence 223, App
55 56 11.5 426 7 US-11-098-686-10340 Sequence 10340, App
56 56 11.5 427 7 US-11-186-284-91 Sequence 91, App
57 56 11.5 581 6 US-10-793-626-28 Sequence 28, App
58 56 11.5 697 6 US-10-485-517-1202 Sequence 1202, App
59 56 11.5 752 6 US-10-793-626-1036 Sequence 1036, App
60 56 11.5 1168 6 US-10-942-072-11 Sequence 11, App
61 56 11.5 1188 7 US-11-115-639-43 Sequence 43, App
62 56 11.5 1188 7 US-11-115-639-43 Sequence 43, App
63 56 11.5 1404 6 US-10-878-556A-169 Sequence 169, App
64 55.5 11.4 207 7 US-11-124-367A-437 Sequence 437, App
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66 55.5 11.4 328 7 US-11-124-367A-436 Sequence 436, App
67 55.5 11.4 440 7 US-11-072-512-3856 Sequence 3856, App
68 55.5 11.4 623 7 US-11-072-512-2547 Sequence 2547, App
69 55.5 11.4 2101 6 US-10-857-780-23 Sequence 23, App
70 55 11.3 257 6 US-10-667-295-61 Sequence 61, App
71 55 11.3 257 7 US-11-054-515-1710 Sequence 1710, App
72 55 11.3 286 6 US-10-667-295-60 Sequence 60, App
73 55 11.3 327 6 US-10-667-295-59 Sequence 59, App
74 55 11.3 359 7 US-11-087-227-8 Sequence 8, App
75 55 11.3 359 7 US-11-192-450-6 Sequence 6, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 / Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502a-14

Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGDPRQ.....SFLFEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database:

A_Geneseq_21.*
1: geneseq1980s.*
2: geneseq1990s.*
3: geneseq2000s.*
4: geneseq2001s.*
5: geneseq2002s.*
6: geneseq2003as.*
7: geneseq2003bs.*
8: geneseq2004s.*
9: geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	100.0	91	5	ABR78161
2	488	100.0	91	5	ABR78159
3	488	100.0	91	5	ABR78162
4	474	97.1	91	5	ABR78163
5	472	96.7	88	5	ABR78160
6	469	96.1	91	5	ABR78158
7	469	96.1	91	5	ABR78157
8	469	96.1	91	5	ABR78156
9	445	91.2	107	7	ABO65445
10	393	80.5	90	5	ABR78165
11	389	79.7	90	5	ABR78155
12	386	79.1	78	5	ABR78164
13	385	78.9	87	5	ABR78152
14	383	78.5	91	5	ABR78150
15	383	78.5	93	7	ADP05158
16	377	77.3	87	5	ABR78151
17	371	76.0	87	5	ABR78153
18	336	68.9	88	5	ABR78154
19	259	53.1	76	5	ABR78166
20	249	51.0	87	5	ABR78148
21	249	51.0	87	5	ABR78147
22	235	48.2	86	5	ABR78149
23	228	46.7	87	5	ABR78170
24	228	46.7	122	7	ABO74609

ALIGNMENTS

25	224.5	46.0	89	9	ABR41576	Abd41576 L. pneumo
26	224.5	46.0	95	5	ABR38294	Abb38294 L. pneumo
27	222.5	45.6	90	5	ABR78167	Abb78167 Amino aci
28	222	45.5	90	5	ABR78168	Abb78168 Amino aci
29	218	44.7	87	5	ABR78169	Abb78169 Amino aci
30	218	44.7	88	5	ABR78178	Abb78178 Amino aci
31	211	43.2	88	5	ABR78171	Abb78171 Amino aci
32	211	43.2	88	5	ABR78172	Abb78172 Amino aci
33	211	43.2	88	5	ABR78173	Abb78173 Amino aci
34	211	43.2	88	5	ABR78172	Abb78172 Amino aci
35	206	42.2	87	5	ABR78175	Abb78175 Amino aci
36	200	41.0	87	5	ABR78176	Abb78176 Amino aci
37	197	40.4	87	5	ABR78176	Abb78176 Amino aci
38	195.5	40.1	92	6	ADA34169	Ada34169 Acinetoba
39	195	40.0	87	5	ABR78177	Abb78177 Amino aci
40	130	26.6	110	8	ADL05173	Adl05173 M. catarr
41	77	15.8	1647	4	ABG10750	Abg10750 Novel hum
42	72	14.8	309	8	ADN46828	Adn46828 Thermococ
43	72	14.8	506	6	AAV74371	Aay74371 Neisseria
44	72	14.8	507	6	ABU40210	Abu40210 Protein e
45	71.5	14.7	184	3	AAE16290	Aab16290 pinus rad
46	71	14.5	447	2	AAE52657	Aae52657 Rat N-ace
47	71	14.5	447	7	ADE55944	Ade55944 Rat Prote
48	71	14.5	507	3	AAV74372	Aay74372 Neisseria
49	71	14.5	507	3	AAV74373	Aay74373 Neisseria
50	71	14.5	546	6	ABU38097	Abu38097 protein e
51	71	14.5	548	4	AAE04737	Aae04737 Brugia ma
52	70.5	14.4	184	3	AAE16325	Aab16325 pinus rad
53	70.5	14.4	184	4	AAE5734	Aab5734 Annexin-1
54	70.5	14.4	184	7	ADB94702	Adb94702 Programme
55	70.5	14.4	593	4	ABG19947	Abg19947 Novel hum
56	70	14.3	257	3	AAE31203	Aag31203 Arabidops
57	70	14.3	297	3	AAE31202	Aag31202 Arabidops
58	70	14.3	324	3	AAE31201	Aag31201 Arabidops
59	70	14.3	758	9	ADW71760	Adw71760 Salimone1
60	69.5	14.2	1377	8	AAE38052	Aag38052 Arabidops
61	69.5	14.2	1377	8	ADV81847	Adv81847 Streptoco
62	69.5	14.2	1387	8	ADV88434	Adv88434 Streptoco
63	69.5	14.2	1387	8	ADV79687	Adv79687 Streptoco
64	69	14.1	503	4	ABG16577	Abg16577 Novel hum
65	69	14.1	679	5	ADZ85056	Adz85056 Partial F
66	68.5	14.0	608	5	ABP73745	Abp73745 Candida a
67	68.5	14.0	632	8	ADS29711	Ads29711 Bacterial
68	68	13.9	239	8	ADP07537	Adp07537 Human col
69	68	13.9	280	3	AAE54284	Aay54284 Amino aci
70	68	13.9	280	5	ABG39905	Abg39905 Lactuca s
71	68	13.9	280	8	ADJ50292	Adj50292 O11-aesoc
72	68	13.9	285	4	AAE32683	Aab32683 Human pro
73	68	13.9	302	4	AAE88379	Aab88379 Human mem
74	68	13.9	302	9	ADY63123	Ady63123 Human CLO
75	68	13.9	414	6	ABU11747	Abu11747 Human MDD

RESULT 1
ID ABR78161 standard; protein; 91 AA.
XX ABR78161;
XX

DT 05-NOV-2002 (first entry)
XX

XX Amino acid sequence of a Yggx homologue.
DE

XX Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
KW

XX hydroxyl radical; DNA damage; Yggx homologue.
OS

XX Unidentified.
XX

XX US2002072118-A1.
XX

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from *Salmonella*
XX *enterica* serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTFCYTLQRDAGQDPQLYPGEIGKRIYNEISKDAWAQOHKQTMLINEKLLMNNNA 60
DB 1 MSRTTFCYTLQRDAGQDPQLYPGEIGKRIYNEISKDAWAQOHKQTMLINEKLLMNNNA 60

QY 61 EHRKLLQEEMVSLFEGKDVHIEGYTPEDKK 91
DB 61 EHRKLLQEEMVSLFEGKDVHIEGYTPEDKK 91

RESULT 2
ABB78159
ID ABB78159 standard; protein; 91 AA.
XX
XX ABB78159;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX

SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTFCYTLQRDAGQDPQLYPGEIGKRIYNEISKDAWAQOHKQTMLINEKLLMNNNA 60
DB 1 MSRTTFCYTLQRDAGQDPQLYPGEIGKRIYNEISKDAWAQOHKQTMLINEKLLMNNNA 60

QY 61 EHRKLLQEEMVSLFEGKDVHIEGYTPEDKK 91
DB 61 EHRKLLQEEMVSLFEGKDVHIEGYTPEDKK 91

RESULT 3
ABB78162
ID ABB78162 standard; protein; 91 AA.
XX
XX ABB78162;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX *Salmonella* typhi.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from *Salmonella*

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-14

Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAGQDFQ.....SFLFGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	100.0	91	2	AH0879 conserved hypothet
2	469	96.1	91	2	A85854 hypothetrical prote
3	469	96.1	91	2	A65082 hypothetrical prote
4	469	96.1	91	2	P91108 hypothetrical prote
5	393	80.5	90	2	A10116 conserved hypothet
6	389	79.7	90	2	C82320 conserved hypothet
7	385	78.9	90	2	C64013 hypothetrical prote
8	259	53.1	93	2	E84894 hypothetrical prote
9	222	47.5	105	2	C82624 conserved hypothet
10	228	46.7	90	2	H83003 conserved hypothet
11	211	43.2	88	2	H81014 conserved hypothet
12	163	16.3	1638	2	D87749 protein unc-73b [i
13	79.5	16.3	2488	2	T42739 guanine nucleotide
14	78	16.0	1260	2	T04440 hypothetrical prote
15	73.5	15.1	495	2	AH0985 probable zinc-prot
16	71.5	14.7	209	2	I64172 alpha-1,3-mannosyl
17	71	14.5	447	2	JC2076 fumarate hydratase
18	71	14.5	507	2	C81063 fumarate hydratase
19	71	14.5	546	2	A81807 63k antigen - nema
20	71	14.5	548	2	A54510 chitosulfate reduct
21	70	14.3	324	2	T05429 chitosulfate-dithio
22	70	14.3	758	2	A57143 hypothetrical prote
23	70	14.3	859	2	T29630 hypothetrical prote
24	69.5	14.2	265	2	T46013 hypothetrical prote
25	69	14.1	265	2	T16527 hypothetrical prote
26	68.5	14.0	447	2	AC2256 alpha-1,3-mannosyl
27	68	13.9	445	1	XUHMB beta-galactosidase
28	68	13.9	445	1	XUHMB beta-galactosidase
29	68	13.9	689	2	F83902

30	67.5	13.8	166	2	F70562 hypothetrical prote
31	67	13.7	447	1	A38561 alpha-1,3-mannosyl
32	67	13.7	1111	2	T23047 hypothetrical prote
33	66.5	13.6	410	1	KHMSD cathepsin D (Ec 3,
34	66	13.5	447	1	A42500 alpha-1,3-mannosyl
35	66	13.5	703	2	B82148 ATP-dependent heli
36	66	13.5	1085	2	S62265 hypothetrical coile
37	65.5	13.4	287	2	F82265 conserved hypothet
38	65.5	13.4	365	2	B54128 PC-binding protein
39	65	13.3	433	2	A70465 probable GTP bindi
40	65	13.3	507	2	A83105 probable fumate
41	65	13.3	511	2	A95574 ABC transporter at
42	65	13.3	593	2	C64097 probable soluble 1
43	65	13.3	1230	2	S56850 SMCI protein homol
44	64.5	13.2	327	2	AD2129 transcription regu
45	64.5	13.2	385	2	D87723 protein R06A10.2 [
46	64.5	13.2	401	2	AE1978 hypothetrical prote
47	64.5	13.2	544	2	T40058 probable chromatin
48	64.5	13.2	1197	2	S26947 DNA-directed DNA p
49	64	13.1	251	2	E90428 hypothetrical prote
50	64	13.1	548	2	A28209 60K filarial anti
51	64	13.1	643	2	A43547 paraaporal crystal
52	63.5	13.0	379	2	S70709 type II site-spect
53	63.5	13.0	438	2	T37786 probable RNA-bind
54	63.5	13.0	2672	2	A48126 translation activa
55	63	12.9	205	2	C26135 keratin, 50K type
56	63	12.9	235	2	G65212 hypothetrical 26.7K
57	63	12.9	258	2	A97991 hypothetrical prote
58	63	12.9	258	2	B95121 phosphotesterase, p
59	63	12.9	483	2	G64799 ybev protein - Esc
60	63	12.9	543	2	T16015 hypothetrical prote
61	63	12.9	549	2	T16016 hypothetrical prote
62	63	12.9	1119	2	T15842 hypothetrical prote
63	63	12.9	1166	2	H71609 hypothetrical prote
64	63	12.9	1209	2	T46027 hypothetrical prote
65	63	12.9	1337	2	T14594 guandidine nucleoti
66	63	12.9	1572	2	S45251 SNF2alpiha protein
67	63	12.9	1586	2	S39580 HBRM protein - hum
68	62.5	12.8	165	2	A81382 shikimate kinase (
69	62.5	12.8	259	2	G83203 conserved hypothet
70	62.5	12.8	305	2	A75211 asparaginase (EC 3
71	62.5	12.8	375	2	T37245 GTP-binding regula
72	62.5	12.8	498	2	G91179 hypothetrical prote
73	62.5	12.8	498	2	H86025 hypothetrical prote
74	62.5	12.8	498	2	S47748 53.1K protein prec
75	62.5	12.8	629	2	B83107 chemotactic transd

ALIGNMENTS

RESULT 1
AH0879 conserved hypothetrical protein SRY3266 [imported] - Salmonella enterica subsp. enterica
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #ext_change 05-Oct-2004
C/Accession: AH0879
R/Parikhili, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Comerston, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero-
A/Reference number: AB0502; WUID:21534947; PMID:11677608
A/Accession: AH0879
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <PAR>
A/Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:G16504189;
C/Genetics:
A/Genes: SRY3266
C/Superfamily: Fe(II) trafficking protein YggX

Query Match	100.0%;	Score 488;	DB 2;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 2.1e-42;		
Matches 91; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	QY	QY	QY
1 MSRTFCTYTORADEGDDPOLYFGEGLGKRYNINISDAMAMQWQHKOTMLINEKGNMNNNA 60	1 MSRTFCTYTORADEGDDPOLYFGEGLGKRYNINISDAMAMQWQHKOTMLINEKGNMNNNA 60	1 MSRTFCTYTORADEGDDPOLYFGEGLGKRYNINISDAMAMQWQHKOTMLINEKGNMNNNA 60	1 MSRTFCTYTORADEGDDPOLYFGEGLGKRYNINISDAMAMQWQHKOTMLINEKGNMNNNA 60
61 EHRLLLEQEMVSPFLFEGKDVHIEGYPDEDK 91	61 EHRLLLEQEMVSPFLFEGKDVHIEGYPDEDK 91	61 EHRLLLEQEMVSPFLFEGKDVHIEGYPDEDK 91	61 EHRLLLEQEMVSPFLFEGKDVHIEGYPDEDK 91

RESULT 2
AB5954
Hypochemical protein YggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: AB5954
R:Perma.N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, B.U.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 528-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: AB5954
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO-
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB005174; NID:g12517511; E
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: YggX
A:Superfamily: fe(II) trafficking protein YggX

Query Match	96.1%;	Score 469;	DB 2;	Length 91;
Best Local Similarity	94.5%;	Pred. No. 1.8e-40;		
Matches	86;	Conservative	5;	Mismatches 0;
			Indels	0;
			Gaps	0;
Qy	1	MSRTITFCYTDAGAGODFOLYPGELGRININISKDMAOMOHQOTWLINKEKLLMNNA	60	
		: : : : : : : : : : :		
Db	1	MSRTITFCYTDORERBAGODFOLYPGELGRININISKEAMAOMOHQOTWLINKEKLLMNNA	60	
Qy	61	EHRKLLBOEMVSLFPEGKDVHIEGTPEDDK	91	
		: : : : : : : : : :		
Db	61	EHRKLLBOEMVSLFPEGKDVHIEGTPEDDK	91	

RESULT 3
A:5082
hypothetical protein b2962 - *Escherichia coli* (strain K-12)
C:Species: *Escherichia coli*
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.V.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; PMID:9278503
A:Accession: A65082
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-91 <Blast>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:G000000000
A:Experimental source: strain K-12, Substrain MG655
A:Superfamily: Fe(II) trafficking protein YggX

```
Query Match      96.1% Score 469; DB 2; length 91;
Best Local Similarity 94.5%; Pred. No.1.8e-40;
Matches      86; Conservative    5; Mismatches    0; Indels    0; Gaps
OY      1 MSRTIFCTYVQRDGGDPQLYPGELGKRYNYSISKDAWQWQHKKQTMLINEKLMMNNA 60
|||||:::|||||||:::|||||:
```

Db 1 MSRTICTFLQRAAEQODPOLYPGELGRIIYNEISKEAAMQOHQITMLINKEULMMA 60

Qy 61 EHRKLLQEMVSTFLFEGKDVHIEGTYTPEDK 91

Db 61 EHRKLLQEMVNFLEFGKDVHIEGTYTPEDK 91

```

RESULT 4
P91108
Hypothetical protein ECa3838 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #next_change 05-Oct-2004
C:Accession: F91108
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
  gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
  Nucleic Acids Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
  A:Reference number: A93629; WUID:21156231; PMID:11258796
A:Accession: F91108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <HAY>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI000013A04; GB:BA000007; PIDD:BA837261.1.
A:Experimental source: strain O157:H7, substrain R1MD 0509552
C:Genetics:
A:Gene: ECa3838
A:Superfamily: fe(II) trafficking protein YggX

```

Query Match	96.1%	Score 469	DB 2	Length 91
Best Local Similarity	94.5%	Pred No. 1	8e-40	
Matches	86	Conservative	5	Mismatches 0; Indels 0; Gaps
Qy	1	MSRTICTCTLOHDAAGDGFOLYPBGLSKRIYNEISKDAAWAOHQMTLINEKLLMNNA	60	
Dy	1	MSRTICTCTLOHDAAGDGFOLYPBGLSKRIYNEISKDAAWAOHQMTLINEKLLMNNA	60	
Dy	61	EHRKLLEQEWVSFLFEGKDVIHEGYTPEDKK	91	
Dy	61	EHRKLLEQEWVNFLEFGKEVHIIEGTTPEKK	91	

RESULT 5
A10116
conserved hypothetical protein YP00953 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: A10116
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, T.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; PMID:21470413; PMID:11586360
A:Accession: A10116
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 190 <R>
A:Cross-references: UNIPARC:UP100000DCCC4; GB:AL550842; PIDD:G15979022;
C:Genetic:
A:Gene: YP00953
A:Superfamily: fe(ii) trafficking protein YggX

Query Match	80.5%	Score 393;	DB 2;	Length 90;
Best Local Similarity	81.1%	Pred. No. 8, 1e-33;		
Matches	73;	Conservative 9;	Mismatches 8;	Indels 0; Gaps
QY	1	MSRTICTYIGRAEGQDFQLYPGEIGKRIYNEISDKDAWQHQKTMILNEKKLNNMNA	60	
		:::		
Db	1	MSRTICTFLKDAERQDFQLYPGEIGKRIYNEISKAWSQWITQKTMILNEKLSMMNI	60	
QY	61	EHRKLEQEMVSLFEGKDVHIEGYTPBPK	90	
Db	61	EDRKLEQEMVNLFLFEGKDVHLAGYTPBPK	90	

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0561 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-14

Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAGQDFQ.....SFLFGKDVHIGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	483	99.0	90	1	PERT_SALCH
2	483	99.0	90	1	PERT_SALPA
3	483	99.0	90	1	PERT_SALTI
4	483	99.0	90	1	PERT_SALTY
5	464	95.1	90	1	PERT_ECO57
6	464	95.1	90	1	PERT_ECOLI
7	464	95.1	90	1	PERT_SHIFL
8	460	94.3	90	1	PERT_ECOL6
9	416	85.2	90	1	PERT_ERWCT
10	401	82.2	90	1	PERT_YERPS
11	393	80.5	90	1	PERT_VIBPA
12	393	80.5	90	1	PERT_YERPA
13	389	79.7	90	1	PERT_VIBCH
14	389	79.7	90	1	PERT_VIBVU
15	389	79.7	90	1	PERT_VIBVY
16	387	79.3	91	1	PERT_MANSW
17	385	78.9	90	1	PERT_HABIN
18	385	78.9	90	2	O4QMD9_HABH8
19	383	78.5	90	1	PERT_PHOPR
20	377	77.3	90	1	PERT_PASMU
21	376	77.0	90	1	PERT_PASLU
22	371	76.0	94	1	PERT_HABDU
23	365	74.8	90	1	PERT_VIBF1
24	341	69.9	90	1	PERT_IDILO
25	336	68.9	92	1	PERT_SHEON
26	259	53.1	77	1	PERT_BUCAT
27	249	51.0	90	1	PERT_BORBR
28	249	51.0	90	1	PERT_BORPA
29	249	51.0	90	1	PERT_BORPE
30	243	49.8	78	1	PERT_BUCAP
31	239	49.0	91	1	PERT_XANAC

32	232	47.5	90	1	PERT_XYLEA	09pc73 xylella fas
33	232	47.5	92	1	PERT_XANOR	059722 xanthomonas
34	228.5	46.8	89	1	PERT_LEGPI	05wv44 legionella
35	228	46.7	90	1	PERT_PSEAB	09h36 pseudomonas
36	228	46.7	90	1	PERT_XYLEP	087d06 xylella fas
37	228	46.7	92	1	PERT_XANCP	08p829 xanthomonas
38	228	46.7	92	2	O4UW14_XANCP	04uw14 xanthomonas
39	225	46.1	78	1	PERT_WIGBR	08d305 wigleswort
40	224.5	46.0	89	1	PERT_LEGPA	05x3x9 legionella
41	224.5	46.0	89	1	PERT_LEGPH	05x806 legionella
42	222	45.5	90	1	PERT_NITBU	082x52 nitrosomonas
43	222	45.5	90	1	PERT_PSEBS	087u55 pseudomonas
44	222	45.5	90	2	O4ZLP3_PSEBS	04zlp3 pseudomonas
45	218	44.7	90	1	PERT_COXBU	083d06 coxiella bu
46	218	44.7	90	1	PERT_PSEPK	088499 pseudomonas
47	218	44.7	90	2	O4J228_AZOVI	04j228 azotobacter
48	215	44.1	90	2	O6T7F6_PSEPL	06t7f6 pseudomonas
49	213	43.6	90	1	PERT_CHRVO	06t7f6 pseudomonas
50	212	43.4	79	1	PERT_CANBF	07vix9 chromobacte
51	211	43.2	88	1	PERT_NEIG1	05f553 neisseria g
52	211	43.2	88	1	PERT_NEIMA	05f553 neisseria m
53	211	43.2	88	1	PERT_NEIMA	05f553 neisseria m
54	207	42.4	87	1	PERT_BUCBP	089444 buchiera ap
55	206	42.2	91	1	PERT_BURMA	062i09 burkholderi
56	206	42.2	91	1	PERT_BURPS	063e14 burkholderi
57	205	42.0	90	2	O4KJ12_PSEPS	04kj12 pseudomonas
58	205	42.0	91	1	PERT_RALSO	08y010 ralstonia s
59	203	41.6	91	2	O4LSI9_9BURK	04lsi9 burkholderi
60	195	40.0	90	1	PERT_METCA	060417 methylococc
61	192	39.3	87	1	PERT_FRATT	05nh18 francisella
62	190.5	39.0	90	1	PERT_ACTAD	06f5b3 acinetobact
63	146	29.9	96	2	O4FVJ7_9GAMM	04fvj7 psychrobact
64	145	29.7	92	2	O4NMQ4_9DELT	04nmq4 anaeromyxob
65	82.5	16.9	482	2	O5NXY1_9BURK	05nxy1 ralstonia m
66	82.5	16.9	514	2	O6AIZ9_DSBS	06aiz9 desulfocale
67	79.5	16.3	1638	2	O7KBP4_CABEL	07kbp4 caenorhabdi
68	79.5	16.3	2400	2	O6BEM2_CABEL	06bem2 caenorhabdi
69	78.5	16.3	2488	2	O6I528_CABEL	06i528 caenorhabdi
70	78.5	16.1	337	2	O81AR8_BACCR	081ar8 bacillus ce
71	78	16.0	1260	2	O49677_ARATH	049677 arabidopsis
72	77.5	15.9	1047	2	O5CJ53_CRYHO	05cj53 cryptospori
73	76.5	15.7	486	2	O7WXS1_ALCEU	07wxs1 alcaligenes
74	75.5	15.5	1278	2	O5CYM7_CRYPV	05cym7 cryptospori
75	75	15.4	385	2	O734A2_BACCI	0734a2 bacillus ce

ALIGNMENTS

RESULT 1
PERT_SALCH STANDARD; PRT; 90 AA.
ID PERT_SALCH
AC O57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yg9x; Ordered locusNames=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_Taxid=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-867;
RC PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.,
"The genome sequence of Salmonella enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen.";
Nucleic Acids Res. 33:1690-1698(2005).
RT -I- FUNCTION: Could be a mediator in iron transfections between iron
acquisition and iron-regulating processes, such as synthesis and/or

```
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE017220; AAX66958.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
PT INIT_MER 0
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE225553C CRC64;
By similarity.
Query Match 99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTTCTTYQRDAEGODPOLYPGELGKRIYNEISKDAWAQWQHKOTMLINEKKLNMMNAE 61
DB 1 SRTTCTTYQRDAEGODPOLYPGELGKRIYNEISKDAWAQWQHKOTMLINEKKLNMMNAE 60
QY 62 HRLLEQEWVSFLPEGKDVHIEGYTPEDKK 91
DB 61 HRLLEQEWVSFLPEGKDVHIEGYTPEDKK 90
RESULT 2
FETP_SALPA STANDARD; PRT; 90 AA.
ID FETP_SALPA
AC Q5PMH1;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=SPA2974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxId=54388;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozerov P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du P., Carter J., Krenitzki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Mink P.,
RA Deleantony K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spiech J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RT Nat. Genet. 36:1268-1274(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
DR SMR; Q5PMH1; 1-91.
DR HAMAP; MF_00686; -; 1.
```

```
DR InterPro; IPR007457; YggX.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
PT INIT_MER 0
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE225553C CRC64;
By similarity.
Query Match 99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SRTTCTTYQRDAEGODPOLYPGELGKRIYNEISKDAWAQWQHKOTMLINEKKLNMMNAE 61
DB 1 SRTTCTTYQRDAEGODPOLYPGELGKRIYNEISKDAWAQWQHKOTMLINEKKLNMMNAE 60
QY 62 HRLLEQEWVSFLPEGKDVHIEGYTPEDKK 91
DB 61 HRLLEQEWVSFLPEGKDVHIEGYTPEDKK 90
RESULT 3
FETP_SALTI STANDARD; PRT; 90 AA.
ID FETP_SALTI
AC P67618; Q8XFE6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=STY3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
NCBI_TaxId=601;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Haque A., Hien T.T., Holtroyd S., Jagsis K.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagsis K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RT Nature 413:848-852(2001).
[2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1126/JCB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G., III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomes of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RT RT J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
DR EMBL; AE016844; AAO70576.1; -; Genomic_DNA.
DR SMR; P67618; 1-90.
DR HAMAP; MF_00686; -; 1.
```


Query Match	91.2%	Score 445;	DB 2;	Length 107;
Best Local Similarity	89.0%	Pred. No. 3.5e-49;		
Matches	81;	Conservative	7;	Mismatches 3;
			Indels	0;
			Gaps	0;

Qy I MSRTICTYLRDAEGDFFLYPGELGRINYSKIDANAQWQHQTMLINEKLIMMNA 60
| | | | : | : | | | | | | | | | | | | | | | | | | | | | |
Db 17 MSRTICTFLRDAEGDFFLYPGELGRINYSKIDANAQWQHQTMLINEKLIMMNP 76

```

Qy      61 EHRKLIQEMVSLFPEGKDVIHIGYTPDEKK 91
          |||||
Db      77 EHRKLIQEMVQLFPEGKDVIHIGYTPPEKQ 107

```

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A

APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09

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; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
;

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Query Match	78.5%;	Score 383;	DB 2;	Length 93;
Best Local Similarity	77.8%;	Pred. No. 2.5e-41;		
Matches 70;	Conservative	9;	Mismatches 11;	Indels 0;
			Gaps	0;

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Qy      1 MSRTICTYLRDAEGODFOLYGEELGRIRYNESKIDAMAWOHQOTMLINEKLMMNA 60
        |||||:::|||||::|||::|||::|||::|||::|||::|||::|||::|||
Db      4 MSRTIETPLNKADGDLFLYGEELGRIRFNESKBAWQMMAQTMLINEKLTMTNP 63
```

```

QY      61 EHRKLLIQEMVSLFPEGKDVHIEGTYRPEDK 90
          : ||||| ||||| : ||| :
DB      64 DDRKLLIQEMVRFLFEGHVDVHIDGTYRPEEK 93

```

RESULT 3
US-09-252-991A-2335
; Sequence 23355, Application US/09252991A

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18

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; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122

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Query Match 46.7%; Score 228; DB 2; Length 122;

Matches 46; Conservative 11; Mismatches 29; Indels 2; Gaps 1

```

Db      33 MSRTWCRKYYHELPGIDRPPYFGAKGDIYNNYSRKAMDEWQKHOTMLIERRLANNNA 922
      |||: | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Qy 61 EHRKLTLEQEMVSFLFEGKD-VHIEGYTP 87
| | | | | : | | : | |
Db 93 EDRKFLQEQEMDKFL-SGEDYAKADGYTP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

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; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456

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ORGANISM: *Acinetobacter baumannii*
US-09-328-352-5456

Best Local Similarity 41.6%; Pred. No. 2.4e-17;
Matches 37; Conservative 15; Mismatches 36; Indels 1; Gaps 1

4 MSRQVFCRKRYQKEMEGLDFAFPFGAKGQEFFEE

Db 64 BAKKFLBEOREKPFNNDSEVEKAEGWKPE 92

Sequence 2859, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:

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; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2109.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236

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; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT

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US-09-540-236-2859	26.6%	Score 130;	DB 2;	Length 110;
Query Match				

Matches 29; Conservative 13; Mismatch 5

65 LLEQEMVSFLFECKDVHIEGYTP 87

RESULT 6
US-09-167-299-3
; Sequence 3, Application US/09167299

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502a-14

Perfect score: 488

Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLPEKQVHIGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US108_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	100.0	91	3	US-09-955-502-14
2	488	100.0	91	3	US-09-955-502-16
3	488	100.0	91	3	US-09-955-502-17
4	474	97.1	91	3	US-09-955-502-18
5	472	96.7	88	3	US-09-955-502-15
6	469	96.1	91	3	US-09-955-502-11
7	469	96.1	91	3	US-09-955-502-12
8	469	96.1	91	3	US-09-955-502-13
9	393	80.5	90	3	US-09-955-502-20
10	389	79.7	90	3	US-09-955-502-10
11	386	79.1	78	3	US-09-955-502-19
12	385	78.9	87	3	US-09-955-502-7
13	383	78.5	87	3	US-09-955-502-5
14	377	77.3	87	3	US-09-955-502-6
15	371	76.0	87	3	US-09-955-502-8
16	336	68.9	88	3	US-09-955-502-9
17	259	53.1	76	3	US-09-955-502-21
18	249	51.0	87	3	US-09-955-502-2
19	249	51.0	87	3	US-09-955-502-3
20	235	48.2	86	3	US-09-955-502-4
21	232	47.5	89	3	US-09-955-502-22
22	228	46.7	87	3	US-09-955-502-25
23	222	45.5	90	3	US-09-955-502-23
24	218	44.7	87	3	US-09-955-502-24
25	218	44.7	88	3	US-09-955-502-33
26	211	43.2	88	3	US-09-955-502-26
27	211	43.2	88	3	US-09-955-502-27

28	211	43.2	88	3	US-09-955-502-28	Sequence 28, Appl
29	206	42.2	87	3	US-09-955-502-29	Sequence 29, Appl
30	206	42.2	87	3	US-09-955-502-30	Sequence 30, Appl
31	197	40.4	87	3	US-09-955-502-31	Sequence 31, Appl
32	195	40.0	87	3	US-09-955-502-32	Sequence 32, Appl
33	177	15.8	1647	5	US-10-450-763-41109	Sequence 41109, A
34	72.5	14.9	786	5	US-10-732-923-4885	Sequence 4885, Ap
35	72	14.8	507	4	US-10-282-122A-68134	Sequence 68134, A
36	72	14.8	1261	4	US-10-437-963-189166	Sequence 189166, A
37	71.5	14.7	184	4	US-10-393-840-52	Sequence 52, Appl
38	71	14.5	546	4	US-10-282-122A-66021	Sequence 66021, A
39	70.5	14.4	184	4	US-10-219-220-66	Sequence 66, Appl
40	70.5	14.4	184	4	US-10-393-840-118	Sequence 118, Appl
41	70.5	14.4	593	5	US-10-450-763-50306	Sequence 50306, A
42	69	14.1	503	5	US-10-450-763-46936	Sequence 46936, A
43	69	14.1	679	5	US-10-805-684-105	Sequence 105, App
44	68.5	14.0	449	4	US-10-424-599-278212	Sequence 278212, A
45	68.5	14.0	608	4	US-10-032-585-7582	Sequence 7582, Ap
46	68.5	14.0	632	4	US-10-369-493-18744	Sequence 18744, A
47	68	13.9	280	3	US-09-323-998D-37	Sequence 37, Appl
48	68	13.9	280	4	US-10-389-566-2296	Sequence 2296, Ap
49	68	13.9	445	4	US-10-844-874-14	Sequence 14, Appl
50	68	13.9	445	5	US-10-713-970-13	Sequence 13, Appl
51	68	13.9	478	4	US-10-087-192-378	Sequence 378, App
52	68	13.9	689	4	US-10-369-493-17280	Sequence 17280, A
53	68	13.9	764	4	US-10-416-330-37	Sequence 37, Appl
54	68	13.9	764	5	US-10-491-467-15	Sequence 15, Appl
55	68	13.9	1206	4	US-10-085-198-144	Sequence 144, App
56	68	13.9	1214	5	US-10-717-665-24	Sequence 24, App
57	67.5	13.8	166	5	US-10-482-706-269	Sequence 269, Appl
58	67	13.7	119	4	US-10-389-566-1126	Sequence 1126, Ap
59	67	13.7	167	4	US-10-437-963-158697	Sequence 158697, A
60	67	13.7	306	4	US-10-424-599-241560	Sequence 241560, A
61	66.5	13.6	315	4	US-10-282-122A-57222	Sequence 57222, A
62	66.5	13.6	315	5	US-10-958-216-464	Sequence 464, App
63	66.5	13.6	315	5	US-10-958-216-466	Sequence 466, App
64	66.5	13.6	561	4	US-10-437-963-169643	Sequence 169643, A
65	66.5	13.6	638	5	US-10-831-070-272	Sequence 272, App
66	66.5	13.6	2910	5	US-10-732-923-3342	Sequence 3342, App
67	66	13.5	120	4	US-10-389-566-1079	Sequence 1079, Ap
68	66	13.5	120	4	US-10-389-566-1125	Sequence 1125, Ap
69	65.5	13.4	459	4	US-10-087-192-375	Sequence 375, App
70	65.5	13.4	221	4	US-10-767-701-41912	Sequence 41912, A
71	65.5	13.4	481	5	US-10-732-923-982	Sequence 982, App
72	65.5	13.4	546	5	US-10-732-923-9369	Sequence 9369, Ap
73	65.5	13.4	546	3	US-09-874-923-2	Sequence 2, Appl
74	65.5	13.4	546	3	US-09-991-496-2	Sequence 2, Appl
75	65.5	13.4	546	4	US-10-098-732A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-09-955-502-14
Sequence 14, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 91
TYPE: PRT
ORGANISM: *Salmonella paratyphi*

US-09-955-502-14

Query Match 100.0%; Score 488; DB 3; Length 91;

Best Local Similarity 100.0%; Pred. No. 6.8e-49; Mismatches 0; Indels 0; Gaps 0;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

DB 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 2

US-09-955-502-16

Sequence 16, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downe, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 16

LENGTH: 91

TYPE: PRT

ORGANISM: Salmonella dublin

US-09-955-502-16

Query Match 100.0%; Score 488; DB 3; Length 91;

Best Local Similarity 100.0%; Pred. No. 6.8e-49; Mismatches 0; Indels 0; Gaps 0;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

DB 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 3

US-09-955-502-17

Sequence 17, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downe, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 17

LENGTH: 91

TYPE: PRT

ORGANISM: Salmonella typhi CT18

US-09-955-502-17

Query Match 100.0%; Score 488; DB 3; Length 91;

Best Local Similarity 100.0%; Pred. No. 6.8e-49; Mismatches 0; Indels 0; Gaps 0;

Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTFCYTLORDABGQDPOLYPGELGKRIYNEISKDAWAQOHKQTMLINEKKNMNA 60

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QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

DB 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 4

US-09-955-502-18

Sequence 18, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downe, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 18

LENGTH: 91

TYPE: PRT

ORGANISM: Salmonella typhimurium

US-09-955-502-18

Query Match 97.1%; Score 474; DB 3; Length 91;

Best Local Similarity 97.8%; Pred. No. 2.9e-47; Mismatches 2; Indels 0; Gaps 0;

Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

DB 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 5

US-09-955-502-15

Sequence 15, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downe, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 15

LENGTH: 88

TYPE: PRT

ORGANISM: Salmonella enteritidis

US-09-955-502-15

Query Match 96.7%; Score 472; DB 3; Length 88;

Best Local Similarity 100.0%; Pred. No. 4.8e-47; Mismatches 0; Indels 0; Gaps 0;

Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:15:00 ; Search time 5.07859 Seconds
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Title: US-09-955-502a-14

Perfect score: 488
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

Database : Published Applications AA New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	13.9	478	6	US-10-821-234-915	Sequence 915, App
3	65	13.3	593	US-11-194-246-317	Sequence 317, App
4	64.5	13.2	177	US-10-467-657-1658	Sequence 1658, App
5	63.5	13.0	1432	US-10-510-386-218	Sequence 218, App
6	62	12.7	251	US-11-054-515-1496	Sequence 1496, App
7	62	12.7	604	US-10-942-072-4	Sequence 4, Appli
8	62	12.7	1167	US-10-942-072-6	Sequence 6, Appli
9	60.5	12.4	504	US-11-072-512-3467	Sequence 3467, App
10	59.5	12.2	264	US-10-821-234-1555	Sequence 1555, App
11	59.5	12.2	285	US-10-467-657-222	Sequence 222, App
12	59.5	12.2	285	US-10-467-657-8230	Sequence 8230, App
13	59.5	12.2	650	US-10-467-657-1948	Sequence 1948, App
14	59.5	12.2	834	US-10-453-372-658	Sequence 658, App
15	59.5	12.2	1995	US-11-069-834-60	Sequence 60, Appl
16	59	12.1	257	US-11-054-515-1710	Sequence 1710, App
17	59	12.1	697	US-10-485-517-202	Sequence 202, App
18	59	12.1	1168	US-10-942-072-11	Sequence 11, Appl
19	59	12.1	1450	US-10-485-517-152	Sequence 152, App
20	58.5	12.0	695	US-10-453-372-648	Sequence 648, App
21	58.5	12.0	700	US-10-995-561-922	Sequence 922, App
22	58.5	12.0	700	US-10-995-561-922	Sequence 922, App
23	58.5	12.0	749	US-11-098-686-10505	Sequence 10505, A
24	58.5	12.0	782	US-10-793-626-2352	Sequence 2352, App
25	58	11.9	448	US-10-618-320A-25	Sequence 25, Appl

26	58	11.9	480	6	US-10-510-386-12	Sequence 12, Appl
27	58	11.9	1501	6	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.8	242	7	US-11-022-562-220	Sequence 220, App
29	57.5	11.8	336	6	US-10-453-372-640	Sequence 640, App
30	57.5	11.8	577	7	US-11-072-175-187	Sequence 187, App
31	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
32	57.5	11.8	793	6	US-10-453-372-656	Sequence 656, App
33	57.5	11.8	793	6	US-10-995-561-925	Sequence 925, App
34	57.5	11.8	804	6	US-10-453-372-650	Sequence 650, App
35	57.5	11.8	847	6	US-10-453-372-654	Sequence 654, App
36	57.5	11.8	857	6	US-10-453-372-652	Sequence 652, App
37	57.5	11.8	905	6	US-10-453-372-658	Sequence 658, App
38	57.5	11.8	905	6	US-10-453-372-662	Sequence 662, App
39	57.5	11.8	905	6	US-10-453-372-664	Sequence 664, App
40	57.5	11.8	963	6	US-10-995-561-923	Sequence 923, App
41	57.5	11.8	963	6	US-10-453-372-660	Sequence 660, App
42	57.5	11.8	1012	6	US-10-453-372-664	Sequence 664, App
43	57.5	11.8	3803	6	US-10-995-561-773	Sequence 773, App
44	57.5	11.8	3960	6	US-10-995-561-771	Sequence 771, App
45	57.5	11.8	5335	6	US-10-995-561-777	Sequence 777, App
46	57.5	11.8	5406	6	US-10-995-561-774	Sequence 774, App
47	57.5	11.8	5415	6	US-10-995-561-779	Sequence 779, App
48	57.5	11.8	5464	6	US-10-995-561-775	Sequence 775, App
49	57.5	11.8	5935	6	US-10-995-561-776	Sequence 776, App
50	57	11.7	234	6	US-10-524-647-120	Sequence 120, App
51	57	11.7	234	6	US-10-524-647-120	Sequence 120, App
52	57	11.7	432	6	US-10-821-234-163	Sequence 163, App
53	57	11.7	440	7	US-11-072-512-3856	Sequence 3856, App
54	56.5	11.6	647	7	US-11-000-463-722	Sequence 722, App
55	56.5	11.6	1254	6	US-10-528-031-47	Sequence 47, Appl
56	56.5	11.6	1897	6	US-10-821-234-1635	Sequence 1635, App
57	56.5	11.6	1907	7	US-11-000-463-260	Sequence 260, App
58	56.5	11.6	3433	6	US-10-714-781A-67	Sequence 67, Appl
59	56	11.5	206	7	US-11-124-368A-116	Sequence 316, App
60	55.5	11.4	136	6	US-10-793-626-580	Sequence 580, App
61	55.5	11.4	279	7	US-11-098-686-10812	Sequence 10812, A
62	55.5	11.4	1188	7	US-11-115-639-42	Sequence 42, Appl
63	55.5	11.4	188	7	US-11-115-639-43	Sequence 43, Appl
64	55	11.3	1189	7	US-11-071-262-1	Sequence 1, Appli
65	55	11.3	667	6	US-10-793-626-188	Sequence 188, App
66	55	11.3	692	7	US-11-038-284-33	Sequence 33, Appl
67	55	11.3	783	7	US-11-037-243-67	Sequence 67, Appl
68	55	11.3	873	7	US-11-038-284-35	Sequence 35, Appl
69	55	11.3	889	7	US-11-038-284-15	Sequence 15, Appl
70	55	11.3	1142	7	US-11-109-156-22	Sequence 22, Appl
71	55	11.3	2665	7	US-11-124-368A-214	Sequence 214, App
72	55	11.3	2668	7	US-11-124-368A-215	Sequence 215, App
73	54.5	11.2	317	6	US-10-523-503-74	Sequence 74, Appl
74	54.5	11.2	450	6	US-10-618-320A-26	Sequence 26, Appl
75	54.5	11.2	496	7	US-11-069-642-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2001-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqman99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 43.2%; Score 211; DB 6; Length 88;
Best Local Similarity 43.8%; Pred. No. 3.2e-17;
Matches 39; Conservative 19; Mismatches 29; Indels 2; Gaps 2;

QY 1 MSRTITCTYLDAGDGF--OLYRG-----ELGKRIYNEISKDAMQOHQOTMLINEKLMNNA 60
DB 1 MARWFFCVKLNKKEAGMKFPPLPNELGKRIYNEISKDAMQOHQOTMLINEKLMNNA 60

QY 61 EHRKLEQEMVSFLF-BGKDVHIBGYTPE 88
DB 61 RAREYLAQOMEOYFPGDADA-VQGYVPO 88

RESULT 2
US-10-821-234-915
Sequence 915, Application US/10821234
Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andaman, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes version 1.0
SEQ ID NO 915
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-915

Query Match 13.9%; Score 68; DB 6; Length 478;
Best Local Similarity 25.5%; Pred. No. 3.4;
Matches 26; Conservative 20; Mismatches 28; Indels 28; Gaps 5;

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QY 52 EKKLMNNAEHRKLEQEMVSFLFEGKDVHI-----BGYTP 87
DB 439 DLKSGVPRAGYRGI-----VTFQFRKRVHLAPPTWBSYDP 475

RESULT 3
US-11-194-246-317

Sequence 317, Application US/11194246
Publication No. US20050272089A1
GENERAL INFORMATION:
APPLICANT: Mott, John
APPLICANT: Treped, Catherine
APPLICANT: Arvidson, Stefan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
FILE REFERENCE: 00592.US1 (MAR 268,05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621

SOFTWARE: PatentIn version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 13.3%; Score 65; DB 7; Length 593;
Best Local Similarity 24.1%; Pred. No. 9.6;
Matches 20; Conservative 10; Mismatches 23; Indels 30; Gaps 2;

QY 9 YLOR--DAEGDFOLYRGELGKRIYNE-----ISKDA 38
DB 240 FLNFFDIENTDFQKWRDEQIRQLQTDVITERRLRMAIWQKTELTSWNLNLSAESKSKOE 299

QY 39 WAQOHQOTMLINEKLMNNAE 61
DB 300 WRWYEAQODILNKTKLTALSK 322

RESULT 4
US-10-467-657-1658

Sequence 1658, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin9, version 1.04
SEQ ID NO 1658
LENGTH: 177
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1658

Query Match 13.2%; Score 64.5; DB 6; Length 177;
Best Local Similarity 28.6%; Pred. No. 2.6;
Matches 20; Conservative 11; Mismatches 38; Indels 1; Gaps 1;

QY 20 QLYPDELGKRIYNEISKDAMQOHQOTMLINEKLMNNAEHRKLEQEMVSFLFEGKD 79
DB 63 EYTRSEIIDYLSNEL-LVTRTKFSFKNIFFSTNEKKYKEIKRKINFLYKNDWYLFNNND 121

QY 80 VHIETPTED 89
DB 122 ITLDEYTGND 131

RESULT 5
US-10-510-386-218

Sequence 218, Application US/10510386
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.3

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 72.2642 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502a-15

Perfect score: 474
Sequence: 1 MSPITCTYTLQRDARGQDFQ.....EMVSLFEGKDVHISGYPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	98.1	88	5	ABB78160 Amino aci
2	465	98.1	91	5	ABB78161 Amino aci
3	465	98.1	91	5	ABB78159 Amino aci
4	465	98.1	91	5	ABB78162 Amino aci
5	451	95.1	91	5	ABB78163 Amino aci
6	446	94.1	91	5	ABB78158 Amino aci
7	446	94.1	91	5	ABB78157 Amino aci
8	446	94.1	91	5	ABB78156 Amino aci
9	431	90.9	107	7	ABO65445 Klebsiell
10	382	80.6	90	5	ABB78165 Amino aci
11	380	80.2	90	5	ABB78155 Amino aci
12	379	80.0	78	5	ABB78164 Amino aci
13	378	79.7	87	5	ABB78152 Amino aci
14	371	78.3	91	5	ABB78150 Amino aci
15	370	78.1	87	5	ABB78151 Amino aci
16	370	78.1	93	7	AD705158 Bacteri
17	364	76.8	87	5	ABB78153 Amino aci
18	329	63.4	88	5	ABB78154 Amino aci
19	252	53.2	76	5	ABB78166 Amino aci
20	242	51.1	87	5	ABB78147 Amino aci
21	242	51.1	87	5	ABB78148 Amino aci
22	228	48.1	86	5	ABB78149 Amino aci
23	221	46.6	87	5	ABB78170 Amino aci
24	221	46.6	122	7	ABO74609 Pseudomon

25	217.5	45.9	89	9	ABE41576 L. pneumo
26	217.5	44.9	95	9	ABE38294 L. pneumo
27	212.5	44.8	90	5	ABB78167 Amino aci
28	211	44.5	87	5	ABB78169 Amino aci
29	209	44.1	88	5	ABB78178 Amino aci
30	204	43.0	88	5	ABB78171 Amino aci
31	204	43.0	88	5	ABB78172 Amino aci
32	204	43.0	88	5	ABB78173 Amino aci
33	204	43.0	88	5	ABB78172 Amino aci
34	204	43.0	88	5	ABB78172 Amino aci
35	199	42.0	87	5	ABB78175 Amino aci
36	193	40.7	87	5	ABB78174 Amino aci
37	190	40.1	87	5	ABB78176 Amino aci
38	188.5	39.8	92	6	ADA34169 Actinoba
39	188	39.7	87	5	ABB78177 Amino aci
40	130	27.4	110	8	ADL05173 M. catarr
41	72	15.2	309	8	ADN46828 Thermoco
42	72	15.2	506	6	AA74371 Neisseria
43	72	15.2	507	6	ABU40210 Protein e
44	71	15.0	447	2	AAR52657 Rat N-ace
45	71	15.0	447	7	ADSS5944 Rat Prote
46	71	15.0	507	3	AA74372 Neisseria
47	71	15.0	507	3	AA74373 Neisseria
48	71	15.0	546	6	ABU38097 Protein e
49	70	14.8	758	9	ADW71760 Salmonell
50	69.5	14.7	184	3	AA816290 P. rad
51	69.5	14.7	1377	8	ADV81847 Streptoco
52	69.5	14.7	1387	8	ADV88434 Streptoco
53	69.5	14.7	1387	8	ADV79687 Streptoco
54	69	14.6	503	4	ABG16577 Novel hum
55	69	14.6	679	9	ADZ85056 Partial F
56	68.5	14.5	184	3	AA816325 P. rad
57	68.5	14.5	184	4	AA865734 Annexin-I
58	68.5	14.5	184	7	ADB94702 Programme
59	68.5	14.5	608	5	ABP73745 Candida a
60	68	14.3	239	8	ADT07537 Human col
61	68	14.3	257	3	AA631203 Arabidops
62	68	14.3	280	3	AA54294 Amino aci
63	68	14.3	280	5	ABG93905 Lactuca s
64	68	14.3	280	8	ADJ50292 O11-488oc
65	68	14.3	285	4	AA892683 Human pro
66	68	14.3	297	3	AA631202 Arabidops
67	68	14.3	302	4	AA888379 Human mem
68	68	14.3	302	9	AA631323 Human cto
69	68	14.3	324	3	AA631201 Arabidops
70	68	14.3	414	6	ABU11747 Human MDD
71	68	14.3	445	2	AA824781 Human Gnt
72	68	14.3	445	4	AA657094 Human bet
73	68	14.3	445	7	ADSS5946 Human Pro
74	68	14.3	445	7	ADL63026 Human apo
75	68	14.3	445	7	ADL63046 Human apo

ALIGNMENTS

RESULT 1	ABB78160 standard; protein; 88 AA.
ID	ABB78160;
AC	ABE41576;
XX	05-NOV-2002 (first entry)
DT	XX
XX	XX
DE	Amino acid sequence of a YggX homologue.
XX	XX
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	XX
OS	hydroxyl radical; DNA damage; YggX homologue.
XX	XX
PN	Unidentified.
XX	XX
XX	US2002072118-A1.

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI, 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgxB protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YgxB protein (a protein identified from *Salmonella*
XX *enterica* serovar Typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YgxB reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YgxB homologues
SQ Sequence 88 AA;

Query Match 98.1%; Score 465; DB 5; Length 88;
Best Local Similarity 98.9%; Pred. No. 5.4e-47;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPTFTCTYLGRDAGQDFOLYPGELGRIYNEISKDAWAQWQHKTMLINEKLMNNA 60
DB 1 MSRTTFTCTYLGRDAGQDFOLYPGELGRIYNEISKDAWAQWQHKTMLINEKLMNNA 60

QY 61 EHRKLLQEMWVSFLPEGKDVHIEGYTPE 88
DB 61 EHRKLLQEMWVSFLPEGKDVHIEGYTPE 88

RESULT 2
ABB78161
ID ABB78161 standard; protein; 91 AA.

XX
XX ABB78161;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YgxB homologue.

XX Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
XX hydroxyl radical; DNA damage; YgxB homologue.

XX Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;

DR WPI, 2002-589476/63.

XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgxB protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.

XX Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YgxB protein (a protein identified from *Salmonella*
XX *enterica* serovar Typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YgxB reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YgxB homologues
SQ Sequence 91 AA;

Query Match 98.1%; Score 465; DB 5; Length 91;
Best Local Similarity 98.9%; Pred. No. 5.6e-47;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPTFTCTYLGRDAGQDFOLYPGELGRIYNEISKDAWAQWQHKTMLINEKLMNNA 60
DB 1 MSRTTFTCTYLGRDAGQDFOLYPGELGRIYNEISKDAWAQWQHKTMLINEKLMNNA 60

QY 61 EHRKLLQEMWVSFLPEGKDVHIEGYTPE 88
DB 61 EHRKLLQEMWVSFLPEGKDVHIEGYTPE 88

RESULT 3
ABB78159
ID ABB78159 standard; protein; 91 AA.

XX
XX ABB78159;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YgxB homologue.

XX Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
XX hydroxyl radical; DNA damage; YgxB homologue.

XX Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;

DR WPI, 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YgxB protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.

XX Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more YgxB
XX native amount of YgxB protein (a protein identified from *Salmonella*

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.62187 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-15
Percent score: 474
Sequence: 1 MSPITFCTYLQRDAEGQDFQ.....EMVSFLFGKDVHIGTYPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	98.1	91	2 AH0879	conserved hypotet
2	446	94.1	91	2 A85954	hypothetical prote
3	446	94.1	91	2 A65082	hypothetical prote
4	446	94.1	91	2 F91108	hypothetical prote
5	382	80.6	90	2 A10116	conserved hypotet
6	380	80.2	90	2 C82320	conserved hypotet
7	378	79.7	90	2 C64013	hypothetical prote
8	252	53.2	93	2 B84994	hypothetical prote
9	222	46.8	105	2 C82624	conserved hypotet
10	221	46.6	90	2 H83003	conserved hypotet
11	204	43.0	88	2 H81014	conserved hypotet
12	195	16.8	1638	2 D87749	protein unc-73b [i
13	195	16.8	1638	2 T42739	guanine nucleotide
14	174	15.6	1260	2 T04440	hypothetical prote
15	173.5	15.5	495	2 A40985	probable zinc-pro
16	171.5	15.1	209	2 I64172	hypothetical prote
17	171	15.0	447	2 JC2076	alpha-1,3-mannosyl
18	150	15.0	507	2 C81063	finarate hydratase
19	150	15.0	507	2 A81807	thiosulfate reduct
20	150	15.0	507	2 A80763	thiosulfate reduct
21	148	14.8	758	2 A57143	thiosulfate reduct
22	147	14.7	859	2 T29630	hypothetical prote
23	146	14.6	265	2 T46013	hypothetical prote
24	143	14.3	324	2 T05429	hypothetical prote
25	143	14.3	445	1 X0HUMB	alpha-1,3-mannosyl
26	143	14.3	689	2 F83902	beta-galactosidase
27	142	14.2	166	2 F70562	hypothetical prote
28	141	14.1	1	2 A38561	alpha-1,3-mannosyl
29	141	14.1	1111	2 T23047	hypothetical prote

30	66.5	14.0	548	2 A54510	63K antigen - nema
31	66.5	14.0	618	2 A71364	probable phosphoen
32	66	13.9	447	1 A42500	alpha-1,3-mannosyl
33	66	13.9	1085	2 S62516	hypothetical colle
34	65.5	13.8	365	2 B54128	Fc-binding protein
35	65	13.7	251	2 B90428	hypothetical prote
36	65	13.7	507	2 A83105	hypothetical prote
37	65	13.7	593	2 C64097	probable fumarsae
38	65	13.7	628	2 A82193	probable soluble 1
39	65	13.7	1230	2 S56850	hypothetical prote
40	64.5	13.6	401	2 A81978	SMC1 protein homol
41	64.5	13.6	511	2 A99574	hypothetical prote
42	64.5	13.6	544	2 T40058	ABC transporter at
43	63.5	13.4	327	2 AD2129	probable chromatin
44	63.5	13.4	379	2 S70709	type II site-speci
45	63.5	13.4	410	1 KXMSD	cathelin D (BC 3.
46	63.5	13.4	1119	2 T15842	hypothetical prote
47	63.5	13.4	2672	2 A48126	translation activa
48	63	13.3	235	2 G65212	hypothetical 26.7K
49	63	13.3	258	2 A97991	hypothetical prote
50	63	13.3	258	2 B95121	phosphoserine, p
51	63	13.3	447	2 T16527	hypothetical prote
52	63	13.3	483	2 G64799	ydev protein - Bsc
53	63	13.3	543	2 T16015	hypothetical prote
54	63	13.3	549	2 T16016	hypothetical prote
55	63	13.3	703	2 B82148	ATP-dependent heli
56	63	13.3	1209	2 T46027	hypothetical prote
57	63	13.3	1327	2 T14594	guanidine nucleoti
58	63	13.3	1572	2 S45251	SNF2alpha protein
59	63	13.3	1586	2 S39580	HBW protein - hum
60	62.5	13.2	165	2 A81382	shikimate kinase (
61	62.5	13.2	259	2 G83203	conserved hypotet
62	62.5	13.2	287	2 P82265	conserved hypotet
63	62.5	13.2	305	2 A75211	asparaginase (BC 3
64	62.5	13.2	498	2 G91179	hypothetical prote
65	62.5	13.2	498	2 H86025	hypothetical prote
66	62.5	13.2	498	2 S47748	53.1K protein proc
67	62.5	13.2	906	2 G69531	alanyl-tRNA synth
68	62.5	13.2	1141	2 T29185	hypothetical prote
69	62	13.1	156	2 F70382	conserved hypotet
70	62	13.1	643	2 A43647	parasporel crystal
71	62	13.1	898	2 D95123	phosphoenolpyruvat
72	62	13.1	898	2 P97993	phosphoenolpyruvat
73	62	13.1	3388	1 GNMVDP	genome polypeptid
74	61.5	13.0	305	2 A71247	probable L-asparag
75	61.5	13.0	414	2 T49916	hypothetical prote

ALIGNMENTS

RESULT 1

AH0879 conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C/Species: Salmonella enterica subsp. enterica serovar Typhi

A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004

C/Accession: AH0879
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AH0879

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-91 <PAB>

A/Cross-references: UNIPARC:UP1000005A44C; GB:AL513382; PTDN:CAD02936.1; PTD:g16504189;

A/Gene: STY3266

C/Superfamily: fe(II) trafficking protein YggX

Query Match 98.1%; Score 446; DB 2; Length 91;
Best Local Similarity 93.2%; Pred. No. 7,2e-41;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60
Db 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 88
Db 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 88

RESULT 2
A:Accession: A85954
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7, substrain EDL93
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Hiller, D.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE005174; NID:g12517511; F
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: y9gX
C:Superfamily: fe(II) trafficking protein Y9gX

Query Match 94.1%; Score 446; DB 2; Length 91;
Best Local Similarity 93.2%; Pred. No. 6,4e-39;
Matches 82; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60
Db 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 88
Db 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 88

RESULT 3
A:Accession: A65082
A:Title: The complete genome sequence of *Escherichia coli* K-12.
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65082
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE000378; GB:U00096; NID:g
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein Y9gX

Query Match 94.1%; Score 446; DB 2; Length 91;
Best Local Similarity 93.2%; Pred. No. 6,4e-39;
Matches 82; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60
Db 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 88
Db 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 88

RESULT 4
A:Accession: P91108
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: P91108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <HAY>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:BA000007; PIDN:BA037261.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECA3838
C:Superfamily: fe(II) trafficking protein Y9gX

Query Match 94.1%; Score 446; DB 2; Length 91;
Best Local Similarity 93.2%; Pred. No. 6,4e-39;
Matches 82; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60
Db 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 88
Db 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 88

RESULT 5
A:Accession: A10116
A:Title: conserved hypothetical protein YPO0953 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: A10116
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
H. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A10116
A:Status: preliminary
A:Molecule type: DNA
A:Cross-references: UNIPARC:UP100000DDCC4; GB:AL590842; PIDN:CA089796.1; PID:g15979022;
C:Genetics:
A:Gene: YPO0953
C:Superfamily: fe(II) trafficking protein Y9gX

Query Match 80.6%; Score 382; DB 2; Length 90;
Best Local Similarity 81.6%; Pred. No. 2,4e-32;
Matches 71; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60
Db 1 MSRTIFCTYLRDABGODPOLYPGELGKRIYNEISKDAMQWQHQTMLINEKLLNMNNA 60

Qy 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 87
Db 61 EHRKLLBQEMVNFLEPGKDVHIEGYTP 87

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 18:51:36 ; Search time 64.8474 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-15

Perfect score: 474
Sequence: 1 MSPRIFTYLRDAEGQDFQ.....EMVSFLREGKDVHIEGYTPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	460	97.0	90	1	FETP_SALCH
2	460	97.0	90	1	FETP_SALPA
3	460	97.0	90	1	FETP_SALTI
4	460	97.0	90	1	FETP_SALTY
5	441	93.0	90	1	FETP_ECOS7
6	441	93.0	90	1	FETP_ECOS7
7	441	93.0	90	1	FETP_ECOS7
8	437	92.2	90	1	FETP_ECOS7
9	409	86.3	90	1	FETP_ERWCT
10	390	82.3	90	1	FETP_ERWCT
11	386	81.4	90	1	FETP_ERWCT
12	382	80.6	90	1	FETP_ERWCT
13	380	80.2	90	1	FETP_ERWCT
14	380	80.2	90	1	FETP_ERWCT
15	378	79.7	90	1	FETP_ERWCT
16	378	79.7	90	1	FETP_ERWCT
17	378	79.7	90	1	FETP_ERWCT
18	378	79.7	90	1	FETP_ERWCT
19	372	78.5	90	1	FETP_ERWCT
20	370	78.1	90	1	FETP_ERWCT
21	364	76.8	90	1	FETP_ERWCT
22	363	76.6	90	1	FETP_ERWCT
23	358	75.5	90	1	FETP_ERWCT
24	333	70.3	90	1	FETP_ERWCT
25	329	69.4	90	1	FETP_ERWCT
26	322	53.2	90	1	FETP_ERWCT
27	242	51.1	90	1	FETP_ERWCT
28	242	51.1	90	1	FETP_ERWCT
29	242	51.1	90	1	FETP_ERWCT
30	236	49.8	78	1	FETP_ERWCT
31	232	48.9	91	1	FETP_ERWCT

32	225	47.5	92	1	FETP_XANOR	05gy22 xanthomonas
33	222	46.8	90	1	FETP_XYLF	09pc73 xyella fas
34	221.5	46.7	89	1	FETP_LEGP	05vrc4 legionella
35	221	46.6	90	1	FETP_PSEB	09nu16 pseudomonas
36	221	46.6	92	1	FETP_XANP	08b829 xanthomonas
37	221	46.6	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
38	218	46.0	78	1	FETP_WIGR	08b3c5 wigleswort
39	218	46.0	90	1	FETP_XYLF	08b3c5 xyella fas
40	217.5	45.9	89	1	FETP_LEGP	05x3x9 legionella
41	217.5	45.9	89	1	FETP_LEGP	05x3x9 legionella
42	211	44.5	90	1	FETP_COXU	083d06 coxiella bu
43	211	44.5	90	1	FETP_PSEB	08b829 pseudomonas
44	211	44.5	90	2	Q4J228_AZOV1	Q4J228 azotobacter
45	209	44.1	79	1	FETP_CAMP	07vrg9 candidatus
46	209	44.1	90	1	FETP_PSEB	08uf5 pseudomonas
47	209	44.1	90	2	Q4Z1P3_PSEB	Q4Z1P3 pseudomonas
48	208	43.9	90	2	Q6T7F6_PSEB	Q6T7F6 pseudomonas
49	206	43.5	90	1	FETP_CHRO	07nsr4 chromobacte
50	205	43.2	90	1	FETP_NEIG	082xf2 neisseria g
51	204	43.0	88	1	FETP_NEIG	082xf2 neisseria g
52	204	43.0	88	1	FETP_NEIG	082xf2 neisseria g
53	204	43.0	88	1	FETP_NEIG	082xf2 neisseria g
54	201	42.4	87	1	FETP_BURP	083a44 burkholderi
55	199	42.0	91	1	FETP_BURP	083a44 burkholderi
56	199	42.0	91	1	FETP_BURP	083a44 burkholderi
57	198	41.8	90	2	Q4K1T2_PSEB	Q4K1T2 pseudomonas
58	198	41.8	91	1	FETP_RALS	08y010 raietonia s
59	196	41.4	91	2	Q4L819_PSEB	Q4L819 burkholderi
60	192	40.5	87	1	FETP_FRAT	05nhj8 francisella
61	188	39.7	90	1	FETP_METC	06oa73 methylococc
62	183.5	38.7	90	1	FETP_METC	06fb3 acinetobact
63	145	30.6	96	2	Q4FVJ7_PSEB	Q4FVJ7 pseudomonas
64	135	28.5	92	2	Q4NMQ4_PSEB	Q4NMQ4 pseudomonas
65	82.5	17.4	482	2	Q5N1Y1_PSEB	Q5N1Y1 pseudomonas
66	82.5	17.4	514	2	Q6A1Z9_PSEB	Q6A1Z9 pseudomonas
67	79.5	16.8	1638	2	Q6BEM2_CABE	Q6BEM2 caenorhabdi
68	79.5	16.8	2140	2	Q6BEM2_CABE	Q6BEM2 caenorhabdi
69	79.5	16.8	2488	2	Q6BEM2_CABE	Q6BEM2 caenorhabdi
70	77	16.2	1047	2	Q5CJ53_CRYO	Q5CJ53 cryptospori
71	76.5	16.1	486	2	Q7WXS1_ALCE	Q7WXS1 alcaligenes
72	75	15.8	508	2	Q7NSF0_CRYO	Q7NSF0 cryptospori
73	75	15.8	1278	2	Q5CYM7_CRYO	Q5CYM7 cryptospori
74	74	15.6	1260	2	Q46777_ARAT	Q46777 arabidopsis
75	73.5	15.5	495	1	YHJ1_SALTI	08x286 salmoneilla

ALIGNMENTS

RESULT 1
ID FETP_SALCH STANDARD, PRT; 90 AA.
AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gX; OrderedLocNames=SC3052;
OS Salmoneilla choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmoneilla.
OX NCBI_TaxID=591;
RX NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RC PubMed=15781495; DOI=10.1093/nar/gk1297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmoneilla enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen."
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or

CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; AE017220; AAX66958.1; -; Genomic_DNA.
DR HAVAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Prodrom; PD029191; DUF495; 1.
DR Prodrom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
FT INIT MET 0
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1BE2255E3C CRC64;

Query Match 97.0%; Score 460; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 2.7e-41;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 SPITFCYTLORDAEGQDPOLYPGELGKRIYNEISKDAAQWQHOKTMLINEKLMNNAE 61
DB 1 SRTIFCYTLORDAEGQDPOLYPGELGKRIYNEISKDAAQWQHOKTMLINEKLMNNAE 60
OY 62 HRKLEQEMVSFLFEGKDVHIEGYTPE 88
DB 61 HRKLEQEMVSFLFEGKDVHIEGYTPE 87

RESULT 2
FETP_SALPA STANDARD; PRT; 90 AA.
AC QSPMM1:
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=Y9GX; OrderedlocusNames=SPA2974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 9150 / SAR842;
RC PubMed=15531862; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter U., Krenitzki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Mink P.,
RA Diekhant J., Wilson R.K.;
RA "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid";
RL Nat. Genet. 36:1268-1274(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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DR EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
DR SMR; QSPMM1; 1-91.
DR HAVAP; MF_00686; -; 1.

DR InterPro; IPR007457; Y9GX.
DR Prodrom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
FT INIT MET 0
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1BE2255E3C CRC64;

Query Match 97.0%; Score 460; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 2.7e-41;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 SPITFCYTLORDAEGQDPOLYPGELGKRIYNEISKDAAQWQHOKTMLINEKLMNNAE 61
DB 1 SRTIFCYTLORDAEGQDPOLYPGELGKRIYNEISKDAAQWQHOKTMLINEKLMNNAE 60
OY 62 HRKLEQEMVSFLFEGKDVHIEGYTPE 88
DB 61 HRKLEQEMVSFLFEGKDVHIEGYTPE 87

RESULT 3
FETP_SALTI STANDARD; PRT; 90 AA.
AC P67618; Q8XFW6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=Y9GX; OrderedlocusNames=STY3266, C3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=CT18;
RC MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jogle K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RA "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18";
RL Nature 413:848-852(2001).
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=TY2 / ATCC 700931;
RC MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyranski V., Schwartz D.C., Blattner F.R.;
RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.

DR EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
DR EMBL; AE016844; AAO70576.1; -; Genomic_DNA.
DR SMR; P67618; 1-90.
DR HAVAP; MF_00686; -; 1.

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 17.8405 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-15

Perfect score: 474
Sequence: 1 MSPRTCTYLRDAGQDFQ.....EMVSFLFGKVHIGTYPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

Issued Patents, AA: *
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/7 COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/8 COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/9 COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/10 COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	431	90.9	107	2	US-09-489-039A-11962
2	370	78.1	93	2	US-09-543-681A-5443
3	221	46.6	122	2	US-09-252-991A-23355
4	188.5	39.8	92	2	US-09-328-352-5456
5	130	27.4	110	2	US-09-540-235-2859
6	68.5	14.5	184	2	US-09-323-932A-66
7	68.5	14.5	544	2	US-09-248-796A-18911
8	68	14.3	280	2	US-09-323-998E-37
9	68	14.3	1214	2	US-10-164-595-24
10	66.5	14.0	548	2	US-09-167-299-3
11	66	13.9	292	2	US-09-328-352-5836
12	65	13.7	474	2	US-09-252-991A-24473
13	64	13.5	337	2	US-09-270-767-41746
14	64	13.5	1176	2	US-09-489-039A-8879
15	63	13.3	1586	2	US-09-538-092-1171
16	62.5	13.2	260	2	US-09-252-991A-17498
17	62.5	13.2	419	2	US-09-543-681A-7295
18	62.5	13.2	662	2	US-09-583-110-5119
19	62.5	13.2	664	2	US-09-107-463-2775
20	62	13.1	227	2	US-09-270-767-58283
21	62	13.1	238	2	US-09-323-998E-41
22	62	13.1	448	2	US-09-270-767-42959
23	62	13.1	604	2	US-09-008-097-4
24	62	13.1	604	2	US-09-472-667-4
25	62	13.1	644	2	US-08-793-331-7
26	62	13.1	898	2	US-09-583-110-3750
27	62	13.1	899	2	US-09-107-433-3196

28	62	13.1	1167	2	US-09-008-097-6	Sequence 6, Appl
29	62	13.1	1167	2	US-09-472-667-6	Sequence 6, Appl
30	61.5	13.0	591	2	US-09-370-368-8	Sequence 8, Appl
31	61	12.9	143	2	US-09-270-767-45872	Sequence 45872, A
32	61	12.9	184	2	US-09-270-767-61571	Sequence 61571, A
33	61	12.9	325	2	US-09-134-000C-4346	Sequence 4346, Ap
34	61	12.9	389	2	US-09-270-767-46116	Sequence 46116, A
35	60.5	12.8	223	2	US-09-543-681A-5667	Sequence 5667, Ap
36	60.5	12.8	525	2	US-09-540-235-2250	Sequence 2250, Ap
37	60.5	12.8	527	2	US-09-489-039A-10883	Sequence 10883, A
38	60.5	12.8	701	2	US-09-252-991A-22288	Sequence 22288, A
39	60	12.7	232	2	US-09-201-641-8	Sequence 8, Appl
40	60	12.7	232	2	US-09-323-998E-36	Sequence 36, Appl
41	60	12.7	421	2	US-09-489-039A-7512	Sequence 7512, Ap
42	59.5	12.6	139	2	US-09-513-999C-4802	Sequence 4802, Ap
43	59.5	12.6	258	2	US-09-513-999C-4800	Sequence 4800, Ap
44	59.5	12.6	264	2	US-09-949-016-6012	Sequence 6012, Ap
45	59.5	12.6	276	2	US-09-949-016-11703	Sequence 11703, A
46	59.5	12.6	434	2	US-09-303-518D-334	Sequence 334, App
47	59.5	12.6	680	2	US-09-298-924-4	Sequence 4, Appl
48	59.5	12.6	687	2	US-09-538-092-539	Sequence 539, App
49	59.5	12.6	720	1	US-08-840-235-1	Sequence 1, Appl
50	59.5	12.6	720	1	US-08-503-448A-1	Sequence 1, Appl
51	59.5	12.6	921	2	US-09-248-796A-14950	Sequence 14950, A
52	59	12.4	98	2	US-09-270-767-56301	Sequence 41085, A
53	59	12.4	113	2	US-08-894-173-93	Sequence 56301, A
54	59	12.4	113	2	US-09-398-193-93	Sequence 93, Appl
55	59	12.4	119	2	US-09-328-352-7391	Sequence 7391, Ap
56	59	12.4	234	2	US-09-296-754-2	Sequence 2, Appl
57	59	12.4	284	1	US-08-624-125-16	Sequence 16, Appl
58	59	12.4	284	2	US-08-937-155-16	Sequence 16, Appl
59	59	12.4	284	2	US-09-323-998E-16	Sequence 16, Appl
60	59	12.4	381	2	US-09-328-352-6400	Sequence 16, Appl
61	59	12.4	431	2	US-09-861-451A-16	Sequence 16, Appl
62	59	12.4	697	2	US-08-816-177-2	Sequence 16, Appl
63	59	12.4	1094	2	US-09-949-016-8755	Sequence 8755, Ap
64	59	12.4	1094	2	US-09-949-016-8756	Sequence 8756, Ap
65	59	12.4	1147	2	US-09-949-016-8861	Sequence 8861, Ap
66	59	12.4	1147	2	US-09-949-016-8862	Sequence 8862, Ap
67	59	12.4	1147	2	US-09-949-016-8862	Sequence 8862, Ap
68	59	12.4	1165	1	US-08-240-357-2	Sequence 2, Appl
69	59	12.4	1168	2	US-09-474-076-2	Sequence 2, Appl
70	59	12.4	1168	2	US-09-472-667-11	Sequence 11, Appl
71	59	12.4	1168	2	US-10-201-000-2	Sequence 2, Appl
72	58.5	12.3	57	2	US-09-562-737-134	Sequence 124, App
73	58.5	12.3	116	2	US-09-562-737-135	Sequence 125, App
74	58.5	12.3	233	1	US-08-557-305B-40	Sequence 40, Appl
75	58.5	12.3	233	2	US-08-834-306-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Bretton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709 2004/001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 55.7267 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502a-15

Perfect score: 474

Sequence: 1 MSPTFTYLRDAGQDFQ.....EMVSLFRGKVHIGTYPE 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_AA_Main:*

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6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	465	98.1	91	3	US-09-955-502-14
3	465	98.1	91	3	US-09-955-502-16
4	465	98.1	91	3	US-09-955-502-17
5	451	95.1	91	3	US-09-955-502-18
6	446	94.1	91	3	US-09-955-502-11
7	446	94.1	91	3	US-09-955-502-12
8	446	94.1	91	3	US-09-955-502-13
9	382	80.6	90	3	US-09-955-502-20
10	380	80.2	90	3	US-09-955-502-10
11	379	80.0	78	3	US-09-955-502-19
12	378	79.7	78	3	US-09-955-502-7
13	371	78.3	91	3	US-09-955-502-5
14	370	78.1	87	3	US-09-955-502-6
15	364	76.8	87	3	US-09-955-502-8
16	329	63.4	88	3	US-09-955-502-9
17	252	53.2	76	3	US-09-955-502-21
18	242	51.1	87	3	US-09-955-502-2
19	242	51.1	87	3	US-09-955-502-3
20	228	48.1	86	3	US-09-955-502-4
21	222	46.8	89	3	US-09-955-502-22
22	221	46.6	87	3	US-09-955-502-25
23	211	44.5	87	3	US-09-955-502-24
24	211	44.5	88	3	US-09-955-502-33
25	209	44.1	90	3	US-09-955-502-23
26	204	43.0	88	3	US-09-955-502-26
27	204	43.0	88	3	US-09-955-502-27

ALIGNMENTS

28	204	43.0	88	3	US-09-955-502-28	Sequence 28, Appl
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30	199	42.0	87	3	US-09-955-502-30	Sequence 30, Appl
31	190	40.1	87	3	US-09-955-502-31	Sequence 31, Appl
32	188	39.7	87	3	US-09-955-502-32	Sequence 32, Appl
33	188	39.7	87	3	US-09-955-502-32	Sequence 32, Appl
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RESULT 1
US-09-955-502-15
Sequence 15, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downe, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 15
LENGTH: 88
TYPE: PR
ORGANISM: Salmonella enteritidis

US-09-955-502-15

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Best Local Similarity	98.9%	Pred. No. 1e-46;		
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Db 1 MSRTICTYLRDABGD¹FLY²Y³EGELGRI⁴YNEIS⁵KDAM⁶QW⁷QHK⁸QTM⁹L¹⁰NEK¹¹KL¹²MM¹³NA 600

QY 61 EHRKLLBQEMVSPFLFEGKDVHIEGYTPE 88
Db 61 EHRKLLBQEMVSPFLFEGKDVHIEGYTPE 88

RESULT 2
US-09-955-502-14

; Sequence 14, Application US/09955502
; Patent No. US2002007211BA1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
 ; APPLICANT: Gralnick, Jeff A.
 ; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
 ; TITLE OF INVENTION: Oxygen-labile Proteins

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; SEQ ID NO 14
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; LENGTH: 91
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; TYPE: PRT
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; ORGANISM: Salmonella paratyphi
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US-09-955-502-14

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Query Match	98.1%	Score 465	DB 3	Length 91
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RESULT 3
US-09-955-502-16

; Sequence 16, Application US/09955502
; Patent No. US2002007211BA1
; GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins

Query Match 98.1%; Score 465; DB 3; Length 91;

Best Local Similarity 98.9%; Pred. No. 1e-46;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 EHRKLLLEQEMVSFLFEKGDVHIIEGYTPE 88
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RESULT 4
US-09-955-502-17

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; Sequence 17, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

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APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and Tissues
TITLE OR INVENTION: Oxygen-Labile Proteins

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; SEQ ID NO 17
;
; LENGTH: 91
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; TYPE: prt
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; ORGANISM: Salmonella typhi CT18
;
US-09-955-502-17

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RESULT 5
US-09-955-502-18

; Sequence 18, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins

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			Indels	0;
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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:15:00 ; Search time 4.9116 Seconds

(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502a-15

Perfect score: 474

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Scoring table:

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	68	14.3	478	US-10-821-234-915	Sequence 915, App
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5	62	13.1	604	US-10-942-072-4	Sequence 4, App1
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8	60.5	12.8	1432	US-10-510-386-218	Sequence 218, App
9	59.5	12.6	264	US-10-821-234-1555	Sequence 1555, App
10	59.5	12.6	650	US-10-467-657-1948	Sequence 1948, App
11	59.5	12.6	834	US-10-453-372-658	Sequence 658, App
12	59.5	12.6	1995	US-11-069-834-60	Sequence 60, App1
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14	59	12.4	1168	US-10-942-072-11	Sequence 11, App1
15	59	12.4	1450	US-10-485-517-152	Sequence 152, App
16	58.5	12.3	285	US-10-467-657-222	Sequence 222, App
17	58.5	12.3	285	US-10-467-657-8230	Sequence 8230, App
18	58.5	12.3	695	US-10-453-372-648	Sequence 648, App
19	58.5	12.3	700	US-10-995-561-922	Sequence 922, App
20	58.5	12.3	700	US-10-995-561-924	Sequence 924, App
21	58.5	12.3	749	US-11-098-686-10505	Sequence 10505, App
22	58.5	12.3	782	US-10-793-626-2352	Sequence 2352, App
23	58	12.2	257	US-11-054-515-1710	Sequence 1710, App
24	58	12.2	480	US-10-510-386-12	Sequence 12, App
25	57.5	12.1	336	US-10-453-372-640	Sequence 640, App

26	57.5	12.1	752	US-11-072-512-3003	Sequence 3003, App
27	57.5	12.1	775	US-10-453-372-656	Sequence 656, App
28	57.5	12.1	793	US-10-995-561-925	Sequence 925, App
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31	57.5	12.1	857	US-10-453-372-652	Sequence 652, App
32	57.5	12.1	905	US-10-453-372-638	Sequence 638, App
33	57.5	12.1	905	US-10-453-372-662	Sequence 662, App
34	57.5	12.1	905	US-10-453-372-664	Sequence 664, App
35	57.5	12.1	963	US-10-995-561-923	Sequence 923, App
36	57.5	12.1	963	US-10-453-372-660	Sequence 660, App
37	57.5	12.1	1012	US-10-453-372-646	Sequence 646, App
38	57	12.0	234	US-10-524-647-120	Sequence 120, App
39	57	12.0	234	US-10-524-972-108	Sequence 108, App
40	57	12.0	432	US-10-821-234-1463	Sequence 1463, App
41	57	12.0	504	US-11-072-512-3467	Sequence 3467, App
42	56.5	11.9	242	US-11-022-562-220	Sequence 220, App
43	56.5	11.9	647	US-11-000-463-722	Sequence 722, App
44	56.5	11.9	692	US-11-038-284-33	Sequence 33, App1
45	56.5	11.9	889	US-11-038-284-35	Sequence 35, App1
46	56.5	11.9	1254	US-10-528-031-47	Sequence 15, App1
47	56.5	11.9	1897	US-10-821-234-1635	Sequence 15, App1
48	56.5	11.9	1907	US-11-000-463-250	Sequence 1635, App
49	56.5	11.9	206	US-11-124-367A-316	Sequence 250, App
50	56	11.8	1011	US-11-098-686-10257	Sequence 316, App
51	56	11.8	3433	US-10-714-781A-67	Sequence 10257, App
52	56	11.8	279	US-11-098-686-10812	Sequence 67, App1
53	55.5	11.7	189	US-11-071-262-1	Sequence 10812, App
54	55	11.6	667	US-10-793-626-198	Sequence 1, App1
55	55	11.6	1142	US-11-109-156-22	Sequence 198, App
56	55	11.6	1501	US-10-793-626-2850	Sequence 22, App1
57	55	11.5	317	US-10-523-503-74	Sequence 2850, App
58	54.5	11.5	496	US-11-069-642-20	Sequence 74, App1
59	54.5	11.5	111	US-10-771-257-34	Sequence 20, App1
60	54	11.4	426	US-11-127-677-34	Sequence 34, App1
61	54	11.4	7	US-11-098-686-10340	Sequence 34, App1
62	54	11.4	179	US-11-037-243-67	Sequence 10340, App
63	54	11.4	783	US-10-467-657-6542	Sequence 67, App1
64	53.5	11.3	313	US-10-995-561-972	Sequence 6542, App
65	53.5	11.3	335	US-10-995-561-970	Sequence 972, App
66	53.5	11.3	345	US-10-995-561-971	Sequence 970, App
67	53.5	11.3	384	US-10-467-657-2024	Sequence 971, App
68	53.5	11.3	774	US-11-070-627-7	Sequence 2024, App
69	53.5	11.3	3803	US-10-995-561-773	Sequence 7, App1
70	53.5	11.3	3860	US-10-995-561-771	Sequence 773, App
71	53.5	11.3	5335	US-10-995-561-777	Sequence 771, App
72	53.5	11.3	5406	US-10-995-561-774	Sequence 777, App
73	53.5	11.3	5415	US-10-995-561-779	Sequence 774, App
74	53.5	11.3	5464	US-10-995-561-775	Sequence 779, App
75	53.5	11.3			Sequence 775, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

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/ SEQ ID NO 968
/ LENGTH: 88
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968
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Best Local Similarity 42.7%; Pred. No. 9,9e-17;
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DB 61 RAREYLAQOEYFPGDGADA-VQGYVPQ 88
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RESULT 2
US-10-821-234-915
/ Sequence 915, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmant, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ PRIOR FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 915
/ LENGTH: 478
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-915
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Query Match          14.3%; Score 68; DB 6; Length 478;
Best Local Similarity 25.5%; Pred. No. 2.8;
Matches 26; Conservative 20; Mismatches 28; Indels 28; Gaps 5;
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QY 8 TYLQORDAEGODF-QLYPG-----ELGKRIYNEISKDAMAWOHKQTMLIN 51
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 380 SYLQREAYDRDPLFARYGAPQLQVEKVRTNDRKEIGSVRVQYGRDSFKAFK-KALGVMD 438
```

```
QY 52 EKLKLNMMNAHRKLEBEMVSPLEEGKDVHI-----EGYTP 87
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 439 DLKSGVPRAGYRGJ-----VTFQFRGRVHLADPPPTWEGYDP 475
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```
RESULT 3
US-11-194-246-317
/ Sequence 317, Application US/11194246
/ Publication No. US20050272089A1
/ GENERAL INFORMATION:
/ APPLICANT: Mott, John
/ APPLICANT: Trepod, Catherine
/ APPLICANT: Atvidson, Steffen
/ TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
/ FILE REFERENCE: 00592.US1 (M&R 268.05920101)
/ CURRENT APPLICATION NUMBER: US/11/194,246
/ PRIOR FILING DATE: 2005-08-01
/ PRIOR APPLICATION NUMBER: US/10/274,586
/ PRIOR FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US 60/345,438
/ PRIOR FILING DATE: 2001-10-19
/ NUMBER OF SEQ ID NOS: 621
```

```
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 317
/ LENGTH: 593
/ TYPE: PRT
/ ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317
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Query Match          13.7%; Score 65; DB 7; Length 593;
Best Local Similarity 24.1%; Pred. No. 7.9;
Matches 20; Conservative 10; Mismatches 23; Indels 30; Gaps 2;
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```
QY 9 YLQD--DAEGODFQLYPGLGKRIYNE-----ISKDA 38
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 240 FLNRFEDNENTDFQKWRBQIRQLQTDNLTERRLMAIWKQTELTSLWNLISAEKSKQE 299
```

```
QY 39 WAQOHKQTMLINEKLMNMAE 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 300 WRYWEAKODILNTTKLTALSKR 322
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```
RESULT 4
US-11-054-515-1496
/ Sequence 1496, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS
/ FILE REFERENCE: PFS23P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1496
/ LENGTH: 251
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1496
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Query Match          13.3%; Score 63; DB 7; Length 251;
Best Local Similarity 41.0%; Pred. No. 4.8;
Matches 16; Conservative 5; Mismatches 14; Indels 4; Gaps 1;
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```
QY 2 SPPICTYQORDAEGODFQLYPGLGKRIYNEISK 36
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 157 SVTISCTGSSDVGVGYVSWYQYFGKAPKLIWVVK 195
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```
RESULT 5
US-10-942-072-4
/ Sequence 4, Application US/10942072
/ Publication No. US20050250721A1
/ GENERAL INFORMATION:
/ APPLICANT: Hammon, H. K.
```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-16
Perfect score: 490
Sequence: 1 MSPTFCTYLQRDAEQDFQ.....SFLFEKGVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21:*

1: geneeqp1980s:*

2: geneeqp1990s:*

3: geneeqp2000s:*

4: geneeqp2001s:*

5: geneeqp2002s:*

6: geneeqp2003as:*

7: geneeqp2003bs:*

8: geneeqp2004s:*

9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481	98.2	91	5	ABB78161 Amino aci
2	481	98.2	91	5	ABB78159 Amino aci
3	481	98.2	91	5	ABB78162 Amino aci
4	467	95.3	91	5	ABB78163 Amino aci
5	465	94.9	88	5	ABB78160 Amino aci
6	462	94.3	91	5	ABB78158 Amino aci
7	462	94.3	91	5	ABB78157 Amino aci
8	462	94.3	91	5	ABB78156 Amino aci
9	438	89.4	107	7	ABO65445 Amino aci
10	386	78.8	90	5	ABB78165 Amino aci
11	382	78.0	90	5	ABB78155 Amino aci
12	379	77.3	78	5	ABB78164 Amino aci
13	378	77.1	87	5	ABB78152 Amino aci
14	376	76.7	91	5	ABB78150 Amino aci
15	376	76.7	93	7	ADP05158 Amino aci
16	370	75.5	87	5	ABB78151 Amino aci
17	364	74.3	87	5	ABB78153 Amino aci
18	329	67.1	88	5	ABB78154 Amino aci
19	252	51.4	76	5	ABB78166 Amino aci
20	242	49.4	87	5	ABB78148 Amino aci
21	242	49.4	87	5	ABB78147 Amino aci
22	228	46.5	86	5	ABB78149 Amino aci
23	221	45.1	87	5	ABB78170 Amino aci
24	221	45.1	122	7	ABO74609 Pseudomon

25	217.5	44.4	89	9	ABB41576	Aeb41576 L. pneumo
26	217.5	44.4	95	5	ABB38294	Aeb38294 L. pneumo
27	215.5	44.0	90	5	ABB78167	Abb78167 Amino aci
28	215	43.9	90	5	ABB78168	Abb78168 Amino aci
29	211	43.1	87	5	ABB78169	Abb78169 Amino aci
30	211	43.1	88	5	ABB78178	Abb78178 Amino aci
31	204	41.6	88	5	ABB78171	Abb78171 Amino aci
32	204	41.6	88	5	ABB78172	Abb78172 Amino aci
33	204	41.6	88	5	ABB78173	Abb78173 Amino aci
34	204	41.6	88	5	ABB77219	Abb77219 N. gonorr
35	199	40.6	87	5	ABB78175	Abb78175 Amino aci
36	193	39.4	87	5	ABB78174	Abb78174 Amino aci
37	190	38.8	87	5	ABB78176	Abb78176 Amino aci
38	188.5	38.5	92	6	ADA34169	Ada34169 Acinetoba
39	188	38.4	87	5	ABB78177	Abb78177 Amino aci
40	130	26.5	110	8	ADL05173	Adl05173 M. catar
41	77	15.7	1647	4	ABG10750	Abg10750 Novel Hum
42	72	14.7	309	8	ADN46828	Adn46828 Thermococ
43	72	14.7	506	6	AAV74371	Aay74371 Neisseria
44	72	14.7	507	6	ABU40210	Abu40210 Protein e
45	71.5	14.6	184	3	ABAB16290	Abab16290 Pinnus rad
46	71	14.5	447	2	ABR52657	Aar52657 Rat N-ace
47	71	14.5	447	7	ABR55944	Aar55944 Rat Prote
48	71	14.5	507	3	AAV74372	Aay74372 Neisseria
49	71	14.5	507	3	AAV74373	Aay74373 Neisseria
50	71	14.5	546	6	ABU38097	Abu38097 Protein e
51	70.5	14.4	184	3	ABAB16325	Abab16325 Pinnus rad
52	70.5	14.4	184	4	ABAB65734	Abab65734 Annexin-1
53	70.5	14.4	184	7	ADB94702	Adb94702 Programme
54	70	14.3	758	9	ADW71760	Adw71760 Salmonell
55	69.5	14.2	1377	8	ADV81847	Adv81847 Streptoco
56	69.5	14.2	1387	8	ADV88434	Adv88434 Streptoco
57	69.5	14.2	1387	8	ADV79687	Adv79687 Streptoco
58	69	14.1	503	4	ABG16577	Abg16577 Novel Hum
59	69	14.1	679	9	ADZ85056	Adz85056 Partial F
60	68.5	14.0	608	5	ABP73745	Abp73745 Candida a
61	68.5	14.0	632	8	ADS29711	Ads29711 Bacterial
62	68	13.9	239	3	ADT07537	Adt07537 Human col
63	68	13.9	257	3	AAAG31203	Aag31203 Arabidops
64	68	13.9	280	3	AAAY54294	Aay54294 Amino aci
65	68	13.9	280	5	ABG93905	Abg93905 Lactuca s
66	68	13.9	280	8	ADJ50292	Adj50292 Oil-asso
67	68	13.9	285	4	AAAB92683	Aab92683 Human pro
68	68	13.9	297	3	AAAG31202	Aag31202 Arabidops
69	68	13.9	302	4	AAAB88379	Aab88379 Human mem
70	68	13.9	302	3	ADY63123	Ady63123 Human cto
71	68	13.9	324	3	AAAG31201	Aag31201 Arabidops
72	68	13.9	414	6	ABU11747	Abu11747 Human MDD
73	68	13.9	445	2	AAAR24781	Aar24781 Human GNT
74	68	13.9	445	4	AAAG67094	Aag67094 Human bet
75	68	13.9	445	7	ADBS5946	Adbs5946 Human Pro

ALIGNMENTS

RESULT 1
ID ABB78161 standard; protein; 91 AA.
AC ABB78161;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
OS
XX
XX US2002072118-A1.
XX
XX

PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC enterica serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 91 AA;

Query Match 98.2%; Score 481; DB 5; Length 91;
 Best Local Similarity 98.9%; Pred. No. 2e-48; 1; Indels 0; Gaps 0;
 Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPTIFCTYLOBDAGQDFOLYPGELGKRIYNEISKDAMQWQHOKTMLINEKKLANMNA 60
 Db 1 MSRTIFCTYLOBDAGQDFOLYPGELGKRIYNEISKDAMQWQHOKTMLINEKKLANMNA 60
 Qy 61 EHRKLEQEMVSPFEGKDVHIEGYTPEDKK 91
 Db 61 EHRKLEQEMVSPFEGKDVHIEGYTPEDKK 91

RESULT 2

ABB78159
 ID ABB78159 standard; protein; 91 AA.

AC ABB78159;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

KM Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC enterica serovar typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 91 AA;

Query Match 98.2%; Score 481; DB 5; Length 91;
 Best Local Similarity 98.9%; Pred. No. 2e-48; 1; Indels 0; Gaps 0;
 Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPTIFCTYLOBDAGQDFOLYPGELGKRIYNEISKDAMQWQHOKTMLINEKKLANMNA 60
 Db 1 MSRTIFCTYLOBDAGQDFOLYPGELGKRIYNEISKDAMQWQHOKTMLINEKKLANMNA 60
 Qy 61 EHRKLEQEMVSPFEGKDVHIEGYTPEDKK 91
 Db 61 EHRKLEQEMVSPFEGKDVHIEGYTPEDKK 91

RESULT 3

ABB78162
 ID ABB78162 standard; protein; 91 AA.

AC ABB78162;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

KM Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
 KM hydroxyl radical; DNA damage; YggX homologue.

OS *Salmonella typhi*.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-16
Perfect score: 490
Sequence: 1 MSPTFCTYLQRDAEGQDFQ.....SFLPEGKVHIEGYTPEDKK 91

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	481	98.2	91	2	AH0879 conserved hypotet
2	462	94.3	91	2	A65954 hypotetrical prote
3	462	94.3	91	2	A65082 hypotetrical prote
4	462	94.3	91	2	F91108 hypotetrical prote
5	386	78.8	90	2	A10116 conserved hypotet
6	382	78.0	90	2	C82320 conserved hypotet
7	378	77.1	90	2	C64013 hypotetrical prote
8	252	51.4	93	2	B84994 hypotetrical prote
9	225	45.9	105	2	C82624 conserved hypotet
10	221	45.1	90	2	H83003 conserved hypotet
11	204	41.6	88	2	H81014 conserved hypotet
12	79.5	16.2	1638	2	D87749 protein unc-73b [i
13	79.5	16.2	2488	2	T42739 guanine nucleotide
14	78	15.3	1260	2	T04440 hypotetrical prote
15	73.5	15.0	495	2	AH0985 probable zinc-prot
16	71.5	14.6	209	2	I64172 hypotetrical prote
17	71	14.5	447	2	JC2076 alpha-1,3-mannosyl
18	71	14.5	507	2	C81063 fumarate hydratase
19	71	14.5	546	2	A81807 thiosulfate reduct
20	70	14.3	758	2	AD0763 thiosulfate reduct
21	70	14.3	758	2	A57143 thiosulfate-dithio
22	69.5	14.2	859	2	T29630 hypotetrical prote
23	69	14.1	265	2	T46013 hypotetrical prote
24	69	14.1	447	2	T16527 hypotetrical prote
25	68.5	14.0	683	2	AC2256 hypotetrical prote
26	68	13.9	324	2	T05429 alpha-1,3-mannosyl
27	68	13.9	445	1	X05429 beta-galactosidase
28	68	13.9	689	2	P83902 hypotetrical prote
29	67.5	13.8	166	2	P70562 hypotetrical prote

30	67	13.7	447	1	A38561 alpha-1,3-mannosyl
31	67	13.7	1111	2	T23047 hypotetrical prote
32	66.5	13.6	548	2	A54510 63k antigen - nema
33	66.5	13.6	618	2	A71364 probable phosphoen
34	66	13.5	447	1	A42500 alpha-1,3-mannosyl
35	66	13.5	1085	2	S62516 hypotetrical colle
36	65.5	13.4	287	2	P82265 conserved hypotet
37	65.5	13.4	365	2	B54128 Fc-binding protein
38	65	13.3	251	2	B90428 hypotetrical prote
39	65	13.3	433	2	A70465 probable GTP bindi
40	65	13.3	507	2	A83105 probable fumarase
41	65	13.3	511	2	A99574 ABC transporter at
42	65	13.3	593	2	C64097 probable soluble 1
43	65	13.3	628	2	AF2393 hypotetrical prote
44	65	13.3	1230	2	S56850 SWC1 protein homol
45	64.5	13.2	401	2	A81978 hypotetrical prote
46	64.5	13.2	544	2	T40058 probable chromatin
47	64.5	13.2	1119	2	T15842 hypotetrical prote
48	64.5	13.2	1197	2	S26947 DNA-directed DNA p
49	64	13.1	643	2	A43647 parasporal crystal
50	63.5	13.0	327	2	AD2129 transcription regu
51	63.5	13.0	379	2	S70709 type II site-speci
52	63.5	13.0	410	1	K4MSD cathepsin D (EC 3.
53	63.5	13.0	2672	2	A48126 keratin, 50K type
54	63	12.9	205	2	C26135 hypotetrical prote
55	63	12.9	235	2	G65212 ATP-dependent heli
56	63	12.9	258	2	A97991 hypotetrical prote
57	63	12.9	258	2	B55121 phosphoesterase, p
58	63	12.9	483	2	G64799 ydev protein - Bsc
59	63	12.9	543	2	T16015 hypotetrical prote
60	63	12.9	549	2	T16016 ATP-dependent heli
61	63	12.9	703	2	B82148 hypotetrical prote
62	63	12.9	1165	2	H71609 hypotetrical prote
63	63	12.9	1209	2	T46027 guanidine nucleoti
64	63	12.9	1327	2	T14594 SNF2alpha protein
65	63	12.9	1572	2	S45251 HBH protein - hum
66	63	12.9	1586	2	S39580 shikimate kinase (
67	62.5	12.8	165	2	A81382 conserved hypotet
68	62.5	12.8	259	2	G83203 asparaginase (EC 3
69	62.5	12.8	305	2	A75211 GTP-binding regula
70	62.5	12.8	375	2	T37245 protein R06A10.2 f
71	62.5	12.8	385	2	D87723 hypotetrical prote
72	62.5	12.8	498	2	G91179 hypotetrical prote
73	62.5	12.8	498	2	H86025 53.1K protein prec
74	62.5	12.8	498	2	S47748 chemocactic cran
75	62.5	12.8	629	2	B83107

ALIGNMENTS

RESULT 1

AH0879 conserved hypotetrical protein STY3266 [Imported] - Salmonella enterica subsp. enterica

C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004

C:Accession: AH0879
R:Parthall, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; T. Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Nature 413, 848-852, 2001

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0879

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-91 <PAR>

A:Cross-References: UNIPARC:UPI000005A44C; GB:AL513382; PIRN:CAD02936.1; PID:g16504189;
C:Gene: STY3266

C:Superfamily: fe(II) trafficking protein YggX

Query Match 98.2%; Score 481; DB 2; Length 91;
Best Local Similarity 98.9%; Pred. No. 7.8e-42;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60
1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Qy 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91
61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

Db 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 2
A:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
Hiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 523-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE005174; NID:g12517511; F
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: y9gX
C:Superfamily: fe(II) trafficking protein Y9gX

Query Match 94.3%; Score 462; DB 2; Length 91;
Best Local Similarity 93.4%; Pred. No. 6.5e-40;
Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60
1 MSPTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Qy 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91
61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

Db 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 3
A:Species: Escherichia coli (strain K-12)
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65082
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE000378; GB:U00096; NID:G
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein Y9gX

Query Match 94.3%; Score 462; DB 2; Length 91;
Best Local Similarity 93.4%; Pred. No. 6.5e-40;
Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60
1 MSPTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Qy 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91
61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

Db 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 4
A:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C:Accession: F91108
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gawara, N.; Yasunaga, T.; Kunara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <HAY>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:BA000007; PIDN:BA037261.1;
A:Experimental source: strain O157:H7, substrain RIMD 0509552
C:Genetics:
A:Gene: EC93838
C:Superfamily: fe(II) trafficking protein Y9gX

Query Match 94.3%; Score 462; DB 2; Length 91;
Best Local Similarity 93.4%; Pred. No. 6.5e-40;
Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60
1 MSPTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Qy 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91
61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

Db 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 91

RESULT 5
A:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: A10116
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A10116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <KUP>
A:Cross-references: UNIPARC:UP100000DDCC4; GB:AL590842; PIDN:CA089796.1; PID:g15979022;
C:Genetics:
A:Gene: YPO0953
C:Superfamily: fe(II) trafficking protein Y9gX

Query Match 78.8%; Score 386; DB 2; Length 90;
Best Local Similarity 80.0%; Pred. No. 3.2e-32;
Matches 72; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MSPTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60
1 MSPTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Db 1 MSRTIFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKLLNMNNA 60

Qy 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 90
61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 90

Db 61 EHRKLLBOEMVSLFPEGKDVHIEGYTPEDKK 90

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OM protein - protein search, using SW model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-16

Perfect score: 490
Sequence: 1 MSPIFCTYLQRDAEGDFFQ.....SFLFEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	476	97.1	90	1	FETP_SALCH
2	476	97.1	90	1	FETP_SALCH
3	476	97.1	90	1	FETP_SALCH
4	476	97.1	90	1	FETP_SALCH
5	457	93.3	90	1	FETP_SALCH
6	457	93.3	90	1	FETP_SALCH
7	457	93.3	90	1	FETP_SALCH
8	453	92.4	90	1	FETP_SALCH
9	409	83.5	90	1	FETP_SALCH
10	394	80.4	90	1	FETP_SALCH
11	386	78.8	90	1	FETP_SALCH
12	386	78.8	90	1	FETP_SALCH
13	382	78.0	90	1	FETP_SALCH
14	382	78.0	90	1	FETP_SALCH
15	382	78.0	90	1	FETP_SALCH
16	380	77.6	90	1	FETP_SALCH
17	378	77.1	90	1	FETP_SALCH
18	378	77.1	90	1	FETP_SALCH
19	376	76.7	90	1	FETP_SALCH
20	370	75.5	90	1	FETP_SALCH
21	369	75.3	90	1	FETP_SALCH
22	364	74.3	90	1	FETP_SALCH
23	358	73.1	90	1	FETP_SALCH
24	334	68.2	90	1	FETP_SALCH
25	329	67.1	90	1	FETP_SALCH
26	252	51.4	90	1	FETP_SALCH
27	242	49.4	90	1	FETP_SALCH
28	242	49.4	90	1	FETP_SALCH
29	242	49.4	90	1	FETP_SALCH
30	236	48.2	90	1	FETP_SALCH
31	232	47.3	90	1	FETP_SALCH

32	225	45.9	90	1	FETP_XYLFA	Q9pc73 xylfa
33	225	45.9	92	1	FETP_XANOR	Q5gv22 xanthomonas
34	221.5	45.2	89	1	FETP_LEGPL	Q5vvc4 legionella
35	221	45.1	90	1	FETP_PSEAB	Q9nu36 pseudomonas
36	221	45.1	90	1	FETP_XYLFT	Q87d06 xylfa
37	221	45.1	92	1	FETP_XANCP	Q8p829 xanthomonas
38	221	45.1	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
39	218	44.5	78	1	FETP_WIGER	Q8d3c5 wigleswort
40	217.5	44.4	89	1	FETP_LEGPA	Q53x39 legionella
41	217.5	44.4	89	1	FETP_LEGPH	Q53x80 legionella
42	215	43.9	90	1	FETP_NITRU	Q82xf2 nitrosomonas
43	215	43.9	90	1	FETP_PSEBM	Q87uf5 pseudomonas
44	215	43.9	90	2	Q4ZLP3_PSEBS	Q4ZLP3 pseudomonas
45	211	43.1	90	1	FETP_COXU	Q8d406 coxiella bu
46	211	43.1	90	1	FETP_PSEBK	Q88r49 pseudomonas
47	211	43.1	90	2	Q4J228_AZOCI	Q4J228 azotobacter
48	209	42.7	79	1	FETP_CANBP	Q7vrg9 candidatus
49	208	42.4	90	2	Q6T7F6_PSEFL	Q6T7F6 pseudomonas
50	206	42.0	90	1	FETP_CHRVO	Q7nar4 chromobacte
51	204	41.6	88	1	FETP_NEIG1	Q5f53 neisseria g
52	204	41.6	88	1	FETP_NEIMA	Q5f53 neisseria m
53	204	41.6	88	1	FETP_NEIMB	Q5f53 neisseria m
54	201	41.0	87	1	FETP_BURBP	Q89a44 buchera ap
55	199	40.6	91	1	FETP_BURMA	Q62i19 burkholderi
56	199	40.6	91	1	FETP_BURPS	Q63s14 burkholderi
57	198	40.4	90	2	Q4KJ72_PSEFS	Q4KJ72 pseudomonas
58	198	40.4	90	1	FETP_RALSO	Q8y010 ralstonia s
59	196	40.0	91	2	Q4LS19_PBURK	Q4LS19 burkholderi
60	192	39.2	87	1	FETP_FRATV	Q5nhj8 francisella
61	188	38.4	90	1	FETP_METCA	Q60a17 methylococc
62	183.5	37.4	90	1	FETP_ACIDP	Q6f6b3 acinetobact
63	145	29.6	96	2	Q4FVJ7_PGAMM	Q4FVJ7 psychrobact
64	138	28.2	92	2	Q4NM04_PDELT	Q4NM04 anseromyxob
65	82.5	16.8	482	2	Q5NU11_PBURK	Q5NU11 ralstonia m
66	82.5	16.8	514	2	Q6A129_DSPPS	Q6A129 desulfohalob
67	79.5	16.2	1638	2	Q7KPP4_CABEL	Q7KPP4 caenorhabdi
68	79.5	16.2	2140	2	Q6BEM2_CABEL	Q6BEM2 caenorhabdi
69	79.5	16.2	2488	2	Q6I528_CABEL	Q6I528 caenorhabdi
70	78.5	16.0	337	2	Q8IAR8_BACCR	Q8IAR8 bacillus ce
71	78	15.9	1260	2	Q49677_ARATH	Q49677 arabidopsis
72	77.5	15.8	1047	2	Q5CJ53_CRYHO	Q5CJ53 cryptospori
73	76.5	15.6	486	2	Q7WXS1_ALCEHO	Q7WXS1 alcaligenes
74	75.5	15.4	1278	2	Q5CYM7_CRYPV	Q5CYM7 cryptospori
75	75	15.3	385	2	Q734A2_BACCI	Q734A2 bacillus ce

ALIGNMENTS

RESULT 1

ID FETP_SALCH STANDARD, PRT; 90 AA.

AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_Taxid=591;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gk1297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen";
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-regulating processes, such as synthesis and/or

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502a-16

Perfect score: 490

Sequence: 1 MSPRTFYLYLRDAEGQDFQ.....SFLFKGVHIEGYTPEDKK 91

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents_AA:*

- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PCOMB_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	438	89.4	107	2	US-09-489-039A-11962
2	376	76.7	93	2	US-09-543-681A-5443
3	221	45.1	122	2	US-09-252-991A-23355
4	188.5	38.5	92	2	US-09-328-352-5456
5	130	26.5	110	2	US-09-540-236-2859
6	70.5	14.4	184	2	US-09-325-932A-66
7	68.5	14.0	544	2	US-09-248-796A-18911
8	68	13.9	280	2	US-09-323-998E-37
9	68	13.9	1214	2	US-10-164-595-24
10	66.5	13.6	325	2	US-09-134-000C-4346
11	66.5	13.6	548	2	US-09-167-299-3
12	66	13.5	292	2	US-09-328-352-5836
13	65	13.3	474	2	US-09-252-991A-24473
14	64	13.1	98	2	US-09-270-767-41085
15	64	13.1	98	2	US-09-270-767-56301
16	64	13.1	337	2	US-09-270-767-41746
17	64	13.1	569	2	US-09-107-532A-6689
18	64	13.1	644	2	US-08-793-331-7
19	64	13.1	1176	2	US-09-489-039A-8879
20	63.5	13.0	921	2	US-09-248-796A-14950
21	63	12.9	1586	2	US-09-538-092-1171
22	62.5	12.8	260	2	US-09-252-991A-17498
23	62.5	12.8	419	2	US-09-543-681A-7295
24	62.5	12.8	662	2	US-09-583-110-5119
25	62.5	12.8	664	2	US-09-107-433-2775
26	62.5	12.8	701	2	US-09-252-991A-23288
27	62	12.7	227	2	US-09-270-767-58283

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709, 2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117, 747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 89.4%; Score 438; DB 2; Length 107;
Best Local Similarity 87.9%; Pred. No. 1.6e-48; Indels 0; Gaps 0;
Matches 80; Conservative 7; Mismatches 4;

Qy 1 MSPTIFCTYLORDAEGDGFOLYPGELGKRIYNEISKDAMQOMHQKQTMLINEKLNMMNA 60
17 MSRTIFCTFLORDADGDFOLYPGELGKRIYNEISKDAMQOMHQKQTMLINEKLNMMNP 76

Db 61 EHRKLEQEWVSFLFEGKDVHIEGYTPEDK 91
77 EHRKLEQEWVSFLFEGKDVHIEGYTPEDK 107

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 76.7%; Score 376; DB 2; Length 93;
Best Local Similarity 76.7%; Pred. No. 1.2e-40; Indels 0; Gaps 0;
Matches 69; Conservative 9; Mismatches 12;

Qy 1 MSPTIFCTYLORDAEGDGFOLYPGELGKRIYNEISKDAMQOMHQKQTMLINEKLNMMNA 60
4 MSRTIFCTFLORDADGDFOLYPGELGKRIYNEISKDAMQOMHQKQTMLINEKLNMMNP 63

Db 61 EHRKLEQEWVSFLFEGKDVHIEGYTPEDK 90
64 DDKRLLEQEWVSFLFEGKDVHIEGYTPEDK 93

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 45.1%; Score 221; DB 2; Length 122;
Best Local Similarity 51.1%; Pred. No. 1.5e-20; Indels 2; Gaps 2;
Matches 45; Conservative 11; Mismatches 30;

Qy 1 MSPTIFCTYLORDAEGDGFOLYPGELGKRIYNEISKDAMQOMHQKQTMLINEKLNMMNA 60

Db 33 MSRTWCKRKHEBELPGLDRPPYGAKEGDIYNNVSRKADWQKHQKQTMLINEKLNMMNA 92
Qy 61 EHRKLEQEWVSFLFEGKDVHIEGYTP 87
Db 93 EDRFLQEWVDFLFGKDVHIEGYTP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 38.5%; Score 188.5; DB 2; Length 92;
Best Local Similarity 40.4%; Pred. No. 1.6e-16; Indels 1; Gaps 1;
Matches 36; Conservative 15; Mismatches 37;

Qy 1 MSPTIFCTYLORDAEGDGFOLYPGELGKRIYNEISKDAMQOMHQKQTMLINEKLNMMNA 60
4 MSRTWCKRKHEBELPGLDRPPYGAKEGDIYNNVSRKADWQKHQKQTMLINEKLNMMNP 63

Db 61 EHRKLEQEWVSFLFEGKDVHIEGYTP 88
64 EAKKLEQEWVSFLFEGKDVHIEGYTP 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 26.5%; Score 130; DB 2; Length 110;
Best Local Similarity 34.9%; Pred. No. 6.6e-09; Indels 0; Gaps 0;
Matches 29; Conservative 13; Mismatches 41;

Qy 5 IFCTYLORDAEGDGFOLYPGELGKRIYNEISKDAMQOMHQKQTMLINEKLNMMNAEHRK 64
25 VFCKRYQONLPLKLNPPFPNKAQGEIOTDISAKAMNMBELQTMLINEKLNMMNP 84

Db 65 LLEQEWVSFLFEGKDVHIEGYTP 87
85 YLNEQREKFLDNGDYBKPDAGYKP 107

RESULT 6
US-09-325-932A-66
; Sequence 66, Application US/09325932A

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502A-16
Perfect score: 490
Sequence: 1 MSPRTFCTYLQRDAGQDFQ.....SFLPEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_MA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	481	98.2	91	3	US-09-955-502-14
2	481	98.2	91	3	US-09-955-502-16
3	481	98.2	91	3	US-09-955-502-17
4	467	95.3	91	3	US-09-955-502-18
5	465	94.9	88	3	US-09-955-502-15
6	462	94.3	91	3	US-09-955-502-11
7	462	94.3	91	3	US-09-955-502-12
8	462	94.3	91	3	US-09-955-502-13
9	386	78.8	90	3	US-09-955-502-20
10	382	78.0	90	3	US-09-955-502-10
11	379	77.3	78	3	US-09-955-502-19
12	378	77.1	87	3	US-09-955-502-7
13	376	76.7	91	3	US-09-955-502-5
14	370	75.5	87	3	US-09-955-502-6
15	364	74.3	87	3	US-09-955-502-8
16	329	67.1	88	3	US-09-955-502-9
17	252	51.4	76	3	US-09-955-502-21
18	242	49.4	87	3	US-09-955-502-2
19	242	49.4	87	3	US-09-955-502-3
20	228	46.5	86	3	US-09-955-502-4
21	225	45.9	89	3	US-09-955-502-22
22	221	45.1	87	3	US-09-955-502-25
23	215	43.9	90	3	US-09-955-502-23
24	211	43.1	87	3	US-09-955-502-24
25	211	43.1	88	3	US-09-955-502-33
26	204	41.6	88	3	US-09-955-502-26
27	204	41.6	88	3	US-09-955-502-27

28 204 41.6 88 3 US-09-955-502-28 Sequence 28, Appl
29 199 40.6 87 3 US-09-955-502-29 Sequence 29, Appl
30 199 40.6 87 3 US-09-955-502-30 Sequence 30, Appl
31 190 38.8 87 3 US-09-955-502-31 Sequence 31, Appl
32 188 38.4 87 3 US-09-955-502-32 Sequence 32, Appl
33 188 38.4 87 3 US-09-955-502-33 Sequence 33, Appl
34 72.5 14.8 786 5 US-10-450-763-41109 Sequence 41,09, A
35 72 14.7 507 4 US-10-733-923-4885 Sequence 4885, Ap
36 72 14.7 1261 4 US-10-282-122A-68134 Sequence 68134, A
37 71.5 14.6 184 4 US-10-437-963-189166 Sequence 189166,
38 71 14.5 546 4 US-10-282-122A-66021 Sequence 52, Appl
39 70.5 14.4 184 4 US-10-219-220-66 Sequence 66021, A
40 70.5 14.4 184 4 US-10-393-840-118 Sequence 66, Appl
41 69 14.1 503 5 US-10-450-763-46936 Sequence 118, Appl
42 69 14.1 679 5 US-10-805-664-105 Sequence 46936, A
43 68.5 14.0 449 4 US-10-424-599-279212 Sequence 105, App
44 68.5 14.0 608 4 US-10-032-585-7582 Sequence 279212,
45 68.5 14.0 632 4 US-10-369-493-18744 Sequence 7582, Ap
46 68 13.9 280 3 US-09-323-998D-37 Sequence 18744, A
47 68 13.9 280 4 US-10-389-566-2296 Sequence 37, Appl
48 68 13.9 445 4 US-10-844-874-14 Sequence 2296, Ap
49 68 13.9 445 5 US-10-713-970-13 Sequence 14, Appl
50 68 13.9 478 4 US-10-087-192-378 Sequence 13, Appl
51 68 13.9 689 4 US-10-369-493-17280 Sequence 378, App
52 68 13.9 764 4 US-10-416-330-37 Sequence 17280, A
53 68 13.9 764 5 US-10-491-467-15 Sequence 37, Appl
54 68 13.9 1206 4 US-10-491-467-15 Sequence 144, App
55 68 13.9 1214 5 US-10-085-198-144 Sequence 144, App
56 67.5 13.8 166 5 US-10-482-706-269 Sequence 24, Appl
57 67.5 13.8 593 5 US-10-450-763-50306 Sequence 269, App
58 67.5 13.8 835 4 US-10-282-122A-53271 Sequence 50306, A
59 67 13.7 119 4 US-10-389-566-1126 Sequence 53271, A
60 67 13.7 167 4 US-10-437-963-158697 Sequence 1126, Ap
61 67 13.7 561 4 US-10-437-963-158697 Sequence 158697,
62 66.5 13.6 315 4 US-10-282-122A-53271 Sequence 168643,
63 66.5 13.6 315 5 US-10-958-216-464 Sequence 57222, A
64 66.5 13.6 315 5 US-10-958-216-464 Sequence 464, App
65 66.5 13.6 638 5 US-10-831-070-272 Sequence 466, App
66 66.5 13.6 2910 5 US-10-733-923-3342 Sequence 272, App
67 66 13.5 120 4 US-10-389-566-1079 Sequence 3342, Ap
68 66 13.5 120 4 US-10-389-566-1125 Sequence 1079, Ap
69 66 13.5 459 4 US-10-087-192-375 Sequence 1125, Ap
70 65.5 13.4 221 4 US-10-767-701-41912 Sequence 375, App
71 65.5 13.4 306 4 US-10-424-599-241560 Sequence 41912, A
72 65.5 13.4 481 5 US-10-733-923-982 Sequence 241560,
73 65.5 13.4 1588 4 US-10-437-963-189741 Sequence 982, App
74 65 13.3 290 4 US-10-389-566-2247 Sequence 189741,
75 65 13.3 311 4 US-10-029-386-33838 Sequence 2247, Ap
Sequence 33838, A

ALIGNMENTS

RESULT 1
US-09-955-502-14
Sequence 14, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960236.97559
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 91
TYPE: PRT
ORGANISM: Salmonella paratyphi

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:15:00 ; Search time 5.07859 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502A-16

Perfect score: 490
Sequence: 1 MSPITFCYTORDAEGDFO.....SFLREGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications_AA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	41.6	88	US-10-467-657-968	Sequence 968, App
2	68	13.9	478	US-10-821-234-915	Sequence 915, App
3	65	13.3	593	US-11-194-246-317	Sequence 317, App
4	64.5	13.2	177	US-10-467-657-1658	Sequence 1658, App
5	63.5	13.0	1432	US-10-510-386-218	Sequence 218, App
6	63	12.9	251	US-11-054-515-1496	Sequence 1496, App
7	62	12.7	604	US-10-942-072-6	Sequence 4, App11
8	62	12.7	1167	US-10-942-072-6	Sequence 4, App11
9	60.5	12.3	504	US-11-072-512-3467	Sequence 3467, App
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12	59.5	12.1	834	US-10-453-372-658	Sequence 658, App
13	59.5	12.1	1995	US-11-069-834-60	Sequence 60, App1
14	59	12.0	697	US-10-485-517-202	Sequence 60, App1
15	59	12.0	1168	US-10-942-072-11	Sequence 11, App1
16	59	12.0	1450	US-10-485-517-152	Sequence 152, App
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18	58.5	11.9	285	US-10-467-657-8230	Sequence 8230, App
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21	58.5	11.9	700	US-10-995-561-924	Sequence 924, App
22	58.5	11.9	749	US-11-098-686-10505	Sequence 10505, App
23	58.5	11.9	782	US-10-799-626-2352	Sequence 2352, App
24	58	11.8	257	US-11-054-515-1710	Sequence 1710, App
25	58	11.8	448	US-10-618-320A-25	Sequence 25, App1

26	58	11.8	480	6	US-10-510-386-12	Sequence 12, App1
27	58	11.8	1501	6	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.7	336	6	US-10-453-372-640	Sequence 640, App
29	57.5	11.7	752	7	US-11-072-512-3003	Sequence 3003, App
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31	57.5	11.7	793	6	US-10-995-561-925	Sequence 925, App
32	57.5	11.7	804	6	US-10-453-372-650	Sequence 650, App
33	57.5	11.7	847	6	US-10-453-372-654	Sequence 654, App
34	57.5	11.7	857	6	US-10-453-372-652	Sequence 652, App
35	57.5	11.7	905	6	US-10-453-372-638	Sequence 638, App
36	57.5	11.7	905	6	US-10-453-372-662	Sequence 662, App
37	57.5	11.7	905	6	US-10-453-372-664	Sequence 664, App
38	57.5	11.7	963	6	US-10-995-561-923	Sequence 923, App
39	57.5	11.7	963	6	US-10-453-372-660	Sequence 660, App
40	57.5	11.7	1012	6	US-10-453-372-666	Sequence 666, App
41	57.5	11.7	3803	6	US-10-995-561-773	Sequence 773, App
42	57.5	11.7	3960	6	US-10-995-561-771	Sequence 771, App
43	57.5	11.7	5335	6	US-10-995-561-777	Sequence 777, App
44	57.5	11.7	5406	6	US-10-995-561-774	Sequence 774, App
45	57.5	11.7	5415	6	US-10-995-561-779	Sequence 779, App
46	57.5	11.7	5464	6	US-10-995-561-775	Sequence 775, App
47	57.5	11.7	5935	6	US-10-995-561-776	Sequence 776, App
48	57	11.6	234	6	US-10-524-647-120	Sequence 120, App
49	57	11.6	234	6	US-10-524-972-108	Sequence 108, App
50	57	11.6	432	6	US-10-821-234-1463	Sequence 1463, App
51	57	11.6	440	7	US-11-072-512-3856	Sequence 3856, App
52	56.5	11.5	242	7	US-11-022-562-2820	Sequence 220, App
53	56.5	11.5	647	7	US-11-000-463-722	Sequence 722, App
54	56.5	11.5	692	7	US-11-038-284-33	Sequence 33, App1
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56	56.5	11.5	889	7	US-11-038-284-15	Sequence 15, App1
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60	56.5	11.5	3433	6	US-10-714-761A-67	Sequence 67, App1
61	56	11.4	206	7	US-11-124-367A-316	Sequence 316, App
62	56	11.4	1011	7	US-11-098-686-10257	Sequence 10257, App
63	55.5	11.3	136	7	US-10-793-626-580	Sequence 580, App
64	55.5	11.3	279	7	US-11-098-686-10812	Sequence 10812, App
65	55.5	11.3	1188	7	US-11-115-639-42	Sequence 42, App1
66	55.5	11.3	1188	7	US-11-115-639-43	Sequence 43, App1
67	55	11.2	189	7	US-11-071-262-1	Sequence 1, App11
68	55	11.2	667	6	US-10-793-626-198	Sequence 198, App
69	55	11.2	783	7	US-11-037-243-67	Sequence 67, App1
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75	54	11.0	111	6	US-10-771-257-34	Sequence 34, App1

ALIGNMENTS

RESULT 1
US-10-467-657-968
Sequence 968, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASTIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ IDS NOS: 7218
SOFTWARE: SeqWin99, version 1.04

NUMBER OF SEQ ID NOS: 621

NUMBER OF SEQ ID NOS: 248

; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.3

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 18:38:11 / Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-17
Perfect score: 488
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Gapop 10.0, Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
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- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	474	97.1	91	5	ABB78163 Amino aci
5	472	96.7	88	5	ABB78160 Amino aci
6	469	96.1	91	5	ABB78158 Amino aci
7	469	96.1	91	5	ABB78157 Amino aci
8	469	96.1	91	5	ABB78156 Amino aci
9	445	91.2	107	7	ABO65445 Amino aci
10	393	80.5	90	5	ABB78165 Amino aci
11	389	79.7	90	5	ABB78155 Amino aci
12	386	79.1	78	5	ABB78164 Amino aci
13	385	78.9	87	5	ABB78152 Amino aci
14	383	78.5	91	5	ABB78150 Amino aci
15	383	78.5	93	7	ADP05158 Amino aci
16	377	77.3	87	5	ABB78151 Amino aci
17	371	76.0	87	5	ABB78153 Amino aci
18	336	68.9	88	5	ABB78154 Amino aci
19	259	53.1	76	5	ABB78166 Amino aci
20	249	51.0	87	5	ABB78148 Amino aci
21	249	51.0	87	5	ABB78147 Amino aci
22	235	48.2	86	5	ABB78149 Amino aci
23	228	46.7	87	5	ABB78170 Amino aci
24	228	46.7	122	7	ABO74609 Pseudomon

ALIGNMENTS

25	224.5	46.0	89	9	ABE41576 L. pneumo
26	224.5	46.0	95	9	ABE38294 L. pneumo
27	222.5	45.6	90	5	ABB78167 Amino aci
28	222	45.5	90	5	ABB78168 Amino aci
29	218	44.7	87	5	ABB78169 Amino aci
30	218	44.7	88	5	ABB78178 Amino aci
31	211	43.2	88	5	ABB78171 Amino aci
32	211	43.2	88	5	ABB78172 Amino aci
33	211	43.2	88	5	ABB78173 Amino aci
34	211	43.2	88	6	ABP77219 N. gonorr
35	206	42.2	87	5	ABB78175 Amino aci
36	200	41.0	87	5	ABB78174 Amino aci
37	197	40.4	87	5	ABB78176 Amino aci
38	195.5	40.1	92	6	ADA34169 Acinetoba
39	195	40.0	87	5	ABB78177 Amino aci
40	130	26.6	110	8	ADL05173 M. catarr
41	77	15.8	1647	4	ABG10750 Novel hum
42	72	14.8	309	8	ADN46828 Thermococ
43	72	14.8	506	6	AAV74371 Neisseria
44	72	14.8	507	6	ABU40210 Protein e
45	71.5	14.7	184	3	AAH16290 Pinnus rad
46	71	14.5	447	2	AAH52657 Rat N-ace
47	71	14.5	447	7	ADH55944 Rat Prote
48	71	14.5	507	3	AAV74372 Neisseria
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51	71	14.5	548	4	AAH04737 Brugia ma
52	70.5	14.4	184	3	AAH16325 Pinnus rad
53	70.5	14.4	184	4	AAH65734 Annexin-I
54	70.5	14.4	184	7	ADB94702 Programme
55	70.5	14.4	593	4	AAH19947 Novel hum
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57	70	14.3	297	7	AAH31202 Arabidops
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61	69.5	14.2	1377	8	ADH81847 Streptoco
62	69.5	14.2	1387	8	ADH84834 Streptoco
63	69.5	14.2	1387	8	ADV79687 Streptoco
64	69	14.1	503	4	ABG16577 Novel hum
65	69	14.1	679	9	ADH85056 Partial F
66	68.5	14.0	608	5	ABP73745 Candida a
67	68.5	14.0	632	8	ADS29711 Bacterial
68	68	13.9	239	8	ADT07537 Human col
69	68	13.9	280	3	AAV54294 Amino aci
70	68	13.9	280	5	ABG93905 Lactuca s
71	68	13.9	280	8	ADJ50292 O11-assoC
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73	68	13.9	302	4	AAH88379 Human mem
74	68	13.9	302	9	ADY63123 Human cto
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RESULT 1

ID ABB78161 standard; protein, 91 AA.

AC ABB78161; 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
DR
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more yggx protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX
XX Example; Fig 1A; 16bp; English.
PS
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of yggx protein (a protein identified from *Salmonella*
CC *enterica* serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. Yggx reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent yggx homologues
XX
XX Sequence 91 AA;
SQ

```

Query Match      100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Fred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 MSRTTFCYTLORDAEGODPOLYPGELEGKRIIYNEISKDAAWQHOKOTMLINEKLTNNMNA 60
DB      1 MSRTTFCYTLQDABEQDPQLPFGELGKRIIYNEISKDAWQHOKOTMLINEKLTNNMNA 60
QY      61 EHRKLLBQEMVSPFLFEGKDVHIEGYTPEDKK 91
DB      61 EHRKLLBQEMVSPFLFEGKDVHIEGYTPEDKK 91

RESULT 2
ABB78159
ID      ABB78159 standard; protein; 91 AA.
XX
AC      ABB78159;
XX
DT      05-NOV-2002 (first entry)
XX
DE      Amino acid sequence of a YggX homologue.
XX
KW      Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM      hydroxyl radical; DNA damage; YggX homologue.
XX
OS      Unidentified.
XX
PN      US2002072118-A1.
XX
PD      13-JUN-2002.
XX
PF      18-SEP-2001; 2001US-00955502.
XX
PR      22-SEP-2000; 2000US-0234588P.
XX
PA      (DOWN/) DOWNS D.
XX      (GRAL/) GRALNICK J A.
XX
PI      Downs D, Gralnick JA;
XX

```

DR WPI, 2002-589476/63.

XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgxB protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.

XX
XX
XX PS Example, Fig 1A, 16pp; English.

XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgxB protein (a protein identified from *Salmonella*
CC *enterica* serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgxB homologues

SQ Sequence 91 AA;
XX

	Query Match	Similarity	100.0%	Score 488	DB 5	Length 91
Best Local			100.0%	Prod. No. 2,3e-49		
Matches	91	Conservative	0	Mismatches	0	Indels
					0	Gaps
					0	
QY	1	MSRTFTCYLORDABEGDFOIYPBELGRIRYNEISKAMAMQKHOTMLINEKLLNNMNA				60
DB	1	MSRTFTCYLORDABEGDFOIYPBELGRIRYNEISKAMAMQKHOTMLINEKLLNNMNA				60
QY	61	EHKRLLEQEMWSFLFEGKDVAIEGYTPEDKK				91
DB	61	EHKRLLEQEMWSFLFEGKDVAIEGYTPEDKK				91

RESULT 3
ID ABB78162 standard; protein; 91 AA.
AC ABB78162;
DT 05-NOV-2002 (first entry)
DE Amino acid sequence of a YggX homologue.
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX Salmonella typhi.
OS US2002072118-A1.
PN 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
PF 22-SEP-2000; 2000US-0234588P.
PR (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX Downs D, Gralnicks JA;
PI WPI; 2002-589476/63.
DR Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica serovar Typhimurium.
PS Example; Fig 1A; 16pp; English.

The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-17

Perfect score: 488

Sequence: 1 MSRTIFCTYLRDAEGQDFQ.....SFLFEKQVHIRGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	100.0	91	2 AH0879	conserved hypothet
2	469	96.1	91	2 AH8594	hypothetical prote
3	469	96.1	91	2 A65082	hypothetical prote
4	469	96.1	91	2 F91108	hypothetical prote
5	393	80.5	90	2 A10116	conserved hypothet
6	389	79.7	90	2 C82320	conserved hypothet
7	385	78.9	90	2 C64013	hypothetical prote
8	259	53.1	93	2 B84994	hypothetical prote
9	232	47.5	105	2 C82624	conserved hypothet
10	228	46.7	90	2 H85003	conserved hypothet
11	211	43.2	88	2 H81014	conserved hypothet
12	199.5	16.3	1638	2 D87749	protein unc-73b [i
13	179.5	16.3	2488	2 T47739	guanine nucleotide
14	78	16.0	1260	2 T04440	hypothetical prote
15	73.5	15.1	495	2 AH0985	probable zinc-pro
16	71.5	14.7	209	2 T64172	hypothetical prote
17	71	14.5	507	2 JG2076	alpha-1,3-mannosyl
18	71	14.5	546	2 C81063	funarate hydratase
19	71	14.5	546	2 A81807	63k antigen - nema
20	71	14.5	548	2 A54510	hypothetical prote
21	70	14.3	324	2 T05429	thiosulfate reduct
22	70	14.3	758	2 AD0763	thiosulfate-dithio
23	69.5	14.2	859	2 T29630	hypothetical prote
24	69.5	14.1	265	2 T46013	hypothetical prote
25	69	14.1	447	2 T16527	hypothetical prote
26	68.5	14.0	683	2 AC2256	hypothetical prote
27	68	13.9	445	1 XDHUMB	alpha-1,3-mannosyl
28	68	13.9	689	2 F83902	beta-galactosidase

30	67.5	13.8	166	2 F70562	hypothetical prote
31	67	13.7	447	1 A38561	alpha-1,3-mannosyl
32	67	13.7	1111	2 T23047	hypothetical prote
33	66.5	13.6	410	1 K8MSD	cathepsin D (EC 3.
34	66	13.5	447	1 A42500	alpha-1,3-mannosyl
35	66	13.5	703	2 B82148	ATP-dependent heil
36	66	13.5	1085	2 S62516	hypothetical coile
37	65.5	13.4	287	2 F82265	conserved hypothet
38	65.5	13.4	365	2 B54128	Fe-binding protein
39	65	13.3	433	2 A70465	probable GTP bindi
40	65	13.3	507	2 A83105	probable fumarate
41	65	13.3	511	2 A99574	ABC transporter at
42	65	13.3	593	2 C64097	probable soluble 1
43	65	13.2	1230	2 S56850	SMC1 protein homol
44	64.5	13.2	327	2 AD2129	transcription regul
45	64.5	13.2	385	2 D87723	protein R06A10.2 [
46	64.5	13.2	401	2 AE1978	hypothetical prote
47	64.5	13.2	544	2 T40058	probable chromatin
48	64.5	13.2	1197	2 S26947	DNA-directed DNA p
49	64	13.1	251	2 B90428	hypothetical prote
50	64	13.1	548	2 A28209	60k filarial anti
51	64	13.1	643	2 A43647	parasporeal crystal
52	63.5	13.0	379	2 S70709	type II site-speci
53	63.5	13.0	438	2 T37786	probable RNA-bindi
54	63.5	13.0	2672	2 A48126	translation activa
55	63	12.9	205	2 C26135	keratin, 50K type
56	63	12.9	235	2 G65212	hypothetical 26.7K
57	63	12.9	258	2 A97991	hypothetical prote
58	63	12.9	258	2 B95121	phosphoesterase, p
59	63	12.9	483	2 G64799	yeast protein - Bac
60	63	12.9	543	2 T16015	hypothetical prote
61	63	12.9	549	2 T16016	hypothetical prote
62	63	12.9	1119	2 T15842	hypothetical prote
63	63	12.9	1166	2 H71609	hypothetical prote
64	63	12.9	1209	2 T46027	hypothetical prote
65	63	12.9	1327	2 T14594	guanine nucleoti
66	63	12.9	1572	2 S45251	SNF2alpha protein
67	63	12.9	1586	2 S39580	HBW protein - hum
68	62.5	12.8	165	2 A81382	shikimate kinase (
69	62.5	12.8	259	2 G81203	conserved hypothet
70	62.5	12.8	305	2 A75211	asparaginase (EC 3
71	62.5	12.8	375	2 T37245	GTP-binding regula
72	62.5	12.8	498	2 G91179	hypothetical prote
73	62.5	12.8	498	2 H86025	hypothetical prote
74	62.5	12.8	498	2 S47748	53.1K protein prec
75	62.5	12.8	629	2 B85107	chemotactic transd

ALIGNMENTS

RESULT 1
AH0879
conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C/Accession: AH0879
R/Parthill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AH0879
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <PAR>
A/Cross-References: UNIPARC:UPI00005A44C; GB:A513382; PIDN:CAD02936.1; PID:g16504189; C/Gene: STY3266
C/Superfamily: fe(II) trafficking protein YggX

Query Match	100.0%	Score 488	DB 2	Length 91	
Beat Local Similarity	100.0%	Pred. No. 2.1e-42			
Matches	91	Conservative	0	Mismatches	0
Indels			0	Gaps	0

Oy 1 MSRTIFCTYLRDAGGDPOLYPGELGKRITNEISKDAMAWOHKQTMLINEKLANMNA 60
 |||||
 Db 1 MSRTIFCTYLRDAGGDPOLYPGELGKRITNEISKDAMAWOHKQTMLINEKLANMNA 60

Oy 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
 |||||
 Db 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91

RESULT 2
 A:Accession: A85954
 A:Residues: 1-91 <STO>
 A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; E:11206551
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Y9gX
 C:Superfamily: fe(II) trafficking protein Y9gX

Query Match	96.1%	Score 469	DB 2	Length 91	
Beat Local Similarity	94.5%	Pred. No. 1.8e-40			
Matches	86	Conservative	5	Mismatches	0
Indels			0	Gaps	0

Oy 1 MSRTIFCTYLRDAGGDPOLYPGELGKRITNEISKDAMAWOHKQTMLINEKLANMNA 60
 |||||
 Db 1 MSRTIFCTYLRDAGGDPOLYPGELGKRITNEISKDAMAWOHKQTMLINEKLANMNA 60

Oy 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
 |||||
 Db 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91

RESULT 3
 A:Accession: A65082
 A:Residues: 1-91 <BLAT>
 A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g12517511; E:11206551
 A:Experimental source: strain K-12, substrain MG1655
 C:Superfamily: fe(II) trafficking protein Y9gX

Query Match	96.1%	Score 469	DB 2	Length 91	
Beat Local Similarity	94.5%	Pred. No. 1.8e-40			
Matches	86	Conservative	5	Mismatches	0
Indels			0	Gaps	0

Oy 1 MSRTIFCTYLRDAGGDPOLYPGELGKRITNEISKDAMAWOHKQTMLINEKLANMNA 60
 |||||
 Db 1 MSRTIFCTYLRDAGGDPOLYPGELGKRITNEISKDAMAWOHKQTMLINEKLANMNA 60

Oy 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
 |||||
 Db 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91

RESULT 4
 A:Accession: A65082
 A:Residues: 1-91 <BLAT>
 A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g12517511; E:11206551
 A:Experimental source: strain K-12, substrain MG1655
 C:Superfamily: fe(II) trafficking protein Y9gX

Query Match	96.1%	Score 469	DB 2	Length 91	
Beat Local Similarity	94.5%	Pred. No. 1.8e-40			
Matches	86	Conservative	5	Mismatches	0
Indels			0	Gaps	0

Oy 1 MSRTIFCTYLRDAGGDPOLYPGELGKRITNEISKDAMAWOHKQTMLINEKLANMNA 60
 |||||
 Db 1 MSRTIFCTYLRDAGGDPOLYPGELGKRITNEISKDAMAWOHKQTMLINEKLANMNA 60

Oy 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91
 |||||
 Db 61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK 91

Db 1 MSRTIFCTYFLQREAGGDPOLYPGELGKRIYNEISKEAWAQMOMKOTMLINEKKLANMNA 60

Qy 61 EHRKLEQEWVSTFLPEGKDVHIGYTPEDCK 91

Db 61 EHRKLEQEWVSTFLPEGKDVHIGYTPEDCK 91

RESULT 4

F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C:Accession: F91108
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kunara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A9629; MUID:1156231; PMID:11258796
A:Accession: F91108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <HAX>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA037261.1;
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs3838
C:Superfamily: fe(II) trafficking protein YsgX

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYFLQREAGGDPOLYPGELGKRIYNEISKEAWAQMOMKOTMLINEKKLANMNA 60

Db 1 MSRTIFCTYFLQREAGGDPOLYPGELGKRIYNEISKEAWAQMOMKOTMLINEKKLANMNA 60

Qy 61 EHRKLEQEWVSTFLPEGKDVHIGYTPEDCK 91

Db 61 EHRKLEQEWVSTFLPEGKDVHIGYTPEDCK 91

RESULT 5

A10116
conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: A10116
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
NATURE 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: A10116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <KUR>
A:Cross-references: UNIPARC:UPI00000DCC4; GB:AL590844; PIDN:CAC89796.1; PID:G15979022;
C:Genetics:
A:Gene: YPO0953
C:Superfamily: fe(II) trafficking protein YsgX

Query Match 80.5%; Score 393; DB 2; Length 90;
Best Local Similarity 81.1%; Pred. No. 8.1e-33;
Matches 73; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MSRTIFCTYFLQREAGGDPOLYPGELGKRIYNEISKEAWAQMOMKOTMLINEKKLANMNA 60

Db 1 MSRTIFCTYFLQREAGGDPOLYPGELGKRIYNEISKEAWAQMOMKOTMLINEKKLANMNA 60

Qy 61 EHRKLEQEWVSTFLPEGKDVHIGYTPEDCK 90

Db 61 EHRKLEQEWVSTFLPEGKDVHIGYTPEDCK 90

61 EDRKLEQEWVSTFLPEGKDVHIGYTPEDCK 90

GenCore version 5.1.7
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OM protein - protein search, using bw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-17

Perfect score: 488

Sequence: 1 MSRTIFCTYLGRDAGQDFQ.....SFLPGKDVHIGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: uniprot_05.80:*
2: uniprot_sprot:*
3: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	483	99.0	90	1	FETP_SALCH
2	483	99.0	90	1	FETP_SALPA
3	483	99.0	90	1	FETP_SALTI
4	483	99.0	90	1	FETP_SALTY
5	464	95.1	90	1	FETP_ECO57
6	464	95.1	90	1	FETP_ECOLI
7	464	95.1	90	1	FETP_SHIFL
8	460	94.3	90	1	FETP_ECOL6
9	416	85.2	90	1	FETP_EBWCY
10	401	82.2	90	1	FETP_YBRPS
11	393	80.5	90	1	FETP_VIBPA
12	393	80.5	90	1	FETP_YBRPS
13	389	79.7	90	1	FETP_VIBCH
14	389	79.7	90	1	FETP_VIBVU
15	389	79.7	90	1	FETP_VIBVY
16	387	79.3	91	1	FETP_HAENS
17	385	78.9	90	1	FETP_HAENS
18	385	78.9	90	2	Q4QMD9_HAB18
19	383	78.5	90	1	FETP_PHOPR
20	377	77.3	90	1	FETP_PASMU
21	376	77.0	90	1	FETP_PASMU
22	371	76.0	94	1	FETP_PHOLI
23	365	74.8	90	1	FETP_HABDU
24	341	69.9	90	1	FETP_VIBP1
25	336	68.9	92	1	FETP_IDILO
26	359	53.1	77	1	FETP_SHEON
27	249	51.0	90	1	FETP_BORBR
28	249	51.0	90	1	FETP_BORBR
29	249	51.0	90	1	FETP_BORBR
30	243	49.8	78	1	FETP_BUCAP
31	239	49.0	91	1	FETP_XANAC

32	232	47.5	90	1	FETP_XYLPA	Q9PC73 xylella fas
33	232	47.5	92	1	FETP_XANOR	O59J22 xanthomonas
34	228.5	46.8	89	1	FETP_LEGPI	O59J24 legionella
35	228	46.7	90	1	FETP_PSBAB	O59J26 pseudomonas
36	228	46.7	90	1	FETP_XYLFT	O9HJ36 pseudomonas
37	228	46.7	92	1	FETP_XANCP	O87J06 xylella fas
38	228	46.7	92	2	Q4UW14_XANCP	O8P829 xanthomonas
39	225	46.1	78	1	FETP_WIGBR	O4UW14 xanthomonas
40	224.5	46.0	89	1	FETP_LEGPA	O8J305 wigglewort
41	224.5	46.0	89	1	FETP_LEGPA	O5XJ99 legionella
42	222	45.5	90	1	FETP_NITRU	O5XJ80 legionella
43	222	45.5	90	1	FETP_PSBEM	O82X12 nitrosomonas
44	222	45.5	90	2	Q4ZLP3_PSBESY	O87J05 pseudomonas
45	218	44.7	90	1	FETP_COXBU	O4ZLP3 pseudomonas
46	218	44.7	90	1	FETP_PSEBK	O83J06 coxiella bu
47	218	44.7	90	2	Q4J228_AZOVIT	O88J49 pseudomonas
48	215	44.1	90	2	Q6T7F6_PSEFL	O4J228 azotobacter
49	213	43.6	90	1	FETP_CHRVO	O6T7F6 pseudomonas
50	212	43.4	79	1	FETP_CANBP	O7VXG9 chrysiobacter
51	211	43.2	88	1	FETP_NEIRI	O5F553 neisseria g
52	211	43.2	88	1	FETP_NEIRI	O5F553 neisseria g
53	211	43.2	88	1	FETP_NEIRI	O5F553 neisseria m
54	207	42.4	87	1	FETP_BUCBP	O67616 neisseria m
55	206	42.2	91	1	FETP_BURMA	O89A44 buchnera ap
56	206	42.2	91	1	FETP_BURMA	O62J09 burkholderi
57	205	42.0	90	2	Q4KJ12_PSEBS	O63J14 burkholderi
58	205	42.0	91	1	FETP_RALSO	O4KJ12 pseudomonas
59	203	41.6	91	2	Q4LS19_9BURK	O8Y010 ralsstonia b
60	195	40.0	90	1	FETP_METCA	O4LS19 burkholderi
61	192	39.3	87	1	FETP_FRATT	O60J17 methylococc
62	190.5	39.0	90	1	FETP_ACICD	O5N1J8 franciella
63	146	29.9	96	2	Q4FVJ7_9GAMM	O6FJ33 acinetobact
64	145	29.7	92	2	Q4NMQ4_9DELT	O4FVJ7 psychrobact
65	82.5	16.9	482	2	O5NUV1_9BURK	O4NMQ4 anaeromyxob
66	82.5	16.9	514	2	O6A1Z9_DSPPS	O5NUV1 ralsstonia m
67	79.5	16.3	1638	2	O7XPD4_CABEL	O6A1Z9 deusilfocale
68	79.5	16.3	2140	2	O6BEM2_CABEL	O7XPD4 caenorhabdi
69	79.5	16.3	2488	2	O61528_CABEL	O6BEM2 caenorhabdi
70	78.5	16.1	337	2	O81A8B_BACCR	O61528 caenorhabdi
71	78	16.0	1260	2	O46677_ARATH	O81A8B bacillus ce
72	77.5	15.9	1047	2	O5CJ53_CRYHO	O46677 arabidopsis
73	76.5	15.7	486	2	O7WX51_ALCEU	O5CJ53 cryptospori
74	75.5	15.5	1278	2	O5CYM7_CRYPV	O7WX51 alciogens
75	75	15.4	385	2	Q7J34A2_BACCI	O5CYM7 cryptospori

ALIGNMENTS

RESULT 1
FETP_SALCH STANDARD; PRT; 90 AA.
ID FETP_SALCH
AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Probable Fe(2+) trafficking protein.
DS Name=yggX; OrderedLocustNames=SC3052;
GN Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_Taxid=591;
(1)
NP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gk1297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.,
"The genome sequence of Salmonella enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen."
RL Nucleic Acids Res. 33:1690-1698 (2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or

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CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1 SUBUNIT: Monomer (By similarity).
CC -1 SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB017220; AAK66958.1; -; Genomic_DNA.
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; Y9GX.
CC DR Prodom; PD029191; DUF495; 1.
CC KW Complete proteome; Iron.
CC FT INIT_MET 0
CC SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;
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Query Match 99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 SRTIFCTYLQDAEGDQFQLYPGELGKRIYNEISKDAAQWQHOKTMTLINEKLNMMNAE 60
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DB 61 HRKLEQEMVSPFLPEGKDVHIEGYTPEDKK 90
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PFTP SALPA STANDARD; PRT; 90 AA.
AC QSPMML;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gx; OrderedLocustNames=SPR2974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_Taxid=54388;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.B., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozerky P., McEllan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremliki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Minx P.,
RA Delehanthy K., Fronick C., Magrini V., Nhan M., Warren W., Flores L.,
RA Spiech J., Wilson R.K.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL Nat. Genet. 36:1268-1274(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
CC DR SMR; QSPMML; 1-91.
CC DR HAMAP; MF_00686; -; 1.
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DR InterPro; IPR007457; Y9GX.
DR Prodom; PD029191; DUF495; 1.
CC KW Complete proteome; Iron.
CC FT INIT_MET 0
CC SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;
CC -----
Query Match 99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
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DB 1 SRTIFCTYLQDAEGDQFQLYPGELGKRIYNEISKDAAQWQHOKTMTLINEKLNMMNAE 60
QY 62 HRKLEQEMVSPFLPEGKDVHIEGYTPEDKK 91
DB 61 HRKLEQEMVSPFLPEGKDVHIEGYTPEDKK 90
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RESULT 3
PFTP SALTI STANDARD; PRT; 90 AA.
AC P67618; Q8XFW6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gx; OrderedLocustNames=STR3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_Taxid=601;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatina M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leach A., Moulé S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22533367; PubMed=12644504;
RX DOI=10.1126/DB.185.7.2330-2337.2003;
RA Deng W., Iou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL627277; CADD2936.1; -; Genomic_DNA.
CC DR EMBL; AB016844; AAO70576.1; -; Genomic_DNA.
CC DR SMR; P67618; 1-90.
CC DR HAMAP; MF_00686; -; 1.
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-17

Perfect score: 488

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Issued Patents AA:*

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- 4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445	91.2	107	2	US-09-489-039A-11962
2	383	78.5	93	2	US-09-543-681A-5443
3	228	46.7	122	2	US-09-252-991A-23355
4	195.5	40.1	92	2	US-09-328-352-5456
5	130	26.6	110	2	US-09-540-235-2859
6	71	14.5	548	2	US-09-167-293-3
7	70.5	14.4	184	2	US-09-325-932A-66
8	68.5	14.0	544	2	US-09-248-796A-18911
9	68	13.9	337	2	US-09-323-998B-37
10	68	13.9	337	2	US-09-270-767-41746
11	68	13.9	1214	2	US-10-164-595-24
12	66.5	13.6	325	2	US-09-134-000C-4346
13	66	13.5	292	2	US-09-328-352-5836
14	65.5	13.4	546	1	US-08-533-669A-2
15	65.5	13.4	546	1	US-08-183-861-2
16	65.5	13.4	546	2	US-09-022-765-2
17	65.5	13.4	546	2	US-09-551-974A-2
18	65.5	13.4	546	2	US-09-565-501A-2
19	65.5	13.4	546	2	US-09-639-206A-2
20	65.5	13.4	546	2	US-09-874-923-2
21	65.5	13.4	546	2	US-08-798-841-2
22	65.5	13.4	982	2	US-09-551-974A-95
23	65.5	13.4	982	2	US-09-565-501A-95
24	65.5	13.4	982	2	US-09-639-206A-95
25	65.5	13.4	982	2	US-09-874-923-95
26	65.5	13.4	1427	2	US-09-551-974A-97
27	65.5	13.4	1427	2	US-09-565-501A-97

28	65.5	13.4	1427	2	US-09-639-206A-97	Sequence 97, Appl
29	65.5	13.4	1427	2	US-09-874-923-97	Sequence 97, Appl
30	65.5	13.4	1641	2	US-09-551-974A-96	Sequence 96, Appl
31	65.5	13.4	1641	2	US-09-565-501A-96	Sequence 96, Appl
32	65.5	13.4	1641	2	US-09-639-206A-96	Sequence 96, Appl
33	65.5	13.4	1641	2	US-09-874-923-96	Sequence 96, Appl
34	65.5	13.3	474	2	US-09-252-991A-4085	Sequence 24473, A
35	64	13.1	98	2	US-09-270-767-41746	Sequence 41085, A
36	64	13.1	98	2	US-09-270-767-56301	Sequence 56301, A
37	64	13.1	569	2	US-09-107-532A-6689	Sequence 6689, A
38	64	13.1	644	2	US-08-793-331-7	Sequence 7, Appl
39	64	13.1	1176	2	US-09-489-039A-8879	Sequence 8879, A
40	63.5	13.0	921	2	US-09-248-796A-14950	Sequence 14950, A
41	63	12.9	1586	2	US-09-538-092-1171	Sequence 1171, A
42	62.5	12.8	260	2	US-09-252-991A-17498	Sequence 17498, A
43	62.5	12.8	419	2	US-09-543-681A-7295	Sequence 7295, A
44	62.5	12.8	662	2	US-09-583-110-5119	Sequence 5119, A
45	62.5	12.8	664	2	US-09-107-433-2775	Sequence 2775, A
46	62.5	12.8	701	2	US-09-252-991A-23288	Sequence 23288, A
47	62	12.7	227	2	US-09-270-767-58283	Sequence 58283, A
48	62	12.7	238	2	US-09-323-998B-41	Sequence 41, Appl
49	62	12.7	448	2	US-09-270-767-42959	Sequence 42959, A
50	62	12.7	604	2	US-09-008-097-4	Sequence 4, Appl
51	62	12.7	604	2	US-09-472-667-4	Sequence 4, Appl
52	62	12.7	898	2	US-09-583-110-3750	Sequence 3750, A
53	62	12.7	1167	2	US-09-107-433-3196	Sequence 3196, A
54	62	12.7	1167	2	US-09-008-097-6	Sequence 6, Appl
55	62	12.7	1167	2	US-09-472-667-6	Sequence 6, Appl
56	61.5	12.6	591	2	US-09-370-368-8	Sequence 8, Appl
57	61	12.5	143	2	US-09-270-767-45872	Sequence 45872, A
58	61	12.5	184	2	US-09-270-767-61671	Sequence 61671, A
59	61	12.5	271	2	US-09-248-796A-19265	Sequence 19265, A
60	61	12.5	389	2	US-09-270-767-46116	Sequence 46116, A
61	61	12.5	1394	2	US-09-248-796A-19555	Sequence 19555, A
62	60.5	12.4	223	2	US-09-543-681A-5667	Sequence 5667, A
63	60.5	12.4	504	2	US-10-104-047-3467	Sequence 3467, A
64	60.5	12.4	525	2	US-09-540-235-2250	Sequence 2250, A
65	60.5	12.4	527	2	US-09-489-039A-10883	Sequence 10883, A
66	60	12.3	232	2	US-09-201-641-8	Sequence 8, Appl
67	60	12.3	232	2	US-09-323-998B-36	Sequence 36, Appl
68	60	12.3	421	2	US-09-489-039A-7512	Sequence 7512, A
69	60	12.3	734	2	US-10-008-355-5	Sequence 5, Appl
70	59.5	12.2	139	2	US-09-513-999C-4802	Sequence 4802, A
71	59.5	12.2	209	2	US-09-252-991A-20905	Sequence 20905, A
72	58.5	12.2	258	2	US-09-513-999C-4800	Sequence 4800, A
73	58.5	12.2	264	2	US-09-943-016-6012	Sequence 6012, A
74	59.5	12.2	276	2	US-09-943-016-11703	Sequence 11703, A
75	59.5	12.2	434	2	US-09-303-518D-334	Sequence 334, A

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610835
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity 89.0%; Pred. No. 3.5e-49;
Matches 81; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

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Db 17 MSRTFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQOHKQTMLINEKLNMMNP 76

Qy 61 EHRKLEQEMVSLFPEGKDVHIEGYTPEDK 91
Db 77 EHRKLEQEMVSLFPEGKDVHIEGYTPEDK 107

RESULT 2

US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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RESULT 3

US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rudenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Db 33 MSRTFCTYLRDAGDGFOLYPGELGKRIYNEISKDAMQOHKQTMLINEKLNMMNA 92

Qy 61 EHRKLEQEMVSLFPEGKDVHIEGYTP 87
Db 93 EHRKLEQEMVSLFPEGKDVHIEGYTP 119

RESULT 4

US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 40.1%; Score 195.5; DB 2; Length 92;
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Qy 61 EHRKLEQEMVSLFPEGKDVHIEGYTP 88
Db 64 EHRKLEQEMVSLFPEGKDVHIEGYTP 92

RESULT 5

US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 26.6%; Score 130; DB 2; Length 110;
Best Local Similarity 34.9%; Pred. No. 7.4e-09;
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Qy 65 EHRKLEQEMVSLFPEGKDVHIEGYTP 87
Db 85 EHRKLEQEMVSLFPEGKDVHIEGYTP 107

RESULT 6
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OM protein - protein search, using sw model

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- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	488	100.0	91	US-09-955-502-14	Sequence 14, Appl
2	488	100.0	91	US-09-955-502-16	Sequence 16, Appl
3	488	100.0	91	US-09-955-502-17	Sequence 17, Appl
4	474	97.1	91	US-09-955-502-18	Sequence 18, Appl
5	472	96.7	88	US-09-955-502-15	Sequence 15, Appl
6	469	96.1	91	US-09-955-502-11	Sequence 11, Appl
7	469	96.1	91	US-09-955-502-12	Sequence 12, Appl
8	469	96.1	91	US-09-955-502-13	Sequence 13, Appl
9	393	80.5	90	US-09-955-502-20	Sequence 20, Appl
10	389	79.7	90	US-09-955-502-10	Sequence 10, Appl
11	386	79.1	78	US-09-955-502-19	Sequence 19, Appl
12	385	78.9	87	US-09-955-502-7	Sequence 7, Appl
13	383	78.5	91	US-09-955-502-5	Sequence 5, Appl
14	377	77.3	87	US-09-955-502-6	Sequence 6, Appl
15	371	76.0	87	US-09-955-502-8	Sequence 8, Appl
16	336	68.9	88	US-09-955-502-9	Sequence 9, Appl
17	259	53.1	76	US-09-955-502-21	Sequence 21, Appl
18	249	51.0	87	US-09-955-502-2	Sequence 2, Appl
19	249	51.0	87	US-09-955-502-3	Sequence 3, Appl
20	235	48.2	86	US-09-955-502-4	Sequence 4, Appl
21	232	47.5	89	US-09-955-502-22	Sequence 22, Appl
22	228	46.7	87	US-09-955-502-25	Sequence 25, Appl
23	222	45.5	90	US-09-955-502-23	Sequence 23, Appl
24	218	44.7	87	US-09-955-502-24	Sequence 24, Appl
25	218	44.7	88	US-09-955-502-33	Sequence 33, Appl
26	211	43.2	88	US-09-955-502-26	Sequence 26, Appl
27	211	43.2	88	US-09-955-502-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-955-502-14
Sequence 14, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 14
LENGTH: 91
TYPE: PRT
ORGANISM: Salmonella paratyphi

US-09-955-502-14

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Matches	91;	Conservative	0;	Mismatches 0;
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Db 1 MSRTICTYLRDAGGDFQLYPELGKRIYNEISKDAMQWQHKTMLINEKLLNMNA 6C

Qy 61 EHRKLLQEMVSFLPEGKDVIHIEGYTPEDKK 91
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Db 61 EHRKLLQEMVSFLPEGKDVIHIEGYTPEDKK 91

RESULT 2
US-09-955-502-16

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/ APPLICANT: Downs, Diana M.
/ APPLICANT: Grainick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ TITLE OF INVENTION: Oxygen-Labile Proteins
/ FILE REFERENCE: 960296.97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ PRIOR FILING DATE: 2000-09-22
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/
/ LENGTH: 91

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ORGANISM: Salmonella dublin
US-09-955-502-16

Query Match	100.0%;	Score 488;	DB 3;	length 91;
Best Local Similarity	100.0%;	Pred. No. 6.8e-49;		
Matches 91; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

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Db 1 MSRTICTYLRDPAEGDFFQLYPGELGKRIYNEISKDAWAQWQHKQTMLINEKLNMMNA 6

Qy 61 EHRKLLQEMWSFLPEGKDVIIEGYTPEDKK 91
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Db 61 EHRKLLQEMWSFLPEGKDVIIEGYTPEDKK 91

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?
? APPLICANT : Downs, Diana M.
? APPLICANT : Galinick, Jeff A.
? TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
? TITLE OF INVENTION: Oxygen-labile Proteins
? FILE REFERENCE: 960296, 97559
? CURRENT APPLICATION NUMBER: US/09/955,502
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: 60/234,588
? PRIOR FILING DATE: 2000-09-22
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: SeqIdn Ver. 2.1
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Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 EHRKLLQEAMVSFLPEGKDVIIEGYTPEDKK 91

RESULT 4
US-09-955-502-18

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1  APPLICANT: Gralnick, Jeff A.
2  TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
3  TITLE OF INVENTION: Oxygen-Labile Proteins
4  FILE REFERENCE: 960296, 97559
5  CURRENT APPLICATION NUMBER: US/09/955,502
6  CURRENT FILING DATE: 2001-09-18
7  PRIOR APPLICATION NUMBER: 60/234,588
8  PRIOR FILING DATE: 2000-09-22
9  NUMBER OF SEQ ID NOS: 33
10 SOFTWARE: PatentIn Ver. 2.1

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ORGANISM: *Salmonella typhimurium*
US-09-955-502-18

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Db 1 MSRTICTYTLORDAEGODPOLYPGELGRINYNEISKDAAQWQHQTMLINEKULNMNA 60

QY 61 EHRKLEQEWVSFLPEGKDVIHIGYTPEDKK 91
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Db 61 EHRKLEQEWVSFLPEGKDVIHIEGYPTPEDKK 91

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1  // APPLICANT: Downs, Diana M.
2  // APPLICANT: Gralnick, Jeff A.
3  // TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
4  // TITLE OF INVENTION: Oxygen-Labile Proteins
5  // FILE REFERENCE: 960296.97559
6  // CURRENT APPLICATION NUMBER: US/09/955,502
7  // CURRENT FILING DATE: 2001-09-18
8  // PRIOR APPLICATION NUMBER: 60/234,588
9  // PRIOR FILING DATE: 2000-09-22
10 // NUMBER OF SEQ ID NOS: 33
11 // SOFTWARE: PatentIn Ver. 2.1
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15 // ORGANISM: Salmonella enteritidis
16 US-09-955-502-15

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Best Local Similarity	100.0%	Pred. No. 4.8e-47;		
Matches 88;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0



GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 5.07859 Seconds
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Post-processing: Minimum Match 0%

Listing first 75 summaries

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	68	13.9	478 6 US-10-821-234-915	Sequence 915, App
3	65	13.3	593 7 US-11-194-246-317	Sequence 317, App
4	64.5	13.2	177 6 US-10-467-657-1658	Sequence 1658, App
5	63.5	13.0	1432 6 US-10-510-386-218	Sequence 218, App
6	62	12.7	251 7 US-11-054-515-1496	Sequence 1496, App
7	62	12.7	604 6 US-10-942-072-4	Sequence 4, Appl
8	62	12.7	1167 6 US-10-942-072-6	Sequence 6, Appl
9	60.5	12.4	504 7 US-11-072-512-3467	Sequence 3467, App
10	59.5	12.2	264 6 US-10-821-234-1555	Sequence 1555, App
11	59.5	12.2	285 6 US-10-467-657-222	Sequence 222, App
12	59.5	12.2	285 6 US-10-467-657-8230	Sequence 8230, App
13	59.5	12.2	650 6 US-10-467-657-1948	Sequence 1948, App
14	59.5	12.2	834 6 US-10-453-372-658	Sequence 658, App
15	59.5	12.2	1995 6 US-11-069-834-60	Sequence 60, Appl
16	59	12.1	257 7 US-11-054-515-1710	Sequence 1710, App
17	59	12.1	697 6 US-10-485-517-202	Sequence 202, Appl
18	59	12.1	1168 6 US-10-942-072-11	Sequence 11, Appl
19	59	12.1	1450 6 US-10-485-517-152	Sequence 152, App
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22	58.5	12.0	700 6 US-10-995-561-924	Sequence 924, App
23	58.5	12.0	749 7 US-11-098-686-10505	Sequence 10505, A
24	58.5	12.0	782 6 US-10-793-626-2352	Sequence 2352, App
25	58	11.9	448 6 US-10-618-320A-25	Sequence 25, Appl

26	58	11.9	480 6 US-10-510-386-12	Sequence 12, Appl
27	58	11.8	1501 6 US-10-793-626-2850	Sequence 2850, App
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29	57.5	11.8	336 6 US-10-453-372-640	Sequence 640, App
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31	57.5	11.8	752 7 US-11-072-512-3003	Sequence 3003, App
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43	57.5	11.8	3803 6 US-10-995-561-773	Sequence 773, App
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51	57	11.7	234 6 US-10-524-647-108	Sequence 108, App
52	57	11.7	432 6 US-10-821-234-1463	Sequence 1463, App
53	57	11.7	440 7 US-11-072-512-2856	Sequence 2856, App
54	56.5	11.6	647 7 US-11-000-463-722	Sequence 722, App
55	56.5	11.6	1254 6 US-10-528-031-47	Sequence 47, App
56	56.5	11.6	1897 6 US-10-821-234-1635	Sequence 1635, App
57	56.5	11.6	1907 7 US-11-000-463-250	Sequence 250, App
58	56.5	11.6	3433 6 US-10-714-787A-67	Sequence 67, Appl
59	56	11.5	206 7 US-11-124-367A-316	Sequence 316, App
60	55.5	11.4	136 6 US-10-793-626-580	Sequence 580, App
61	55.5	11.4	279 7 US-11-098-686-10812	Sequence 10812, A
62	55.5	11.4	1188 7 US-11-115-639-42	Sequence 42, Appl
63	55.5	11.4	188 7 US-11-115-639-43	Sequence 43, Appl
64	55	11.3	189 7 US-11-071-262-1	Sequence 1, Appl
65	55	11.3	667 6 US-10-793-626-198	Sequence 198, App
66	55	11.3	692 7 US-11-038-284-33	Sequence 33, Appl
67	55	11.3	783 7 US-11-037-243-67	Sequence 67, Appl
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69	55	11.3	889 7 US-11-038-284-15	Sequence 15, Appl
70	55	11.3	1142 7 US-11-109-156-22	Sequence 22, Appl
71	55	11.3	2668 7 US-11-124-368A-214	Sequence 214, App
72	55	11.3	317 6 US-11-124-368A-215	Sequence 215, App
73	54.5	11.2	450 6 US-10-523-503-74	Sequence 74, Appl
74	54.5	11.2	450 6 US-10-618-320A-26	Sequence 26, Appl
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ALIGNMENTS

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; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWinn9, version 1.04

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 79.0692 Seconds

(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502a-4

Perfect score: 454
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Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	295.5	65.1	91	1	FETP BORP
5	286.5	63.1	91	2	Q4LS19 burkholderi
6	283	62.3	90	1	FETP CHRV
7	282.5	62.2	91	1	FETP BURV
8	282.5	62.2	91	1	FETP BURP
9	272.5	60.0	88	1	FETP NEIG
10	272.5	60.0	88	1	FETP NEIM
11	272.5	60.0	88	1	FETP NEIM
12	269	59.3	90	1	FETP NITB
13	242.5	53.4	90	1	FETP METC
14	242.5	53.4	92	1	FETP SHEON
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19	240	52.9	90	1	FETP IDIO
20	239	52.6	91	1	FETP MANS
21	238.5	52.5	90	1	FETP HARI
22	238.5	52.5	90	2	Q4QMD9 haemophilus
23	238	52.4	90	1	FETP VIBR
24	236	52.0	90	1	FETP ECOS
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26	236	52.0	90	1	FETP ECOS
27	236	52.0	90	1	FETP SHIF
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29	236	52.0	90	1	FETP VIBV
30	235	51.8	90	1	FETP VIBCH
31	233.5	51.4	90	1	FETP PASNU

32	233	51.3	90	1	FETP PHOR	Q61mk7 photobacter
33	232	51.1	90	1	FETP PHOL	Q7n711 photobadu
34	230	50.7	90	1	FETP SALC	Q57k04 salmonella
35	230	50.7	90	1	FETP SALP	Q56mm1 salmonella
36	230	50.7	90	1	FETP SALP	Q67618 salmonella
37	230	50.7	90	1	FETP SALP	Q67617 salmonella
38	228	50.2	90	2	Q4J228 azovi	Q4J228 azotobacter
39	225.5	49.7	94	1	FETP HADU	Q7ykb6 haemophilus
40	225	49.6	90	1	FETP ERWC	Q6d8j9 erwinia car
41	224.5	49.4	90	1	FETP ACIAD	Q6efb3 actinobact
42	223	49.1	90	1	FETP COXU	Q8bd06 coxiella bu
43	222.5	49.0	90	1	FETP PSEB	Q9nu36 pseudomonas
44	220	48.5	78	1	FETP BUCB	Q8K925 buchiera ap
45	220	48.5	90	1	FETP YERP	Q666m3 yerwinia ps
46	220	48.5	91	1	FETP XANC	Q86j17 xanthomonas
47	214	47.1	92	1	FETP XANC	Q5gy22 xanthomonas
48	213	46.9	79	1	FETP CANB	Q7v793 candidatus
49	212	46.7	90	1	FETP YERP	Q8zhe7 yerwinia pe
50	211	46.5	92	1	FETP XANCP	Q86829 xanthomonas
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52	204.5	45.0	90	1	FETP PSEB	Q88r49 pseudomonas
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54	200.5	44.2	90	1	FETP PSEB	Q8rd05 pseudomonas
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56	200	44.1	77	1	FETP BUCB	Q4ZLP3 pseudomonas
57	196.5	43.3	90	2	Q6T7F6 PSEB	Q6T7F6 pseudomonas
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61	184	40.5	87	1	FETP WIGR	Q8d3C5 wiggleswort
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67	77	17.0	330	2	Q5DA35 SCHIA	Q5DA35 schistosoma
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72	71.5	15.7	207	1	COAB STAN	P63830 staphylococ
73	71.5	15.7	207	1	COAB STAN	P63831 staphylococ
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ALIGNMENTS

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DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
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OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			
OC	Alcaligenaceae; Bordetella.			
OX	NCBI_TaxID=518;			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=RB50 / ATCC BAA-588;			
RX	MEBLINE=2827954; PubMed=12910271; DOI=10.1038/ng1227;			
RA	Parshall J., Heideman M., Preston A., Murphy L.D., Thomson N.R.,			
RA	Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,			
RA	Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,			
RA	Achtman M., Atkin R., Baker S., Baason D., Baason N., Cherevach I.,			
RA	Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,			
RA	Fellwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsels K.,			
RA	Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,			

RA Rabbiniwitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: BX640447; CAE33897.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC KW
CC SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;
SQ
Query Match 97.7%; Score 443.5; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 6.9e-39;
Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 1 MSRIYNCVKLRKREAGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNENRLNLADA 60
DB 1 MSRIYNCVKLRKREAGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNENRLNLADA 60
OY 61 RARKYLQOQMERFLFEDGTVGAQG-VP 86
DB 61 RARKYLQOQMERFLFEDGTVGAQGVP 87
RESULT 2
FETP BORPE STANDARD; PRT; 90 AA.
ID FETP BORPE
AC 07W902;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BP1703;
OS *Bordetella parapertussis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; *Bordetella*.
OX NCBI_TaxID=519;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham A., Bason N., Chervach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabbiniwitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

CC
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC removed.

CC EMBL: BX640428; CAE37004.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC KW
CC SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;
SQ
Query Match 97.7%; Score 443.5; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 6.9e-39;
Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
OY 1 MSRIYNCVKLRKREAGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNENRLNLADA 60
DB 1 MSRIYNCVKLRKREAGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNENRLNLADA 60
OY 61 RARKYLQOQMERFLFEDGTVGAQG-VP 86
DB 61 RARKYLQOQMERFLFEDGTVGAQGVP 87
RESULT 3
FETP BORPE STANDARD; PRT; 90 AA.
ID FETP BORPE
AC 07W902;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BP2336;
OS *Bordetella pertussis*.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; *Bordetella*.
OX NCBI_TaxID=520;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parhill J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham A., Bason N., Chervach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabbiniwitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of *Bordetella pertussis*,
RT *Bordetella parapertussis* and *Bordetella bronchiseptica*.";
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CC EMBL: BX640418; CAE32609.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:09:58 ; Search time 20.109 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502a-4

Perfect score: 454
Sequence: 1 MSRLVNCVKNRBAEGLDFP.....QQQMERFLPEDGTVAQGV 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents, AA:*

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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/BCRUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RB_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Dackfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	229	50.4	107	US-09-489-039A-11962	Sequence 11962, A
2	228	50.2	92	US-09-543-681A-5443	Sequence 5443, Ap
3	223.5	49.2	93	US-09-328-352-5456	Sequence 5456, Ap
4	222.5	49.0	122	US-09-252-991A-23355	Sequence 23355, A
5	157.5	34.7	110	US-09-540-236-2859	Sequence 2859, Ap
6	77.5	16.0	303	US-09-902-540-13601	Sequence 13601, A
7	70.5	15.5	200	US-09-710-279-1186	Sequence 1186, Ap
8	70.5	15.5	200	US-09-710-279-2390	Sequence 2390, Ap
9	70.5	15.5	208	US-09-134-001C-3785	Sequence 3785, Ap
10	70.5	15.5	366	US-08-928-213B-59	Sequence 59, Appl
11	69	15.2	219	US-08-928-213B-61	Sequence 61, Appl
12	69	15.2	504	US-08-441-139-18	Sequence 18, Appl
13	69	15.2	521	US-08-557-122A-32	Sequence 32, Appl
14	69	15.2	521	US-09-262-666-32	Sequence 32, Appl
15	69	15.2	522	US-09-368-588-2	Sequence 2, Appl
16	69	15.2	530	US-08-557-122A-35	Sequence 35, Appl
17	69	15.2	530	US-09-262-666-35	Sequence 35, Appl
18	67	14.8	381	US-09-949-016-9788	Sequence 9788, Ap
19	67	14.8	381	US-09-964-899-13	Sequence 13, Appl
20	66.5	14.6	591	US-09-370-368-8	Sequence 8, Appl
21	66.5	14.6	1242	US-09-107-532A-5241	Sequence 5241, Ap
22	66.5	14.6	1245	US-09-716-964B-87	Sequence 87, Appl
23	66	14.5	503	US-09-058-260-26	Sequence 26, Appl
24	64	14.1	1493	US-09-713-273A-20	Sequence 20, Appl
25	63.5	14.0	498	US-09-058-260-16	Sequence 16, Appl
26	63.5	14.0	503	US-08-781-802-2	Sequence 2, Appl
27	63.5	14.0	503	US-08-781-802-10	Sequence 10, Appl

28	63.5	14.0	503	1	US-08-781-802-12	Sequence 12, Appl
29	63.5	14.0	503	2	US-08-694-078-2	Sequence 2, Appl
30	63.5	14.0	503	2	US-09-058-260-2	Sequence 2, Appl
31	63.5	14.0	503	2	US-09-058-260-10	Sequence 10, Appl
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33	63.5	14.0	503	2	US-09-058-260-28	Sequence 28, Appl
34	63.5	14.0	503	2	US-09-058-260-30	Sequence 30, Appl
35	63.5	14.0	805	1	US-08-045-806-2	Sequence 2, Appl
36	63.5	14.0	805	1	US-08-366-051B-2	Sequence 2, Appl
37	63	13.9	581	2	US-09-713-273A-12	Sequence 12, Appl
38	63	13.9	979	2	US-09-543-681A-5466	Sequence 5466, Ap
39	63	13.9	2532	2	US-09-215-694-10	Sequence 10, Appl
40	63	13.9	2532	2	US-10-109-310-10	Sequence 10, Appl
41	62.5	13.8	666	2	US-09-270-767-62249	Sequence 62249, A
42	62.5	13.8	721	2	US-09-270-767-46645	Sequence 46645, A
43	61.5	13.5	292	2	US-09-328-352-5836	Sequence 5836, Ap
44	61.5	13.5	516	2	US-09-248-796A-19517	Sequence 19517, A
45	61.5	13.5	518	2	US-09-045-360-4	Sequence 4, Appl
46	61.5	13.5	518	2	US-09-746-390-4	Sequence 4, Appl
47	61.5	13.5	623	2	US-10-104-047-3378	Sequence 3378, Ap
48	61.5	13.5	1464	2	US-09-045-360-2	Sequence 2, Appl
49	61.5	13.5	1464	2	US-09-713-273A-21	Sequence 21, Appl
50	61.5	13.5	1464	2	US-10-038-224-2	Sequence 2, Appl
51	61.5	13.5	1464	2	US-09-746-390-2	Sequence 2, Appl
52	61	13.4	312	2	US-09-605-703B-2656	Sequence 2656, Ap
53	61	13.4	563	2	US-09-949-016-10801	Sequence 10801, A
54	61	13.4	713	2	US-09-540-236-3595	Sequence 3595, Ap
55	61	13.4	856	2	US-09-252-991A-17850	Sequence 17850, A
56	61	13.4	862	1	US-08-685-118-2	Sequence 2, Appl
57	61	13.4	862	1	US-08-915-495-2	Sequence 2, Appl
58	61	13.4	862	1	US-08-914-520-2	Sequence 2, Appl
59	61	13.4	862	2	US-09-853-180B-4	Sequence 4, Appl
60	61	13.3	864	2	US-09-949-016-7758	Sequence 7758, Ap
61	60.5	13.3	81	2	US-10-290-579A-138	Sequence 138, Ap
62	60	13.2	1308	2	US-09-862-027-79	Sequence 79, Appl
63	59.5	13.1	447	2	US-09-902-540-13195	Sequence 13195, A
64	59.5	13.1	5037	2	US-09-424-783-4	Sequence 4, Appl
65	59	13.0	226	2	US-10-104-047-3820	Sequence 3820, Ap
66	59	13.0	265	2	US-09-710-279-174	Sequence 174, Ap
67	59	13.0	309	2	US-09-248-796A-14939	Sequence 14939, A
68	59	13.0	371	2	US-10-104-047-3421	Sequence 3421, Ap
69	59	13.0	435	2	US-09-248-796A-15070	Sequence 15070, A
70	59	13.0	437	2	US-09-134-001C-5342	Sequence 5342, Ap
71	59	13.0	805	2	US-09-598-401C-77	Sequence 77, Appl
72	59	13.0	1612	2	US-08-545-860D-48	Sequence 48, Appl
73	59	13.0	1612	4	PCT-US94-04496-48	Sequence 48, Appl
74	58.5	12.9	314	2	US-09-252-991A-18752	Sequence 18752, A
75	58.5	12.9	318	1	US-08-695-412B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610036
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 20040001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OW protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 65.403 Seconds

(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502a-4

Perfect score: 454

Sequence: 1 MSRLVNCVKLRKRGALDLP.....QQQMERFLFEDGTVAQGV 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA Main:

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	86	3	US-09-955-502-4
2	443.5	97.7	87	3	US-09-955-502-2
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4	282.5	62.2	87	3	US-09-955-502-29
5	282.5	62.2	87	3	US-09-955-502-30
6	272.5	60.0	88	3	US-09-955-502-26
7	272.5	60.0	88	3	US-09-955-502-27
8	272.5	60.0	88	3	US-09-955-502-28
9	257.5	56.7	87	3	US-09-955-502-31
10	246	54.2	91	3	US-09-955-502-5
11	242.5	53.4	87	3	US-09-955-502-32
12	242.5	53.4	88	3	US-09-955-502-9
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14	241	53.1	91	3	US-09-955-502-12
15	241	53.1	91	3	US-09-955-502-13
16	241	53.1	91	3	US-09-955-502-18
17	238.5	52.5	87	3	US-09-955-502-7
18	235	51.8	88	3	US-09-955-502-15
19	235	51.8	90	3	US-09-955-502-10
20	235	51.8	91	3	US-09-955-502-14
21	235	51.8	91	3	US-09-955-502-16
22	235	51.8	91	3	US-09-955-502-17
23	233.5	51.4	87	3	US-09-955-502-6
24	225.5	49.7	87	3	US-09-955-502-8
25	223	49.1	88	3	US-09-955-502-33
26	222.5	49.0	87	3	US-09-955-502-25
27	222	48.9	78	3	US-09-955-502-19

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73	195	43.0	89	3	US-09-955-502-22	Sequence 22, Appl
74	195	43.0	89	3	US-09-955-502-22	Sequence 22, Appl
75	195	43.0	89	3	US-09-955-502-22	Sequence 22, Appl

RESULT 1
US-09-955-502-4
Sequence 4, Appl
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: DOWNS, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 4
LENGTH: 86
TYPE: PRT
ORGANISM: Bordetella bronchiseptica

US-09-955-502-4

Query Match 100.0%; Score 454; DB 3; Length 86;
Best Local Similarity 100.0%; Pred. No. 5,7e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNNRNLADA 60
Db 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNNRNLADA 60

Qy 61 RARKYLQOQMERFLFEDGTVEAOG-VP 86
Db 61 RARKYLQOQMERFLFEDGTVEAOG-VP 86

RESULT 2

US-09-955-502-2
Sequence 2, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 87
TYPE: PRT
ORGANISM: Bordetella pertussis
US-09-955-502-2

Query Match 97.7%; Score 443.5; DB 3; Length 87;
Best Local Similarity 98.9%; Pred. No. 9,6e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNNRNLADA 60
Db 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNNRNLADA 60

Qy 61 RARKYLQOQMERFLFEDGTVEAOG-VP 86
Db 61 RARKYLQOQMERFLFEDGTVEAOG-VP 86

RESULT 3

US-09-955-502-3
Sequence 3, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 87
TYPE: PRT
ORGANISM: Bordetella parapertussis
US-09-955-502-3

Query Match 97.7%; Score 443.5; DB 3; Length 87;

Best Local Similarity 98.9%; Pred. No. 9,6e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNNRNLADA 60
Db 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNNRNLADA 60

Qy 61 RARKYLQOQMERFLFEDGTVEAOG-VP 86
Db 61 RARKYLQOQMERFLFEDGTVEAOG-VP 87

RESULT 4

US-09-955-502-29
Sequence 29, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia mallei
US-09-955-502-29

Query Match 62.2%; Score 282.5; DB 3; Length 87;
Best Local Similarity 56.3%; Pred. No. 5,5e-25;
Matches 49; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

Qy 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNNRNLADA 60
Db 1 MARMTHCKLDKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNNRNLADA 60

Qy 61 RARKYLQOQMERFLFEDGTVEAOG-VP 86
Db 61 RARKYLQOQMERFLFEDGTVEAOG-VP 87

RESULT 5

US-09-955-502-30
Sequence 30, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

Query Match 62.2%; Score 282.5; DB 3; Length 87;
Best Local Similarity 56.3%; Pred. No. 5,5e-25;
Matches 49; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using SW model

Run on: March 1, 2006, 00:02:41 ; Search time 5.85698 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502a-4

Perfect score: 454
Sequence: 1 MSRLVNCVKLRRAEGLDFP.....OOQMERFLFEDGTVEAGQVP 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA New:

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/BCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272.5	60.0	88	US-10-467-657-968	Sequence 968, App
2	70.5	15.5	200	US-10-793-626-1186	Sequence 1186, Ap
3	70.5	15.5	200	US-10-793-626-2390	Sequence 2390, Ap
4	67	14.8	1320	US-11-098-666-10831	Sequence 10831, A
5	64.5	14.2	567	US-11-033-039-1279	Sequence 1279, Ap
6	63.5	14.0	805	US-11-108-539-2	Sequence 2, Appli
7	62.5	13.8	483	US-11-137-465-40	Sequence 40, Appli
8	62.5	13.8	832	US-11-098-666-10182	Sequence 10182, A
9	61.5	13.5	623	US-11-072-512-3378	Sequence 3378, Ap
10	60	13.2	240	US-11-044-111-10	Sequence 10, Appli
11	59	13.0	226	US-11-072-512-3820	Sequence 3820, Ap
12	59	13.0	265	US-10-793-626-114	Sequence 114, App
13	59	13.0	371	US-11-072-512-3421	Sequence 3421, Ap
14	59	13.0	805	US-10-927-641-77	Sequence 77, Appli
15	58.5	12.9	625	US-11-072-512-3310	Sequence 3310, Ap
16	58	12.8	662	US-11-072-175-184	Sequence 184, App
17	58	12.8	919	US-10-821-234-951	Sequence 951, App
18	57.5	12.7	398	US-10-793-626-44	Sequence 44, Appli
19	57.5	12.7	897	US-10-821-234-1523	Sequence 1523, Ap
20	57.5	12.7	897	US-10-821-234-1523	Sequence 1523, Ap
21	57	12.6	212	US-11-044-111-6	Sequence 6, Appli
22	57	12.6	212	US-11-044-111-26	Sequence 26, Appli
23	57	12.6	239	US-11-044-111-5	Sequence 5, Appli
24	57	12.6	239	US-11-044-111-25	Sequence 25, Appli
25	57	12.6	240	US-11-044-111-9	Sequence 9, Appli

26	57	12.6	464	US-10-959-322-5	Sequence 5, Appli
27	57	12.6	809	US-11-072-512-3367	Sequence 3367, Ap
28	57	12.6	1056	US-11-044-111-22	Sequence 22, Appli
29	56	12.3	183	US-11-072-512-3180	Sequence 3180, Ap
30	56	12.3	1076	US-10-467-657-7916	Sequence 7916, Ap
31	55.5	12.2	563	US-11-040-218-23	Sequence 23, Appli
32	55.5	12.2	3353	US-11-037-243-64	Sequence 64, Appli
33	55	12.1	519	US-11-099-691-10	Sequence 10, Appli
34	55	12.1	702	US-11-072-512-2154	Sequence 2154, Ap
35	54.5	12.0	356	US-11-143-986-8	Sequence 8, Appli
36	54.5	12.0	356	US-11-143-986-9	Sequence 9, Appli
37	54.5	12.0	1190	US-11-043-889-20	Sequence 20, Appli
38	54.5	12.0	1275	US-10-724-598-49	Sequence 49, Appli
39	54.5	12.0	1340	US-11-070-575-6	Sequence 6, Appli
40	54.5	12.0	1344	US-11-091-643-20	Sequence 20, Appli
41	54.5	12.0	1659	US-11-072-175-205	Sequence 205, App
42	54	11.9	331	US-11-098-666-10431	Sequence 10431, A
43	53.5	11.8	372	US-10-467-657-2318	Sequence 2318, Ap
44	53.5	11.8	599	US-11-109-157A-3	Sequence 3, Appli
45	53.5	11.8	618	US-10-454-437-396	Sequence 396, App
46	53.5	11.8	1373	US-11-098-666-11150	Sequence 11150, A
47	53.5	11.8	1686	US-11-109-157A-1	Sequence 1, Appli
48	53.5	11.8	1686	US-11-226-701-2	Sequence 2, Appli
49	53.5	11.8	2250	US-10-922-232B-57	Sequence 57, Appli
50	53.5	11.8	2630	US-11-186-731-2	Sequence 2, Appli
51	53.5	11.8	4060	US-10-922-232B-55	Sequence 55, Appli
52	53.5	11.8	6738	US-10-922-232B-56	Sequence 56, Appli
53	53.5	11.8	7968	US-11-186-731-5	Sequence 5, Appli
54	53	11.7	104	US-11-120-308-74	Sequence 74, Appli
55	53	11.7	200	US-11-194-246-402	Sequence 402, App
56	53	11.7	342	US-11-156-084-25	Sequence 25, Appli
57	53	11.7	342	US-11-156-084-44	Sequence 44, Appli
58	53	11.7	369	US-11-156-084-45	Sequence 45, Appli
59	53	11.7	384	US-11-098-666-10752	Sequence 10752, A
60	53	11.7	453	US-11-072-512-3394	Sequence 3394, Ap
61	53	11.7	619	US-11-156-084-24	Sequence 24, Appli
62	53	11.7	784	US-10-517-939-324	Sequence 324, App
63	52.5	11.6	143	US-10-793-626-1714	Sequence 1714, Ap
64	52.5	11.6	237	US-11-044-111-11	Sequence 11, Appli
65	52.5	11.6	362	US-10-517-939-88	Sequence 88, Appli
66	52.5	11.6	471	US-10-770-726-8	Sequence 8, Appli
67	52.5	11.6	473	US-11-152-366-31	Sequence 31, Appli
68	52.5	11.6	473	US-11-152-366-32	Sequence 32, Appli
69	52.5	11.6	552	US-11-019-711-69	Sequence 69, Appli
70	52.5	11.6	694	US-11-072-512-2469	Sequence 2469, Ap
71	52.5	11.6	863	US-10-793-626-2010	Sequence 2010, Ap
72	52.5	11.6	1043	US-10-821-234-1055	Sequence 1055, Ap
73	52.5	11.6	2871	US-11-124-367A-264	Sequence 264, App
74	52	11.5	230	US-11-072-512-3602	Sequence 3602, Ap
75	52	11.5	274	US-10-467-657-706	Sequence 706, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
Sequence 968, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASTIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match
Best Local Similarity 59.8%; Pred. No. 4,6e-25;
Matches 52; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 1 MSRIIVCYKLRKREAGLDPPYPGELGTRIWQISKAEWEKQIQ-TRLVNNRNLADARAKY----- 60
DB 1 MARWVFCYKLNKAEAGMKFPLPNELGKRIFENVSOBAAWTRHQVTLINENRSLADP 60

QY 61 RAKTKLOOMERFLPEDGTVEAQ-VP 86
DB 61 RAREYLAQOMEQYFPGDADAVQGYVP 87

RESULT 2
US-10-793-626-1186
Sequence 1186, Application US/10793626
Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1186
LENGTH: 200
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1186

Query Match
Best Local Similarity 15.5%; Score 70.5; DB 6; Length 200;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;

QY 17 LDFP-PYBGLGTRIWQISKAEWEK--KQIQ-TRLVNNRNLADARAKY----- 65
DB 109 MDIPLYLENEL-----QDTVDEWVVYTSISIQIDRLMERNNLSLEDAAKAVYSQISIDK 163

QY 66 -----LQOOMERFLPEDGTVEAQ 83
DB 164 KSRMADHVIDNLGDKLEKQNLQKLEBEGYIQSE 198

RESULT 3
US-10-793-626-2390
Sequence 2390, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 2390
LENGTH: 200
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-2390

Query Match
Best Local Similarity 15.5%; Score 70.5; DB 6; Length 200;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;

QY 17 LDFP-PYBGLGTRIWQISKAEWEK--KQIQ-TRLVNNRNLADARAKY----- 65
DB 109 MDIPLYLENEL-----QDTVDEWVVYTSISIQIDRLMERNNLSLEDAAKAVYSQISIDK 163

QY 66 -----LQOOMERFLPEDGTVEAQ 83
DB 164 KSRMADHVIDNLGDKLEKQNLQKLEBEGYIQSE 198

RESULT 4
US-11-098-686-10831
Sequence 10831, Application US/11098686
Publication No. US20060024696A1

GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10831
LENGTH: 1320
TYPE: PRT
ORGANISM: Lawsonia intracellularis
US-11-098-686-10831

Query Match
Best Local Similarity 14.8%; Score 67; DB 7; Length 1320;
Matches 23; Conservative 11; Mismatches 25; Indels 14; Gaps 3;

QY 5 VNCYKLRKREAGLDPPYPGELGTRIWQISKAEWEKQIQ-TRLVNNRNLADARAKY----- 61
DB 217 INLESLSKSKRELQOOYTHLKKRLDIWHQ-----WEEWRLIQTRLEHLPPISASFPDQGA 271

QY 62 ARKYLQOOMERFL 74
DB 272 AR-----MERAL 278

RESULT 5
US-11-033-039-1279
Sequence 1279, Application US/11033039
Publication No. US2006002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: Patent In version 3.3

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OW protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 86.765 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502a-5

Perfect score: 482

Sequence: 1 MARVPCERLKOBAEGLDFO.....NLFEGKDVHIEGYTPPEAK 91

Scoring table: BLOSUM62
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Searched: 2443163 seqs, 439378781 residues

2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
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7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	482	100.0	91	5	ABB78150 Amino aci
2	434	90.0	87	5	ABB78152 Amino aci
3	425	88.2	87	5	ABB78151 Amino aci
4	412	85.5	87	5	ABB78153 Amino aci
5	399	82.8	90	5	ABB78155 Amino aci
6	388	80.5	91	5	ABB78158 Amino aci
7	388	80.5	91	5	ABB78157 Amino aci
8	388	80.5	91	5	ABB78156 Amino aci
9	383	79.5	91	5	ABB78161 Amino aci
10	383	79.5	91	5	ABB78159 Amino aci
11	383	79.5	91	5	ABB78162 Amino aci
12	380	78.8	107	7	ABO65445 K1ebd1e11
13	378	78.4	88	5	ABB78160 Amino aci
14	377	78.2	93	7	ADFO5158 Bacterial
15	369.5	76.7	91	5	ABB78163 Amino aci
16	357	74.1	90	5	ABB78165 Amino aci
17	344	71.4	88	5	ABB78154 Amino aci
18	316	65.6	78	5	ABB78164 Amino aci
19	260	53.9	87	5	ABB78148 Amino aci
20	260	53.9	87	5	ABB78147 Amino aci
21	246	51.0	76	5	ABB78166 Amino aci
22	246	51.0	86	5	ABB78149 Amino aci
23	244	50.6	122	7	ABO74609 Pseudomon
24	244	50.2	87	5	ABB78175 Amino aci

25	239	49.6	90	5	ABB78168 Amino aci
26	236.5	49.1	89	9	ABE41576 L. pneumo
27	236.5	49.1	95	9	ABE38294 L. pneumo
28	236	49.0	87	5	ABB78174 Amino aci
29	233	48.3	87	5	ABB78170 Amino aci
30	230	47.7	88	5	ABB78178 Amino aci
31	228	47.3	87	5	ABB78169 Amino aci
32	228	47.3	88	5	ABB78171 Amino aci
33	228	47.3	88	5	ABB78172 Amino aci
34	228	47.3	88	5	ABB78173 Amino aci
35	228	47.3	88	5	ABP77219 N. gonorr
36	224.5	46.6	90	5	ABB78167 Amino aci
37	223	46.3	87	5	ABB78177 Amino aci
38	215.5	44.7	92	6	ADA34169 Acinetoba
39	208	43.2	87	5	ABB78176 Amino aci
40	161	33.4	110	8	ADLO5173 M. catarr
41	161	33.4	110	8	ADLO5173 M. catarr
42	161	33.4	110	8	ADLO5173 M. catarr
43	161	33.4	110	8	ADLO5173 M. catarr
44	161	33.4	110	8	ADLO5173 M. catarr
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53	161	33.4	110	8	ADLO5173 M. catarr
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55	161	33.4	110	8	ADLO5173 M. catarr
56	161	33.4	110	8	ADLO5173 M. catarr
57	161	33.4	110	8	ADLO5173 M. catarr
58	161	33.4	110	8	ADLO5173 M. catarr
59	161	33.4	110	8	ADLO5173 M. catarr
60	161	33.4	110	8	ADLO5173 M. catarr
61	161	33.4	110	8	ADLO5173 M. catarr
62	161	33.4	110	8	ADLO5173 M. catarr
63	161	33.4	110	8	ADLO5173 M. catarr
64	161	33.4	110	8	ADLO5173 M. catarr
65	161	33.4	110	8	ADLO5173 M. catarr
66	161	33.4	110	8	ADLO5173 M. catarr
67	161	33.4	110	8	ADLO5173 M. catarr
68	161	33.4	110	8	ADLO5173 M. catarr
69	161	33.4	110	8	ADLO5173 M. catarr
70	161	33.4	110	8	ADLO5173 M. catarr
71	161	33.4	110	8	ADLO5173 M. catarr
72	161	33.4	110	8	ADLO5173 M. catarr
73	161	33.4	110	8	ADLO5173 M. catarr
74	161	33.4	110	8	ADLO5173 M. catarr
75	161	33.4	110	8	ADLO5173 M. catarr

ALIGNMENTS

RESULT 1	ABB78150	standard; protein; 91 AA.
ID	ABB78150;	
XX	05-NOV-2002	(first entry)
XX	Amino acid sequence of a YggX homologue.	
XX	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
XX	hydroxyl radical; DNA damage; YggX homologue.	
XX	Unidentified.	
XX	US2002072118-A1.	

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from *Salmonella*
XX *enterica* serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
XX Sequence 91 AA;
XX
XX

Query Match 100.0%; Score 482; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARWVFCERLKOBAEGDLPOLYPGELGKRIFPSISKQAMGEMMKQTMLVNEKLLMMNNA 60
DB 1 MARWVFCERLKOBAEGDLPOLYPGELGKRIFPSISKQAMGEMMKQTMLVNEKLLMMNNA 60

QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYTPPEAK 91
DB 61 EHRKLLBQEMVNFLEFGKDVHIEGYTPPEAK 91

RESULT 2
ABB78152
ID ABB78152 standard; protein; 87 AA.

AC ABB78152;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.

OS Haemophilus influenzae.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from *Salmonella*
XX *enterica* serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
XX Sequence 87 AA;
XX
XX

Query Match 90.0%; Score 434; DB 5; Length 87;
Best Local Similarity 93.1%; Pred. No. 7.2e-44;
Matches 81; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MARWVFCERLKOBAEGDLPOLYPGELGKRIFPSISKQAMGEMMKQTMLVNEKLLMMNNA 60
DB 1 MARWVFCERLKOBAEGDLPOLYPGELGKRIFPSISKQAMGEMMKQTMLVNEKLLMMNNA 60

QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYTP 87
DB 61 EHRKLLBQEMVNFLEFGKDVHIEGYTP 87

RESULT 3
ABB78151
ID ABB78151 standard; protein; 87 AA.

AC ABB78151;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.

OS *Pasteurella multocida*.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from *Salmonella enterica* Serovar Typhimurium.

XX Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from *Salmonella*

hypothetical prote
WD-40 repeat prote
hypothetical prote
hypothetical prote

Query Match	91.5%;	Score 441;	DB 2;	Length 90;
Best Local Similarity	93.2%;	Pred. No. 4.8e-37;		

1 MAR/VFCERLKQEAEGUDF VUIFGSECCV...

61 EHRKLEQEMVNFLECKEVIHIEGYIPEDN

61 EHRKLEQEMVNFLECKEVIHIEGYIPEDN

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 83.6663 Seconds

(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502a-5

Perfect score: 482
Sequence: 1 MARVFCRLKQBAEGLDFQ.....NFLPBGKDVHIGYTPPEAK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Uniprot_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	441	91.5	90	1	P44048 haemophilus
2	441	91.5	90	2	Q4QMD9 HAEB18
3	432	89.6	90	1	PERP_PASMG
4	429	89.0	91	1	PERP_MANSW
5	412	85.5	94	1	PERP_HABDU
6	402	83.4	90	1	PERP_VIBPA
7	400	83.0	90	1	PERP_VIBVU
8	400	83.0	90	1	PERP_VIBCH
9	399	82.8	90	1	PERP_VIBCH
10	392	81.3	90	1	PERP_PROPR
11	383	79.5	90	1	PERP_ECO57
12	383	79.5	90	1	PERP_ECOLI
13	383	79.5	90	1	PERP_SHIFL
14	379	78.6	90	1	PERP_ECOL6
15	378	78.4	90	1	PERP_SALCH
16	378	78.4	90	1	PERP_SALPA
17	378	78.4	90	1	PERP_SALTI
18	378	78.4	90	1	PERP_SALTY
19	374	77.6	90	1	PERP_VIBF1
20	365	75.7	90	1	PERP_YERPS
21	360	74.7	90	1	PERP_YERWT
22	357	74.1	90	1	PERP_PHOIL
23	357	74.1	90	1	PERP_YERPE
24	344	71.4	92	1	PERP_SHEON
25	340	70.5	90	1	PERP_IDILO
26	271	56.2	90	1	PERP_BORBR
27	271	56.2	90	1	PERP_BORPA
28	271	56.2	90	1	PERP_BORPE
29	249	51.7	90	1	PERP_NITRU
30	249	51.7	91	1	PERP_BURMA
31	249	51.7	91	1	PERP_BURPS

32	246	51.0	77	1	PERP_BUCAL	P57618 buchnera ap
33	244	50.6	90	1	PERP_PSEAE	Q9H336 pseudomonas
34	242	50.2	90	1	PERP_XYLPF	Q87406 xylella fas
35	240.5	49.9	89	1	PERP_LEGPI	Q5WVC4 legionella
36	240	49.8	90	2	Q4J228 AZOVI	Q4J228 azotobacter
37	240	49.8	91	1	PERP_RALSO	Q8Y010 ralstonia s
38	239	49.6	90	1	PERP_PSEEM	Q87015 pseudomonas
39	239	49.6	90	2	Q4ZLP3_PSEESY	Q4ZLP3 pseudomonas
40	239	49.6	91	2	Q4LS19_9BURK	Q4LS19 burkholderi
41	238	49.4	90	1	PERP_XYLPF	Q9PC73 xylella fas
42	236.5	49.1	89	1	PERP_LEGPA	Q5X3X9 legionella
43	236.5	49.1	89	1	PERP_LEGPA	Q5X3X9 legionella
44	235	48.8	90	1	PERP_PSEEP	Q5X380 legionella
45	234	48.5	90	2	Q6T7F6_PSEFTL	Q6T7F6 pseudomonas
46	232	48.1	91	1	PERP_XANAC	Q6P1H7 xanthomonas
47	231	47.9	90	1	PERP_METCA	Q606J7 methylococc
48	230	47.7	90	1	PERP_COXRU	Q83066 coxiella bu
49	228	47.3	88	1	PERP_NEIGI	Q5E3S3 neisseria bu
50	228	47.3	88	1	PERP_NEIMA	Q5E3S3 neisseria g
51	228	47.3	88	1	PERP_NEIMA	Q5E3S3 neisseria m
52	227	46.7	92	1	PERP_XANOR	Q5GY22 xanthomonas
53	225	46.7	78	1	PERP_WIGBR	Q8D3C5 wigglewort
54	225	46.7	90	2	Q4KJ12_PSEFS	Q4KJ12 pseudomonas
55	224	46.5	90	1	PERP_CHRVO	Q7A614 chromobacte
56	223	46.3	92	1	PERP_XANCP	Q8P829 xanthomonas
57	223	46.3	92	2	Q4UM14_XANCP	Q4UM14 xanthomonas
58	222.5	46.2	90	1	PERP_ACIAD	Q6FFD3 acinetobact
59	207	42.9	78	1	PERP_BUCAP	Q8K825 buchnera ap
60	202	41.9	79	1	PERP_CANBP	Q7V9G9 candidatus
61	202	41.9	87	1	PERP_BUCBP	Q89644 buchnera ap
62	202	41.9	87	1	PERP_FRATY	Q5N3J8 francisella
63	176	36.5	92	2	Q4NMQ4_9BELT	Q4NMQ4 anaeromyxob
64	152	31.5	96	2	Q4FVJ7_9GAMT	Q4FVJ7 psychrobact
65	86	17.8	2248	2	Q4UB40_THRAN	Q4UB40 theileria a
66	85	17.6	2249	2	Q4UMT4_THRPA	Q4UMT4 theileria p
67	77.5	16.1	187	2	Q9HBF7_HUMAN	Q9HBF7 homo sapien
68	77.5	16.1	218	2	Q7SPV9_9BETR	Q7SPV9 human betar
69	77.5	16.1	281	2	Q6PG71_MOUSE	Q6PG71 mus musculu
70	77.5	16.1	372	2	Q85648_9BETR	Q85648 mouse mamma
71	77.5	16.1	452	2	Q7SPV8_9BETR	Q7SPV8 human betar
72	77.5	16.1	590	1	GAG_MMTVC	P10258 mouse mamma
73	77.5	16.1	590	1	GAG_MMTVC	P11284 mouse mamma
74	77.5	16.1	591	2	Q83391_9BETR	Q83391 mouse mamma
75	77.5	16.1	591	2	Q9J2T6_9BETR	Q9J2T6 exogenous m

ALIGNMENTS

RESULT 1

ID: PERP_HABIN STANDARD; PRT; 90 AA.

AC P44048; PERP_HABIN
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Pe(2+) trafficking protein.
GN Ordered locus names: H10760;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellales; Haemophilus.
RN NCBI_TaxID=727;
RX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=rd / KW20 / ATCC 51907;
RC MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weiman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.; and
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 [2]
 RP IDENTIFICATION BY MASS SPECTROMETRY.
 RX MEDLINE=20137468; PubMed=10675023;
 RX DOI=10.1002/(SICI)1522-2683(20000101)21:2<411::AID-ELBS411>3.3.CO;2-W;
 RA Langen H., Takace B., Evers S., Berndt P., Lahm H.W., Wlft B.,
 RA Gray C., Fountoulakis M.;
 RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
 RL Electrophoresis 21:411-429(2000).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: U32760; AAC22419.1; -; Genomic_DNA.
 CC PIR: C64013; C64013.
 CC SMR: P44048; 1-87.
 CC TIGR: H10760; -.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; YggX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe traffic_YggX; 1.
 DR ProDom: PD029191; DUF495; 1.
 DR Complete proteome; Iron.
 SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;
 QY Query Match 91.5%; Score 441; DB 1; Length 90;
 DB Best Local Similarity 93.2%; Pred. No. 1.6e-37;
 DB Matches 82; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MARWPCERLKOBAEGLDFOLYPGELGKRIIPDSISKQAWGEMWKKQTMLVNEKKLNMNNA 60
 DB 1 MARWPCERLKOBAEGLDFOLYPGELGKRIIPDSISKQAWGEMWKKQTMLVNEKKLNMNNA 60
 QY 61 EHRKLLQEMWNVLPFGKDVHIEGYTP 88
 DB 61 EHRKLLQEMWNVLPFGKDVHIEGYTP 88
 RESULT 2
 Q4QMD9_HAE18 PRELIMINARY; PRT; 90 AA.
 ID Q4QMD9_HAE18 PRELIMINARY; PRT; 90 AA.
 AC Q4QMD9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=VTH10920;
 OS Haemophilus influenzae (strain 86-028NP).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OC NCBI_TaxID=281310;
 OK NCBI_TaxID=281310;
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
 RA Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
 RA Zhong H., Gibson J., Gibson M., Johnson L.S., Lewis L., Bakaletz L.O.,
 RA Munson R.S. Jr.;
 RT "Genomic sequence of an otitis media isolate of nontypeable
 RT Haemophilus influenzae: comparative study with H. influenzae serotype
 RT d, strain KM20.";
 RL J. Bacteriol. 187:4627-4636(2005).
 DR EMBL: CP000057; AA87808.1; -; Genomic_DNA.

DR InterPro: IPR007457; YggX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe traffic_YggX; 1.
 DR ProDom: PD029191; DUF495; 1.
 DR Complete proteome; Hypothetical protein.
 SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;
 QY Query Match 91.5%; Score 441; DB 2; Length 90;
 DB Best Local Similarity 93.2%; Pred. No. 1.6e-37;
 DB Matches 82; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MARWPCERLKOBAEGLDFOLYPGELGKRIIPDSISKQAWGEMWKKQTMLVNEKKLNMNNA 60
 DB 1 MARWPCERLKOBAEGLDFOLYPGELGKRIIPDSISKQAWGEMWKKQTMLVNEKKLNMNNA 60
 QY 61 EHRKLLQEMWNVLPFGKDVHIEGYTP 88
 DB 61 EHRKLLQEMWNVLPFGKDVHIEGYTP 88
 RESULT 3
 PIRP_PASMU STANDARD; PRT; 90 AA.
 ID PIRP_PASMU STANDARD; PRT; 90 AA.
 AC Q9CLB9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 GN OrderedLocustNames=PM1320;
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OK NCBI_TaxID=747;
 RN NCBI_TaxID=747;
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=PM70;
 RX MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittem T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida PM70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
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 CC removed.
 CC -----
 CC EMBL: AE06170; AA03404.1; -; Genomic_DNA.
 CC DR EMBL: AE06170; AA03404.1; -; Genomic_DNA.
 DR SMR: Q9CLB9; 1-87.
 DR HAMAP: MF_00686; -; 1.
 DR InterPro: IPR007457; YggX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe traffic_YggX; 1.
 DR ProDom: PD029191; DUF495; 1.
 DR Complete proteome; Iron.
 SQ SEQUENCE 90 AA; 10744 MW; B583448BAE0EDF7 CRC64;
 QY Query Match 89.6%; Score 432; DB 1; Length 90;
 DB Best Local Similarity 92.0%; Pred. No. 1.4e-36;
 DB Matches 81; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MARWPCERLKOBAEGLDFOLYPGELGKRIIPDSISKQAWGEMWKKQTMLVNEKKLNMNNA 60
 DB 1 MARWPCERLKOBAEGLDFOLYPGELGKRIIPDSISKQAWGEMWKKQTMLVNEKKLNMNNA 60
 QY 61 EHRKLLQEMWNVLPFGKDVHIEGYTP 88
 DB 61 EHRKLLQEMWNVLPFGKDVHIEGYTP 88
 DR EMBL: CP000057; AA87808.1; -; Genomic_DNA.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 21.2781 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502a-5

Perfect score: 482
Sequence: 1 MARWVFCRLKQKAGLDFO.....NFLPEGKVHLEGTTPPEAK 91

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCUTS-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	380	78.8	107	2	US-09-489-039A-11962
2	377	78.2	93	2	US-09-543-681A-5443
3	244	50.6	122	2	US-09-252-991A-23355
4	215.5	44.7	92	2	US-09-328-352-5456
5	161	33.4	110	2	US-09-540-236-2859
6	77.5	16.1	591	2	US-09-370-368-8
7	72	14.9	217	2	US-09-543-681A-7862
8	70	14.5	474	2	US-09-252-991A-24473
9	67.5	14.0	177	2	US-08-647-960-6
10	67.5	14.0	579	2	US-09-949-016-10483
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17	67	13.9	2101	2	US-09-452-294-1
18	67	13.9	2101	2	US-09-296-662-32
19	67	13.9	2101	4	PCT-US93-06160-4
20	67	13.9	2107	2	US-09-949-016-7647
21	67	13.9	2107	2	US-09-949-016-7647
22	67	13.9	2115	2	US-09-296-662-33
23	66	13.7	292	2	US-09-328-352-5836
24	66	13.7	680	2	US-09-298-924-4
25	66	13.7	720	1	US-08-840-236-1
26	66	13.7	720	1	US-08-505-448A-1
27	65.5	13.6	455	2	US-09-270-767-45790

ALIGNMENTS

28	65.5	13.6	644	2	US-08-793-331-7	Sequence 7, Appli
29	65.5	13.6	959	2	US-09-543-681A-6879	Sequence 6879, Ap
30	65	13.5	280	2	US-09-323-998E-37	Sequence 37, Appl
31	65	13.5	1401	2	US-09-750-590A-2	Sequence 2, Appli
32	64	13.3	361	2	US-09-328-352-7863	Sequence 7863, Ap
33	63.5	13.2	623	2	US-10-104-047-2547	Sequence 2547, Ap
34	63	13.1	116	2	US-09-562-737-125	Sequence 125, App
35	63	13.1	586	2	US-09-270-767-44373	Sequence 44373, A
36	63	13.1	1695	2	US-08-866-108A-15753	Sequence 15753, A
37	62.5	13.0	271	2	US-09-248-796A-19265	Sequence 19265, A
38	62.5	13.0	1354	2	US-08-685-871-2	Sequence 2, Appli
39	62	12.9	168	2	US-09-107-532A-17800	Sequence 4480, Ap
40	62	12.9	191	1	US-08-468-576B-13	Sequence 13, Appl
41	62	12.9	191	1	US-08-468-579B-13	Sequence 13, Appl
42	62	12.9	191	1	US-08-468-577B-13	Sequence 13, Appl
43	62	12.9	364	2	US-09-328-352-4659	Sequence 4659, Ap
44	62	12.9	482	2	US-09-248-796A-17800	Sequence 17800, A
45	62	12.9	550	2	US-09-107-532A-17201	Sequence 7201, Ap
46	62	12.9	1581	2	US-09-866-108A-15754	Sequence 15754, A
47	61.5	12.8	656	2	US-09-949-016-7320	Sequence 7320, Ap
48	61.5	12.8	666	2	US-09-270-767-62249	Sequence 62249, A
49	61.5	12.8	721	2	US-09-270-767-46645	Sequence 46645, A
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51	61	12.7	501	2	US-09-640-211A-1027	Sequence 1027, Ap
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53	61	12.7	633	2	US-09-328-352-6519	Sequence 6519, Ap
54	61	12.7	674	2	US-08-961-083-200	Sequence 200, App
55	61	12.7	674	2	US-09-536-784-200	Sequence 200, App
56	61	12.7	674	2	US-09-765-271-200	Sequence 200, App
57	61	12.7	674	2	US-09-765-272A-200	Sequence 200, App
58	61	12.7	922	2	US-09-328-352-5283	Sequence 5283, Ap
59	61	12.7	1129	2	US-08-904-871-11	Sequence 11, Appl
60	61	12.7	1129	2	US-10-134-500-2	Sequence 2, Appli
61	61	12.7	1761	2	US-09-561-709B-1	Sequence 1, Appli
62	60.5	12.6	415	1	US-08-602-010A-10	Sequence 10, Appl
63	60.5	12.6	415	1	US-08-680-766A-10	Sequence 10, Appl
64	60.5	12.6	415	2	US-09-092-409-10	Sequence 10, Appl
65	60.5	12.6	525	2	US-09-540-236-2250	Sequence 2250, Ap
66	60.5	12.6	601	2	US-09-489-039A-8499	Sequence 8499, Ap
67	60.5	12.6	1284	2	US-10-296-144-5	Sequence 5, Appli
68	60.5	12.6	2285	2	US-09-308-375-2	Sequence 2, Appli
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75	60	12.4	279	2	US-09-198-452A-221	Sequence 221, App

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 610835
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity	76.4%	Pred. No. 1.5e-40;		
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Db 17 MSRTFCTFLQREADGDQLPGELGRIFYNLSKSAAWQHKKQTMLINEKSLSMNP 76

Qy	61	EHRKLLQEMVNF	LPFGKDVHIEG	TPPE	89
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RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: prt
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Query Match	78.2%;	Score 377;	DB 2;	Length 93;
Best Local Similarity	76.4%;	Pred. No. 3e-40;		
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				Gaps 0

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Db      4 MSRTIFCTPLNKADAGDLPOLYPBELGKRIFNEISKEAQCMMATQTMLINEKCLTNMP   63
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QY      61 EHRKLLQEEMVNFLEFGKDVHIEGYTPRE 89
      : ||||| ||||| ||||| : |||||
DB      64 DDRKLLQEEMVNFLEFGKDVHIDGYTPRE 92
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US-09-252-991A-23355
; RESULT 3
; US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: prf
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Query Match	50.6%;	Score 244;	DB 2;	Length 122;
Best Local Similarity	51.6%;	Pred. No. 3.4e-23;		
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Db 33 MSKRVQMRKCKHEELPGIDRPYPFGANGEDIIYNNVSKRANDEWQKQITMLINERLRNMA 92

Qy 61 EHRKILEQEMVNFLEFGKD-VHIEGYTPPEA 90

Db 93 EDRKFTLEQEMDKFL-SGEDYAKADGYTPPEA 122

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RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: prf
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Query Match	44.7%	Score 215.5;	DB 2;	Length 92;
Best Local Similarity	44.3%;	Pred. No. 1e-19;		
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Qy 61 EHRKLLIEQEMVNFLEFGKDVH-IEGYTP 87
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Db 64 EAKGFLIEQREKEFTNNDSEVEKAEGWKP 91

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RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PR1
; ORGANISM: M.catarhalis
US-09-540-236-2859

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Query Match	33.4%	Score 161;	DB 2;	Length 110;
Best Local Similarity	37.9%	Pred. No. 1.1e-12;		
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Db      24  MFCRKYQONLPKLPNPPRNNAKQOEIQTTISAKMMNANWELQTMILINEKRLSMIDPOAK 83

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QY 64 KLEQEMVNFLEGGKDVHIEGYTPPEA 90
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Db 84 KYLNEGQREKFLDNGEDYEKAPGYKPLKA 110

RESULT 6
US-09-370-368-8
; Sequence 8, Application US/09370368

GenCore version 5.1.7
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Run on: March 1, 2006, 00:01:31 / Search time 69.2055 Seconds

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549.414 Million cell updates/sec

Title: US-09-955-502a-5

Perfect score: 482

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Post-processing: Minimum Match 0%

Database: Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	412	85.5	87	US-09-955-502-8	Sequence 8, Appl
5	399	82.8	90	US-09-955-502-10	Sequence 10, Appl
6	388	80.5	91	US-09-955-502-11	Sequence 11, Appl
7	388	80.5	91	US-09-955-502-12	Sequence 12, Appl
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10	383	79.5	91	US-09-955-502-16	Sequence 16, Appl
11	383	79.5	91	US-09-955-502-17	Sequence 17, Appl
12	378	78.4	88	US-09-955-502-15	Sequence 15, Appl
13	369.5	76.7	91	US-09-955-502-18	Sequence 18, Appl
14	357	74.1	90	US-09-955-502-20	Sequence 20, Appl
15	344	71.4	88	US-09-955-502-9	Sequence 9, Appl
16	316	65.6	78	US-09-955-502-19	Sequence 19, Appl
17	260	53.9	87	US-09-955-502-2	Sequence 2, Appl
18	260	53.9	87	US-09-955-502-3	Sequence 3, Appl
19	246	51.0	76	US-09-955-502-21	Sequence 21, Appl
20	246	51.0	86	US-09-955-502-4	Sequence 4, Appl
21	242	50.2	87	US-09-955-502-29	Sequence 29, Appl
22	242	50.2	87	US-09-955-502-30	Sequence 30, Appl
23	239	49.6	90	US-09-955-502-23	Sequence 23, Appl
24	234	48.5	89	US-09-955-502-22	Sequence 22, Appl
25	233	48.3	87	US-09-955-502-25	Sequence 25, Appl
26	230	47.7	88	US-09-955-502-33	Sequence 33, Appl
27	228	47.3	87	US-09-955-502-24	Sequence 24, Appl

ALIGNMENTS

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30	228	47.3	88	3	US-09-955-502-28	Sequence 28, Appl
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42	68	14.1	283	4	US-10-425-114-68519	Sequence 68519, A
43	68	14.1	284	4	US-10-425-115-278111	Sequence 278111, A
44	68	14.1	481	5	US-10-732-923-982	Sequence 982, App
45	68	14.1	1086	4	US-10-437-963-189070	Sequence 189070, A
46	67.5	14.0	325	4	US-10-369-493-18793	Sequence 18793, A
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52	67	13.9	2101	5	US-10-977-955-32	Sequence 32, Appl
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54	67	13.9	2115	5	US-10-977-955-33	Sequence 33, Appl
55	66.5	13.8	320	4	US-10-282-122A-6765	Sequence 46765, A
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57	66.5	13.8	723	4	US-10-231-913-119	Sequence 139, App
58	66.5	13.8	723	4	US-10-231-913-140	Sequence 140, App
59	66.5	13.8	723	4	US-10-342-844-22	Sequence 22, Appl
60	66.5	13.8	723	4	US-10-342-844-26	Sequence 26, Appl
61	66	13.7	680	4	US-10-688-276-4	Sequence 4, Appl
62	66	13.7	720	3	US-09-419-305-1	Sequence 1, Appl
63	66	13.7	1129	5	US-10-732-923-12553	Sequence 12553, A
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RESULT 1
US-09-955-502-5
Sequence 5, Application US/09955502
Patent No. US3002072118A1
GENERAL INFORMATION:
APPLICANT: Down, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 91
TYPE: PRT
ORGANISM: Actinobacillus actinomycetemcomitans

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Best Local Similarity	81.8%	Pred. No. 1.5e-37;		
Matches	72;	Conservative	9;	Mismatches 7;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Title: US-09-955-502a-5

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SUMMARIES

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3	67	13.9	2101	US-10-857-780-23	Sequence 23, App
4	64	13.3	834	US-10-453-372-658	Sequence 658, App
5	63.5	13.2	623	US-11-072-512-2547	Sequence 2547, App
6	62	12.9	336	US-10-453-372-640	Sequence 640, App
7	62	12.9	793	US-10-995-561-925	Sequence 925, App
8	62	12.9	804	US-10-453-372-650	Sequence 650, App
9	62	12.9	847	US-10-453-372-654	Sequence 654, App
10	62	12.9	857	US-10-453-372-652	Sequence 652, App
11	62	12.9	905	US-10-453-372-638	Sequence 638, App
12	62	12.9	905	US-10-453-372-664	Sequence 664, App
13	62	12.9	905	US-10-453-372-664	Sequence 664, App
14	62	12.9	963	US-10-995-561-923	Sequence 923, App
15	62	12.9	963	US-10-453-372-660	Sequence 660, App
16	62	12.9	1012	US-10-453-372-646	Sequence 646, App
17	61.5	12.8	455	US-10-714-887-212	Sequence 212, App
18	60	12.4	583	US-11-080-991-64	Sequence 64, App
19	59	12.2	177	US-10-467-657-1658	Sequence 1658, App
20	59	12.2	342	US-11-156-084-25	Sequence 25, App
21	59	12.2	342	US-11-156-084-45	Sequence 44, App
22	59	12.2	369	US-11-156-084-45	Sequence 44, App
23	59	12.2	619	US-11-156-084-24	Sequence 24, App
24	59	12.2	695	US-10-453-372-648	Sequence 648, App
25	59	12.2	700	US-10-995-561-922	Sequence 922, App

26 59 12.2 700 6 US-10-995-561-924 Sequence 924, App

27 59 12.2 775 6 US-10-453-372-656 Sequence 656, App

28 58.5 12.1 465 6 US-10-873-528-164 Sequence 164, App

29 58.5 12.1 577 7 US-11-072-175-187 Sequence 187, App

30 58 12.0 296 7 US-11-087-227-10 Sequence 10, App

31 58 12.0 359 7 US-11-087-227-8 Sequence 8, App

32 58 12.0 359 7 US-11-192-450-6 Sequence 6, App

33 58 12.0 404 7 US-11-087-227-6 Sequence 6, App

34 58 12.0 404 7 US-11-192-450-3 Sequence 3, App

35 58 12.0 504 7 US-11-072-512-3467 Sequence 3467, App

36 57.5 11.9 285 6 US-10-467-657-222 Sequence 222, App

37 57.5 11.9 389 6 US-10-467-657-8230 Sequence 8230, App

38 57.5 11.9 245 7 US-11-098-686-10115 Sequence 10115, App

39 57.5 11.9 3803 6 US-10-995-561-773 Sequence 773, App

40 57.5 11.9 3960 6 US-10-995-561-771 Sequence 771, App

41 57.5 11.9 5335 6 US-10-995-561-777 Sequence 777, App

42 57.5 11.9 5406 6 US-10-995-561-774 Sequence 774, App

43 57.5 11.9 5415 6 US-10-995-561-779 Sequence 779, App

44 57.5 11.9 5464 6 US-10-995-561-775 Sequence 775, App

45 57.5 11.9 5935 6 US-10-995-561-776 Sequence 776, App

46 57 11.8 139 6 US-10-793-626-1310 Sequence 1310, App

47 57 11.8 319 6 US-10-793-626-2760 Sequence 2760, App

48 56.5 11.7 261 6 US-10-467-657-5896 Sequence 5896, App

49 56.5 11.7 299 7 US-11-156-084-288 Sequence 288, App

50 56.5 11.7 674 7 US-11-000-463-471 Sequence 471, App

51 56.5 11.7 782 6 US-10-793-626-2352 Sequence 2352, App

52 56 11.6 175 6 US-10-821-224-1522 Sequence 1522, App

53 56 11.6 234 6 US-10-524-647-120 Sequence 120, App

54 56 11.6 234 6 US-10-524-972-108 Sequence 108, App

55 56 11.6 246 6 US-10-131-826A-436 Sequence 436, App

56 56 11.6 246 7 US-11-240-769-57 Sequence 57, App

57 56 11.6 254 7 US-11-072-512-1198 Sequence 1198, App

58 56 11.6 384 6 US-10-467-657-2024 Sequence 2024, App

59 56 11.6 560 7 US-11-131-479-16 Sequence 16, App

60 55.5 11.5 349 6 US-10-821-234-1387 Sequence 1387, App

61 55.5 11.5 451 7 US-11-072-512-2877 Sequence 2877, App

62 55.5 11.5 397 7 US-11-010-239-85 Sequence 85, App

63 55.5 11.5 1188 7 US-11-115-639-43 Sequence 43, App

64 55.5 11.5 1188 7 US-11-115-639-43 Sequence 43, App

65 55 11.4 266 5 US-09-995-493-6 Sequence 266, App

66 55 11.4 611 6 US-10-793-626-2586 Sequence 2586, App

67 55 11.4 619 7 US-11-072-512-2472 Sequence 2472, App

68 55 11.4 724 7 US-11-126-313-28 Sequence 28, App

69 55 11.4 1219 7 US-11-032-236-4 Sequence 4, App

70 54.5 11.3 165 7 US-11-098-686-10784 Sequence 10784, App

71 54.5 11.3 268 6 US-10-995-561-718 Sequence 718, App

72 54.5 11.3 355 6 US-10-995-561-720 Sequence 720, App

73 54.5 11.3 524 6 US-10-507-106-4 Sequence 4, App

74 54.5 11.3 729 6 US-10-511-538-101 Sequence 101, App

75 54.5 11.3 774 7 US-11-070-627-7 Sequence 7, App

ALIGNMENTS

RESULT 1

US-10-467-657-968

Sequence 968, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

APPLICANT: FORTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SeqWIn9, version 1.04

Wed Mar 1 09:16:00 2006

us-09-955-502a-5.rapbn

Page 2

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 47.3%; Score 228; DB 6; Length 88;
Best Local Similarity 47.7%; Pred. No. 1e-19;
Matches 42; Conservative 20; Mismatches 24; Indels 2; Gaps 2;

QY 1 MAMVFCERIKQAGLDPOLYRGELGKRTFDSISQAMGEMKKQTMVNEKKLMMNNA 60
DB 1 MAMVFCVKINKAEKGGKPPPLNELGKRTFENVSDQAMAAWTRHQMLINERLSTADP 60

QY 61 EHRKLEQEMVNFLE-EGKDVHIEGYTP 87
DB 61 RAREYLAQMEQYFFGSDADA-VQGYVP 87

RESULT 2
US-11-194-246-317
Sequence 317, Application US/11194246
Publication No. US2005027089A1
GENERAL INFORMATION:
APPLICANT: Mott, John
APPLICANT: Treppod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
FILE REFERENCE: 00592.US1 (MER 268.05920101)
CURRENT FILING DATE: 2005-08-01
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 14.1%; Score 68; DB 7; Length 593;
Best Local Similarity 46.7%; Pred. No. 3.6;
Matches 14; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 32 DSISQAMGEMKKQTMVNEKKLMMNNAE 61
DB 293 ESKSKQEMRYEAKQDILKNTKLTALSKS 322

RESULT 3
US-10-857-780-23
Sequence 23, Application US/10857780
Publication No. US20050272043A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOTAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
FILE REFERENCE: SEQ-4069-CP
CURRENT FILING DATE: 2004-05-28
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24

PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 2101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-857-780-23

Query Match 13.9%; Score 67; DB 6; Length 2101;
Best Local Similarity 24.1%; Pred. No. 23;
Matches 27; Conservative 26; Mismatches 27; Indels 32; Gaps 7;

QY 7 CERIKQAGLDPOLYRGELGKRTFDSISK-----QAMGEMKK 45
DB 299 CQDLTKERKQMDKINQSLSENGDLSFKLRFPASHQLOQDALNELTEHSKRTQEWLEK 358

QY 46 QTMVNEKKLMMNNAEHRKLEQEMVNFLEEGKDVHIEGY-----TPPEAK 91
DB 359 QAQI--EKELSA--LQDKKLEK--NEIYQKLSQLEHTLSQLDNPPQEK 405

RESULT 4
US-10-453-372-658
Sequence 658, Application US/10453372
Publication No. US2006003323A1
GENERAL INFORMATION:
APPLICANT: Alsebrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-589 A
CURRENT FILING DATE: 2003-06-03
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/823187
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeq1et version 0.1
SEQ ID NO 658
LENGTH: 834
TYPE: PRT
ORGANISM: Homo sapiens
US-10-453-372-658

Query Match 13.3%; Score 64; DB 6; Length 834;
Best Local Similarity 32.7%; Pred. No. 16;
Matches 17; Conservative 7; Mismatches 22; Indels 6; Gaps 2;

QY 39 WGEEMKKQTMVNEKKLMMNNAEHRKLEQEMVNFLEEGKDVHIEGYTPPEA 90
DB 719 WRNKRK-----NTKSNMFPANPVYRKTTEBEDDELHIGTAQI--GHVYPA 764

RESULT 5
US-11-072-512-2547


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PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnack JA;
PI
XX WPI, 2002-589476/63.
DR
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PR protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from Salmonella
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX
XX Sequence 87 AA;
SQ
Query Match 100.0%; Score 462; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.9e-48;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARTVFCETLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTLVNEKLLMMNNA 60
DB 1 MARTVFCETLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTLVNEKLLMMNNA 60
QY 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
DB 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
RESULT 2
ID ABB78152 standard; protein; 87 AA.
XX
XX ABB78152;
AC
XX
XX 05-NOV-2002 (first entry)
DT
XX
XX Amino acid sequence of a YgX homologue.
DE
XX
XX Superoxide damage; cell; YgX; Salmonella enterica serovar Typhimurium;
KW hydroxyl radical; DNA damage; YgX homologue.
XX
XX Haemophilus influenzae.
OS
XX
XX US2002072118-A1.
PN
XX
XX 13-JUN-2002.
PD
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnack JA;
PI
XX

```

```

DR WPI, 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PR protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from Salmonella
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX
XX Sequence 87 AA;
SQ
Query Match 94.2%; Score 435; DB 5; Length 87;
Best Local Similarity 92.0%; Pred. No. 7.6e-45;
Matches 80; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 MARTVFCETLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTLVNEKLLMMNNA 60
DB 1 MARTVFCETLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTLVNEKLLMMNNA 60
QY 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
DB 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87

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RESULT 3
ID ABB78150 standard; protein; 91 AA.
XX
XX ABB78150;
AC
XX
XX 05-NOV-2002 (first entry)
DT
XX
XX Amino acid sequence of a YgX homologue.
DE
XX
XX Superoxide damage; cell; YgX; Salmonella enterica serovar Typhimurium;
KW hydroxyl radical; DNA damage; YgX homologue.
XX
XX Unidentified.
OS
XX
XX US2002072118-A1.
PN
XX
XX 13-JUN-2002.
PD
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnack JA;
PI
XX
XX WPI, 2002-589476/63.
DR
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PR protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from Salmonella

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-6

Perfect score: 462

Sequence: 1 MARYFCSEYLKQSEGLDFQ.....QEMVNFPEKGVHTEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435	94.2	90	2 C64013	hypothetical prote
2	379	82.0	91	2 A85954	hypothetical prote
3	379	82.0	91	2 A65082	hypothetical prote
4	379	82.0	91	2 F91108	hypothetical prote
5	377	81.6	91	2 AH0879	conserved hypotet
6	375	81.2	90	2 C82320	conserved hypotet
7	346	74.9	90	2 A10116	conserved hypotet
8	248	53.7	93	2 B84994	hypothetical prote
9	237	51.3	105	2 C82624	conserved hypotet
10	230	49.8	90	2 H83003	conserved hypotet
11	217	47.0	88	2 H81014	conserved hypotet
12	75	16.2	1024	2 T41415	probable leucine p
13	74.5	16.1	591	1 FOMVMM	gag polyprotein -
14	74.5	16.1	1526	2 AC2239	WD-40 repeat prote
15	72	15.6	593	2 C64097	probable soluble i
16	70.5	15.3	353	1 FOMVGR	gag polyprotein -
17	70	15.2	946	2 T31488	hypothetical prote
18	69	14.9	169	2 PNO560	phytochrome - wild
19	69	14.9	171	2 PNO558	phytochrome - wild
20	69	14.9	225	2 C88939	protein CO5E4.8 li
21	69	14.9	241	2 T27636	hypothetical prote
22	69	14.9	507	2 A83105	probable fumarate
23	68.5	14.8	511	2 A39340	neurofilament prot
24	68.5	14.8	599	2 H64097	fumarate reductase
25	68.5	14.8	615	2 B39340	neurofilament prot
26	68.5	14.8	1200	2 A46194	ORF MSV202 hypotet
27	68	14.7	328	2 T28363	ketol-acid reducte
28	68	14.7	330	1 B64561	glycosyltransferas
29	68	14.7	720	2 JCS131	

30	67	14.5	507	2 C81063	fumarate hydratase
31	67	14.5	546	2 A81807	fumarate hydratase
32	67	14.5	548	2 A54510	63k antigen - nema
33	67	14.5	1119	2 T18491	hypothetical prote
34	66.5	14.4	152	2 B70423	transcriptional regu
35	66.5	14.4	265	2 T46013	hypothetical prote
36	66	14.3	300	2 T32681	hypothetical prote
37	66	14.3	358	2 T34382	hypothetical prote
38	66	14.3	548	2 A28209	60k filarial antiq
39	66	14.3	1129	2 S00097	phytochrome 4 - oa
40	65.5	14.2	228	2 C26599	clathrin light cha
41	65.5	14.2	229	2 B31775	clathrin light cha
42	65.5	14.2	346	2 D89981	hypothetical prote
43	65.5	14.2	1206	2 E96507	hypothetical prote
44	65	14.1	258	2 S58159	hypothetical prote
45	65	14.1	604	2 F64081	isomerase func (RC
46	65	14.1	796	2 T43782	hypothetical prote
47	64.5	14.0	91	2 H90521	hypothetical prote
48	64.5	14.0	472	2 S74886	phytochrome dehydrog
49	64.5	14.0	853	2 S74609	hypothetical prote
50	64	13.9	179	2 H82921	conserved hypotet
51	64	13.9	423	2 T45030	hypothetical prote
52	64	13.9	501	2 A84784	hypothetical prote
53	64	13.9	583	2 T48365	hypothetical prote
54	64	13.9	847	2 G95843	conserved hypotet
55	64	13.9	895	2 A86410	protein F3M18.22 l
56	64	13.9	1129	2 A29631	phytochrome 3 - oa
57	63.5	13.7	166	2 P70562	hypothetical prote
58	63.5	13.7	324	2 T05429	hypothetical prote
59	63.5	13.7	497	2 F90471	hypothetical prote
60	63.5	13.7	577	1 A41289	reverse gyrase (in
61	63.5	13.7	1613	2 G64488	ferritin light cha
62	63	13.6	183	2 B33355	hypothetical prote
63	63	13.6	511	2 B39600	hypothetical prote
64	63	13.6	635	2 C71021	hypothetical prote
65	63	13.6	959	1 P2XR13	outer capsid prote
66	63	13.6	1079	2 A86220	protein P22013.29
67	63	13.6	1113	2 T00736	hypothetical prote
68	63	13.6	2101	2 A42184	nuclear mitotic ap
69	62.5	13.5	93	2 T17906	hypothetical prote
70	62.5	13.5	165	2 A81382	shikimate kinase (
71	62.5	13.5	165	2 C81915	hypothetical prote
72	62.5	13.5	379	2 S70709	type II site-speci
73	62.5	13.5	394	2 B70206	hypothetical prote
74	62.5	13.5	577	1 S39804	mosin - pig
75	62.5	13.5	610	2 S63667	phragmoplastin 12

ALIGNMENTS

RESULT 1
hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
R/Fietschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:7542800
A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <TIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI0000013B0A4; GB:U32760; GB:LA2023; NID:915
C/Superfamily: fe(III) trafficking protein Y99X
Query Match 94.2%; Score 435; DB 2; Length 90;
Best Local Similarity 92.0%; Pred. No. 2e-37;

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OY      Matches   80; Conservative    6; Mismatches    1; Indels    0; Gaps    0;
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DB      1 MARTVFCGYLKKKEBGLDPOLYPGELGRIPDSYSKAQMGWIKKQTMLVNEKTLNMNNA 60
OY      61 DHRQLLEBMNVFLPEGKDVIIEGVVP 87
        ::::::::::::::::::::
DB      61 EHKRLLEBMNVFLPEGDVHIEGVVP 87
        ::::::::::::::::::::

RESULT 2
A65954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A65954
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca,
Nature 409, 523-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A65480; MUID:21074935; PMID:11206551
A:Accession: A65954
A>Status: preliminary
A:Molecule type: DNA
R:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AEO05174; NID:g12517511; F
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: YggX
C:Superfamily: fe(II) trafficking protein YggX

Query Match          82.0%; Score 379; DB 2; Length 91;
Best Local Similarity 75.9%; Pred. No. 1e-31;
Matches 66; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

OY      1 MARTVFCEYLKQESBGDLPOLYPGELGRIPDSISKQAMREWMKKQTMLVNEKTLNMNNA 60
        :|::||:::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      1 MSRTIFCFPLQEAAGODPOLYPGELGRIRIYNISKEAWMOHQKTMLINEKTLNMNNA 60
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

OY      61 DHRQLLEBMNVFLPEGDVHIEGVVP 87
        ::::::::::::::::::::
DB      61 EHKRLLEBMNVFLPEGEVHIEGVTP 87
        ::::::::::::::::::::

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082
R:Blaetnar, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
R:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AEO00378; GB:U00096; NID:c
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein YggX

Query Match          82.0%; Score 379; DB 2; Length 91;
Best Local Similarity 75.9%; Pred. No. 1e-31;
Matches 66; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

OY      1 MARTVFCEYLKQESBGDLPOLYPGELGRIRIYNISKEAWREWMKKQTMLVNEKTLNMNNA 60
        :|::||:::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB      1 MSRTIFCFPLQEAAGODPOLYPGELGRIRIYNISKEAWMOHQKTMLINEKTLNMNNA 60
        ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

OY      61 DHRQLLEBMNVFLPEGDVHIEGVVP 87
        ::::::::::::::::::::
DB      61 EHKRLLEBMNVFLPEGEVHIEGVTP 87
        ::::::::::::::::::::

```

RESULT 4

P91108
hypothetical protein EC63838 [imported] - *Bacterichia coli* (strain O157:H7, substrain RI)
C1Species: *Escherichia coli*
C1Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C1Accession: F91108
R1Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasaawar, N.; Yasunaga, T.; Kubara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
Data Res. 8, 11-22, 2001
A1Title: Complete genome sequence of enterohemorrhagic *Bacterichia coli* O157:H7 and geno
A1Reference number: A9629; PMID:21156231; PMID:11258796
A1Accession: P91108
A1Status: preliminary
A1Molecule type: DNA
A1Residues: 1-91 <NAV>
A1Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;
A1Experimental source: strain O157:H7, substrain RMD 0509952
C1Genetics:
A1Gene: EC63838
C1Superfamily: fe(II) trafficking protein YggX

Query Match 82.0% Score 379; DB 2; Length 91;
Best Local Similarity 75.9%; Pred. No. 1e-31; Indels 0; Gaps 0;
Matches 66; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

Oy 1 MARTVFCRYLKQESBGLDPOLYPGEIGKRIFFDISISKOAMRENNKKOTMLVNEKKLNMNNA 60
 :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1 MSRTICTFPLQREAGDPPOLYPGEIGKRIYNEISKAMAWOMOHKOTMLINEKKLNMMNA 60
 :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy 61 DHRQLLEQEMVNFLFEKGDAHIEGYTP 87
 :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 61 EHRKLLEQEMVNFLFEKGDAHIEGYTP 87
 :|::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 5

AH0879
conserved hypothetical protein STY3266 [imported] - *Salmonella enterica* subsp. *enterica*
C1Species: *Salmonella enterica* subsp. *enterica* serovar Typh
A1Note: this species has also been called *Salmonella typhi*
C1Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C1Accession: AH0879
R1Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A1Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A1Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
A1Reference number: AB0502; MUID:21534947; PMID:11577608
A1Accession: AH0879
A1Status: preliminary
A1Molecule type: DNA
A1Residues: 1-91 <PAR>
A1Cross-references: UNIPARC:UPI00000544C; GB:A1513382; PIDN:CAD02936.1; PID:G16504189;
C1Genetics:
A1Gene: STY3266
C1Superfamily: fe(II) trafficking protein YggX

Query Match 81.6% Score 377; DB 2; Length 91;
Best Local Similarity 75.9%; Pred. No. 1.6e-31;
Matches 66; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Oy 1 MARTVFCRYLKQESBGLDPOLYPGEIGKRIFFDISISKOAMRENNKKOTMLVNEKKLNMNNA 60
 :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1 MSRTICTFPLQREAGDPPOLYPGEIGKRIYNEISKAMAWOMOHKOTMLINEKKLNMMNA 60
 :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Oy 61 DHRQLLEQEMVNFLFEKGDAHIEGYTP 87
 :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 61 EHRKLLEQEMVNFLFEKGDAHIEGYTP 87
 :|::||::||::||::||::||::||::||::||::||::||::||::||::||

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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 79.9886 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: UB-09-955-502a-6

Perfect score: 462
Sequence: 1 MARYFCBYLKGESGLDFQ.....QEMVNFEGKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Uniprot_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	90	1	FETP_PASMTU
2	437	94.6	90	1	FETP_PASMTU
3	435	94.2	90	1	FETP_PASMTU
4	435	94.2	90	2	O4QMD9_HAB18
5	416	90.0	94	1	FETP_HABDU
6	381	82.5	90	1	FETP_VIBPA
7	375	81.2	90	1	FETP_PHOPR
8	375	81.2	90	1	FETP_VIBCH
9	374	81.0	90	1	FETP_EOCS7
10	374	81.0	90	1	FETP_ECOLI
11	374	81.0	90	1	FETP_SHIFL
12	372	80.5	90	1	FETP_SALCH
13	372	80.5	90	1	FETP_SALPA
14	372	80.5	90	1	FETP_SALTI
15	372	80.5	90	1	FETP_SALTY
16	370	80.1	90	1	FETP_ECOLI
17	369	79.9	90	1	FETP_VIBVU
18	369	79.9	90	1	FETP_VIBVU
19	354	76.6	90	1	FETP_YERPS
20	352	76.2	90	1	FETP_ERMCT
21	349	75.5	90	1	FETP_ERMCT
22	346	74.9	90	1	FETP_YERPE
23	345	74.7	92	1	FETP_SHON
24	343	74.2	90	1	FETP_SHON
25	327	70.8	90	1	FETP_IDILO
26	321	54.3	90	1	FETP_BORBR
27	251	54.3	90	1	FETP_BORPA
28	251	54.3	90	1	FETP_BORPA
29	248	53.7	77	1	FETP_BUCAL
30	243	52.6	91	1	FETP_XANAC
31	241	52.2	90	1	FETP_XYLTF

32	238.5	51.6	89	1	FETP_LEGPL	O5WC4 legionella
33	238	51.5	91	1	FETP_BURMA	O6219 burtholderi
34	238	51.5	91	1	FETP_BURPS	O6314 burtholderi
35	238	51.5	92	1	FETP_XANCP	O8B29 xanthomonas
36	238	51.5	92	1	FETP_XANCP	O5G22 xanthomonas
37	238	51.5	92	2	O4UM14_XANCP	O4UM14 xanthomonas
38	237	51.3	89	1	FETP_XYLPA	O9PC73 xyella fas
39	234.5	50.8	89	1	FETP_LEGPA	O5XJ9 legionella
40	234.5	50.8	89	1	FETP_LEGPA	O5XJ9 legionella
41	230	49.8	78	1	FETP_WIGBR	O8D35 wiglesworth
42	230	49.8	90	1	FETP_PSEBR	O9H36 pseudomonas
43	230	49.8	90	2	O4J228_AZOV1	O4J28 azotobacter
44	229	49.6	90	1	FETP_NITEU	O82F2 nitrosomonas
45	228	49.4	91	2	O4LS19_9BRK	O4LS19 burtholderi
46	225	48.7	90	1	FETP_PSEBP	O8A49 pseudomonas
47	225	48.7	91	1	FETP_RALSO	O8Y10 ralestonia s
48	224	48.5	90	1	FETP_PSEBR	O8Y10 ralestonia s
49	224	48.5	90	2	O6T7F6_PSEBL	O6T7F6 pseudomonas
50	224	48.5	90	2	O4ZLP3_PSEBY	O4ZLP3 pseudomonas
51	223	48.3	90	1	FETP_COXBU	O83D6 coxiella bu
52	222	48.1	90	2	O4KJ12_PSEBS	O4KJ12 pseudomonas
53	219	47.4	90	1	FETP_METCA	O6B17 methylococc
54	217	47.0	88	1	FETP_NEIGI	O5E53 neisseria g
55	217	47.0	88	1	FETP_NEIMA	O5E53 neisseria m
56	217	47.0	88	1	FETP_NEIMA	O5E53 neisseria m
57	215	46.3	78	1	FETP_BUCAP	O6716 buchiera ap
58	214	46.3	90	1	FETP_CHRVO	O7N84 chromobact
59	210.5	45.6	80	1	FETP_NACID	O6F13 acinetobact
60	206	44.6	87	1	FETP_BUCBP	O8B44 buchiera ap
61	204	44.2	79	1	FETP_CANBR	O7V99 candidatus
62	198	42.9	87	1	FETP_FRATY	O5N18 francisella
63	156	33.8	92	2	O4NMQ4_PDELT	O4NMQ4 anaeromyxob
64	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
65	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
66	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
67	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
68	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
69	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
70	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
71	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
72	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
73	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
74	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact
75	154	33.3	96	2	O4FVJ7_9GAMM	O4FVJ7 psychrobact

ALIGNMENTS

RESULT 1	FETP_PASMTU	STANDARD;	PRT;	90 AA.
ID	FETP_PASMTU			
AC	O9CLB9;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	OrderedLocNames=PM1320;			
OS	Pasteurella multocida.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Pasteurella.			
OX	NCBI_TaxID=747;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=Pm70;			
RX	MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;			
RA	May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;			
RT	"Complete genomic sequence of Pasteurella multocida Pm70.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).			
CC	- FUNCTION: Could be a mediator in iron transfections between iron			
CC	acquisition and iron-regulating processes, such as synthesis and/or			
CC	repair of Fe-S clusters in biosynthetic enzymes (By similarity).			
CC	- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.			

```
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CC ----- CC
DR EMBL; AE006170; AAK03404.1; -; Genomic_DNA.
DR SMK; Q9CLB9; 1-87.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10744 MW; B583448BA4E0DFD7 CRC64;

Query March 100.0%; Score 462; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 5.8e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 61 DHRLLEQEMVNFLEFGKDVHIEGYVP 87
1 MARVFCECYLLKQESGLDPOLYPGELGRIPDSISKQAMRMKKQTMLVNEKTLNNWNA 60
MARTVFCECYLLKQESGLDPOLYPGELGRIPDSISKQAMRMKKQTMLVNEKTLNNWNA 60

RESULT 2
FETP_MANSNM STANDARD; PRT; 91 AA.
Q65VT7;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+)-trafficking protein.
GN OrderedLocustNames=MSO316;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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CC removed.
CC ----- CC
DR EMBL; AB016827; AAU36923.1; -; Genomic_DNA.
DR SMK; Q65VT7; 1-88.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10801 MW; 8190EB2DA0B35AACC CRC64;
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-6

Perfect score: 462
Sequence: 1 MARYPCRYLKQSEGLDPQ.....QEMNLFEGKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCYTUS-COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RS-COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	364	78.8	107	2	US-09-489-039A-11962
2	361	78.1	93	2	US-09-543-681A-5443
3	230	49.8	122	2	US-09-252-991A-23355
4	205.5	44.5	92	2	US-09-328-352-5456
5	142	30.7	110	2	US-09-540-236-2859
6	74.5	16.1	591	2	US-09-370-368-8
7	69.5	15.0	683	2	US-09-270-767-46792
8	69	14.9	474	2	US-09-252-991A-24473
9	68	14.7	680	2	US-09-298-924-4
10	68	14.7	720	1	US-08-840-236-1
11	68	14.7	528	1	US-08-505-448A-1
12	67	14.5	740	2	US-09-167-299-3
13	66.5	14.4	623	2	US-10-104-047-2547
14	65	14.1	319	2	US-09-710-279-2760
15	64.5	14.0	443	2	US-09-134-001C-1183
16	64.5	14.0	342	2	US-09-270-767-45174
17	64	13.9	298	2	US-09-248-796A-20663
18	64	13.9	411	2	US-09-902-540-9815
19	64	13.9	1129	2	US-08-904-871-11
20	64	13.9	1129	2	US-10-134-500-2
21	63.5	13.7	496	1	US-09-800-170-20
22	63	13.6	359	1	US-09-092-770-6
23	63	13.6	359	2	US-09-223-851-6
24	63	13.6	359	2	US-10-265-062-6
25	63	13.6	404	1	US-09-092-770-3
26	63	13.6	404	1	US-09-222-851-3
27	63	13.6	404	2	US-10-265-062-3

ALIGNMENTS

28	63	13.6	407	2	US-09-949-016-11184	Sequence 11184, A
29	63	13.6	2101	1	US-08-466-390-4	Sequence 4, Appl1
30	63	13.6	2101	1	US-08-470-950-4	Sequence 4, Appl1
31	63	13.6	2101	1	US-08-467-781-4	Sequence 4, Appl1
32	63	13.6	2101	1	US-08-195-487-4	Sequence 4, Appl1
33	63	13.6	2101	1	US-08-483-924-4	Sequence 4, Appl1
34	63	13.6	2101	2	US-09-452-294-1	Sequence 1, Appl1
35	63	13.6	2101	2	US-09-296-662-32	Sequence 32, Appl1
36	63	13.6	2101	4	PCR-US93-06160-4	Sequence 4, Appl1
37	63	13.6	2107	2	US-09-949-016-7546	Sequence 7546, Ap
38	63	13.6	2107	2	US-09-949-016-7547	Sequence 7547, Ap
39	63	13.6	2115	2	US-09-296-662-33	Sequence 33, Appl1
40	62.5	13.5	610	1	US-08-799-138-4	Sequence 4, Appl1
41	62.5	13.5	610	1	US-08-799-138-6	Sequence 6, Appl1
42	62.5	13.5	610	2	US-09-392-362-4	Sequence 4, Appl1
43	62.5	13.5	610	2	US-09-392-362-6	Sequence 6, Appl1
44	62	13.4	57	2	US-09-562-737-124	Sequence 124, App
45	62	13.4	116	2	US-09-562-737-125	Sequence 125, App
46	62	13.4	381	2	US-09-949-016-9788	Sequence 9788, Ap
47	62	13.4	381	2	US-09-949-016-9788	Sequence 13, Appl
48	62	13.4	455	2	US-09-270-767-45790	Sequence 45790, A
49	62	13.4	482	2	US-09-248-796A-17800	Sequence 17800, A
50	62	13.4	556	2	US-09-800-960-4	Sequence 4, Appl1
51	62	13.4	556	2	US-10-096-960-4	Sequence 4, Appl1
52	62	13.4	565	2	US-09-800-960-2	Sequence 2, Appl1
53	62	13.4	565	2	US-10-096-960-2	Sequence 2, Appl1
54	62	13.4	1401	2	US-09-750-590A-2	Sequence 2, Appl1
55	62	13.4	2388	2	US-09-695-795A-2	Sequence 2, Appl1
56	61.5	13.3	239	2	US-09-270-767-32538	Sequence 32538, A
57	61.5	13.3	239	2	US-09-270-767-47755	Sequence 47755, A
58	61.5	13.3	528	2	US-09-071-035-44	Sequence 44, Appl1
59	61.5	13.3	528	2	US-10-206-576-44	Sequence 42, Appl1
60	61.5	13.3	547	2	US-09-071-035-42	Sequence 42, Appl1
61	61.5	13.3	547	2	US-10-206-576-42	Sequence 42, Appl1
62	61.5	13.3	734	2	US-09-442-055-4	Sequence 4, Appl1
63	61	13.2	179	2	US-09-870-574-2	Sequence 15, Appl1
64	61	13.2	179	2	US-10-090-365-15	Sequence 15, Appl1
65	61	13.2	179	2	US-09-728-911-15	Sequence 15, Appl1
66	61	13.2	179	2	US-10-084-288-2	Sequence 15, Appl1
67	61	13.2	202	2	US-09-949-016-11314	Sequence 11314, A
68	60.5	13.1	139	2	US-08-559-896B-4	Sequence 4, Appl1
69	60.5	13.1	139	2	US-09-351-794A-4	Sequence 4, Appl1
70	60.5	13.1	415	1	US-08-602-010A-10	Sequence 10, Appl1
71	60.5	13.1	415	1	US-08-680-726A-10	Sequence 10, Appl1
72	60.5	13.1	415	2	US-09-092-540-16286	Sequence 16286, A
73	60.5	13.1	652	2	US-08-559-896B-2	Sequence 2, Appl1
74	60.5	13.1	652	2	US-09-351-794A-2	Sequence 2, Appl1
75	60.5	13.1	652	2	US-09-351-794A-2	Sequence 2, Appl1

RESULT 1

US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610636
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709 2004001
CURRENT FILING DATE: US/09/489, 039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 78.8%; Score 364; DB 2; Length 107;
Best Local Similarity 72.4%; Pred. No. 1e-39;
Matches 63; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

QY 1 MARTVCEYLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMVNEKKLMMNNA 60
DB 17 MSRTTFCFLQREAGDQPOLYPGELGKRIYNEISKAMQOHQTMVNEKKLSMNP 76

QY 61 DHRQLLEQEMVNFLEPGKDVHIEGYVP 87
DB 77 EHRKLEQEMVQFLFEGGDVHIEGYTP 103

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 78.1%; Score 361; DB 2; Length 93;
Best Local Similarity 73.6%; Pred. No. 2.1e-39;
Matches 64; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 MARTVCEYLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMVNEKKLMMNNA 60
DB 4 MSRTTFCFLQREAGDQPOLYPGELGKRIYNEISKAMQOHQTMVNEKKLSMNP 63

QY 61 DHRQLLEQEMVNFLEPGKDVHIEGYVP 87
DB 64 DHRKLEQEMVNFLEPGGDVHIEGYTP 90

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfeld et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 49.8%; Score 230; DB 2; Length 122;
Best Local Similarity 51.1%; Pred. No. 3.7e-22;
Matches 45; Conservative 17; Mismatches 24; Indels 2; Gaps 2;

QY 1 MARTVCEYLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMVNEKKLMMNNA 60

DB 33 MSRTVCRKXKHEBLPGDPRPYPGAKGEDYNNVSRKAMDEWQHQTMLINERLMMNNA 92

QY 61 DHRQLLEQEMVNFLEPGKD-VHIEGYVP 87
DB 93 EDRKFLQEMDKFL-SEGSDYKADGYVP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 44.5%; Score 205.5; DB 2; Length 92;
Best Local Similarity 42.0%; Pred. No. 4e-19;
Matches 37; Conservative 21; Mismatches 29; Indels 1; Gaps 1;

QY 1 MARTVCEYLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMVNEKKLMMNNA 60
DB 4 MSRTVCRKXKHEBLPGDPRPYPGAKGEDYNNVSRKAMDEWQHQTMLINERLMMNNA 93

QY 61 DHRQLLEQEMVNFLEPGKDVHIEGYVP 87
DB 64 EAKKFLQEMDKFL-SEGSDYKADGYVP 91

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 30.7%; Score 142; DB 2; Length 110;
Best Local Similarity 36.1%; Pred. No. 9.7e-11;
Matches 30; Conservative 15; Mismatches 38; Indels 0; Gaps 0;

QY 5 VRCVCEYLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMVNEKKLMMNNA 64
DB 25 VRCVCEYLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMVNEKKLMMNNA 84

QY 65 LLEQEMVNFLEPGKDVHIEGYVP 87
DB 85 YLNBQREKFLDNGDYKADGYVP 107

RESULT 6
US-09-370-368-8
; Sequence 8, Application US/09370368

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-6

Perfect score: 462

Sequence: 1 MARVPCRYLQSEGLDFO.....QEMVNFEGKDVHIGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	435	94.2	87	3	US-09-955-502-7
3	425	92.0	87	3	US-09-955-502-5
4	416	90.0	87	3	US-09-955-502-8
5	379	82.0	91	3	US-09-955-502-11
6	379	82.0	91	3	US-09-955-502-12
7	379	82.0	91	3	US-09-955-502-13
8	377	81.6	88	3	US-09-955-502-15
9	377	81.6	91	3	US-09-955-502-14
10	377	81.6	91	3	US-09-955-502-16
11	377	81.6	91	3	US-09-955-502-17
12	375	81.2	90	3	US-09-955-502-10
13	370	80.1	91	3	US-09-955-502-18
14	346	74.9	90	3	US-09-955-502-20
15	345	74.7	88	3	US-09-955-502-9
16	317	68.6	78	3	US-09-955-502-19
17	251	54.3	87	3	US-09-955-502-2
18	251	54.3	87	3	US-09-955-502-3
19	248	53.7	76	3	US-09-955-502-21
20	238	51.5	87	3	US-09-955-502-29
21	238	51.5	87	3	US-09-955-502-30
22	237	51.3	89	3	US-09-955-502-22
23	233.5	50.5	86	3	US-09-955-502-4
24	230	49.8	87	3	US-09-955-502-25
25	225	48.7	87	3	US-09-955-502-24
26	224	48.5	90	3	US-09-955-502-23
27	223	48.3	88	3	US-09-955-502-33

28	219	47.4	87	3	US-09-955-502-32	Sequence 32, Appl
29	217	47.0	88	3	US-09-955-502-26	Sequence 26, Appl
30	217	47.0	88	3	US-09-955-502-27	Sequence 27, Appl
31	217	47.0	88	3	US-09-955-502-28	Sequence 28, Appl
32	200	43.3	87	3	US-09-955-502-31	Sequence 31, Appl
33	75	16.2	1144	4	US-10-369-493-22774	Sequence 22774, A
34	74.5	16.1	591	3	US-09-827-822-8	Sequence 8, Appl
35	73.5	15.9	593	5	US-10-450-763-50306	Sequence 50306, A
36	70	15.2	1261	4	US-10-437-963-189166	Sequence 189166, A
37	69.5	15.0	449	4	US-10-437-963-171997	Sequence 171997, A
38	69.5	15.0	1286	4	US-10-424-599-151745	Sequence 151745, A
39	69.5	15.0	1292	4	US-10-424-599-151745	Sequence 151745, A
40	69.5	15.0	1303	4	US-10-424-599-151745	Sequence 151745, A
41	69	14.9	169	5	US-10-732-923-12562	Sequence 12562, A
42	69	14.9	171	5	US-10-732-923-12562	Sequence 12562, A
43	68.5	14.8	1809	4	US-10-437-963-171999	Sequence 171999, A
44	68.5	14.8	1822	4	US-10-437-963-171999	Sequence 171999, A
45	68.5	14.8	1822	4	US-10-437-963-171999	Sequence 171999, A
46	68	14.7	330	3	US-09-815-242-11319	Sequence 11319, A
47	68	14.7	330	4	US-10-282-122A-58687	Sequence 58687, A
48	68	14.7	720	3	US-10-688-276-4	Sequence 276, A
49	67	14.5	507	4	US-10-419-305-1	Sequence 305, A
50	67	14.5	546	4	US-10-282-122A-68021	Sequence 68021, A
51	66.5	14.4	623	4	US-10-104-047-2547	Sequence 2547, A
52	66.5	14.4	723	4	US-10-205-194-25	Sequence 25, Appl
53	66.5	14.4	723	4	US-10-231-913-139	Sequence 139, App
54	66.5	14.4	723	4	US-10-231-913-140	Sequence 140, App
55	66.5	14.4	723	4	US-10-342-844-22	Sequence 22, Appl
56	66.5	14.4	723	4	US-10-342-844-26	Sequence 26, Appl
57	66	14.3	1129	5	US-10-732-923-12553	Sequence 12553, A
58	65.5	14.2	507	4	US-10-282-122A-69897	Sequence 69897, A
59	65.5	14.2	579	4	US-10-360-849A-21	Sequence 21, Appl
60	65.5	14.2	579	4	US-10-360-849A-24	Sequence 24, Appl
61	65.5	14.2	823	6	US-11-097-143-23151	Sequence 23151, A
62	65.5	14.2	966	4	US-10-424-599-16963	Sequence 16963, A
63	65.5	14.2	2724	5	US-10-756-149-5518	Sequence 5518, A
64	65	14.1	436	4	US-10-282-122A-70602	Sequence 70602, A
65	65	14.1	443	4	US-10-724-972A-4158	Sequence 4158, A
66	65	14.1	645	4	US-10-425-115-368990	Sequence 368990, A
67	65	14.1	647	4	US-10-425-114-51665	Sequence 51665, A
68	65	14.1	671	5	US-10-631-467-1461	Sequence 1461, Ap
69	64.5	14.0	327	6	US-11-097-143-36495	Sequence 36495, A
70	64.5	14.0	634	6	US-11-097-143-36495	Sequence 6804, A
71	64	13.9	179	4	US-10-282-122A-76744	Sequence 76744, A
72	64	13.9	286	4	US-10-424-599-176198	Sequence 276198, A
73	64	13.9	325	4	US-10-425-114-45894	Sequence 45894, A
74	64	13.9	389	4	US-10-049-187-3	Sequence 3, Appl
75	64	13.9	389	5	US-10-732-923-10522	Sequence 10522, A

ALIGNMENTS

RESULT 1
US-09-955-502-6
Sequence 6, Appl
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955, 502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234, 588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 6
LENGTH: 87
TYPE: PRT
ORGANISM: Pasteurella multocida

US-09-955-502-6

Query Match 100.0%; Score 462; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.7e-43; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 0;

QY 1 MARTVFCBYLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTMVNEKKLNMNNA 60
DB 1 MARTVFCBYLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTMVNEKKLNMNNA 60

QY 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
DB 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87

RESULT 2

US-09-955-502-7
Sequence 7, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 87
TYPE: PRT
ORGANISM: Haemophilus influenzae

US-09-955-502-7

Query Match 94.2%; Score 435; DB 3; Length 87;
Best Local Similarity 92.0%; Pred. No. 1.7e-40; Indels 0; Gaps 0;
Matches 80; Conservative 6; Mismatches 1;

QY 1 MARTVFCBYLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTMVNEKKLNMNNA 60
DB 1 MARTVFCBYLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTMVNEKKLNMNNA 60

QY 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
DB 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87

RESULT 3

US-09-955-502-5
Sequence 5, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 91
TYPE: PRT
ORGANISM: Actinobacillus actinomycetemcomitans

US-09-955-502-5

Query Match 92.0%; Score 425; DB 3; Length 91;

Best Local Similarity 92.0%; Pred. No. 2.3e-39; Indels 0; Gaps 0;
Matches 80; Conservative 3; Mismatches 4;

QY 1 MARTVFCBYLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTMVNEKKLNMNNA 60
DB 1 MARTVFCBYLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTMVNEKKLNMNNA 60

QY 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
DB 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87

RESULT 4

US-09-955-502-8
Sequence 8, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 87
TYPE: PRT
ORGANISM: Haemophilus ducreyi

US-09-955-502-8

Query Match 90.0%; Score 416; DB 3; Length 87;
Best Local Similarity 88.5%; Pred. No. 2.2e-38; Indels 0; Gaps 0;
Matches 77; Conservative 6; Mismatches 4;

QY 1 MARTVFCBYLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTMVNEKKLNMNNA 60
DB 1 MARTVFCBYLKQESBGLDPOLYPGELGKRIFDPSISKQAWREMKKQTMVNEKKLNMNNA 60

QY 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
DB 61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87

RESULT 5

US-09-955-502-11
Sequence 11, Application US/09955502
Patent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 91
TYPE: PRT
ORGANISM: Becherichia coli K-12 MG1655

US-09-955-502-11

Query Match 82.0%; Score 379; DB 3; Length 91;
Best Local Similarity 75.9%; Pred. No. 3e-34; Indels 0; Gaps 0;
Matches 66; Conservative 14; Mismatches 7;

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:02:41 ; Search time 5.92509 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502a-6

Perfect score: 462
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Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Published Applications AA New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	72	15.6	593	US-11-194-246-317	Sequence 317, App
3	66.5	14.4	623	US-11-072-512-2547	Sequence 2547, App
4	65.5	14.2	285	US-10-467-657-222	Sequence 222, App
5	65.5	14.2	285	US-10-467-657-8230	Sequence 8230, App
6	65	14.1	319	US-10-793-626-2760	Sequence 2760, App
7	64	13.9	296	US-11-087-227-10	Sequence 10, App1
8	63.5	13.7	496	US-11-069-642-20	Sequence 20, App1
9	63.5	13.7	577	US-11-072-175-187	Sequence 187, App
10	63	13.6	140	US-11-098-686-10643	Sequence 10643, App
11	63	13.6	359	US-11-087-227-8	Sequence 8, App1
12	63	13.6	359	US-11-192-450-6	Sequence 6, App1
13	63	13.6	404	US-11-087-227-6	Sequence 6, App1
14	63	13.6	404	US-11-192-450-3	Sequence 3, App1
15	63	13.6	834	US-10-453-372-658	Sequence 658, App
16	63	13.6	2101	US-10-857-780-23	Sequence 23, App1
17	61	13.2	179	US-10-063-703-154	Sequence 154, App
18	61	13.2	179	US-11-177-987-43	Sequence 43, App1
19	61	13.2	336	US-10-453-372-660	Sequence 660, App
20	61	13.2	342	US-11-156-084-25	Sequence 25, App1
21	61	13.2	342	US-11-156-084-44	Sequence 44, App1
22	61	13.2	369	US-11-156-084-45	Sequence 45, App1
23	61	13.2	619	US-11-156-084-24	Sequence 24, App1
24	61	13.2	695	US-10-453-372-648	Sequence 648, App
25	61	13.2	695	US-10-453-372-648	Sequence 648, App

26	61	13.2	700	US-10-995-561-922	Sequence 922, App
27	61	13.2	700	US-10-995-561-924	Sequence 924, App
28	61	13.2	775	US-10-453-372-656	Sequence 656, App
29	61	13.2	793	US-10-995-561-925	Sequence 925, App
30	61	13.2	804	US-10-453-372-650	Sequence 650, App
31	61	13.2	847	US-10-453-372-654	Sequence 654, App
32	61	13.2	857	US-10-453-372-652	Sequence 652, App
33	61	13.2	905	US-10-453-372-658	Sequence 658, App
34	61	13.2	905	US-10-453-372-662	Sequence 662, App
35	61	13.2	963	US-10-453-372-664	Sequence 664, App
36	61	13.2	963	US-10-995-561-923	Sequence 923, App
37	61	13.2	1012	US-10-453-372-660	Sequence 660, App
38	61	13.2	1012	US-11-072-512-3117	Sequence 3117, App
39	60	13.0	428	US-11-120-308-84	Sequence 84, App1
40	59.5	12.9	765	US-11-120-308-84	Sequence 84, App1
41	59.5	12.9	818	US-11-120-308-94	Sequence 94, App1
42	59	12.8	139	US-10-793-626-1310	Sequence 1310, App
43	58	12.6	635	US-11-098-686-10433	Sequence 10433, App
44	58	12.6	750	US-11-073-347-1	Sequence 1, App1
45	58	12.6	750	US-11-155-288-4	Sequence 4, App1
46	58	12.6	750	US-11-202-516-2	Sequence 2, App1
47	57.5	12.4	96	US-10-485-768A-824	Sequence 824, App
48	57.5	12.4	96	US-11-053-076-289	Sequence 209, App
49	57.5	12.4	469	US-10-793-626-2204	Sequence 2204, App
50	57	12.3	175	US-10-821-234-1522	Sequence 1522, App
51	57	12.3	254	US-11-072-512-3198	Sequence 3198, App
52	57	12.3	403	US-11-192-450-4	Sequence 4, App1
53	56.5	12.2	109	US-11-053-076-196	Sequence 196, App
54	56.5	12.2	1089	US-10-793-626-2352	Sequence 2352, App
55	56.5	12.2	1089	US-11-148-770-32	Sequence 32, App1
56	56.5	12.2	1089	US-11-076-427A-114	Sequence 114, App1
57	56.5	12.2	1089	US-11-075-047A-117	Sequence 117, App
58	56.5	12.2	1451	US-10-995-561-829	Sequence 829, App
59	56	12.1	443	US-10-793-626-1200	Sequence 1200, App
60	56	12.1	668	US-11-098-686-11201	Sequence 11201, App
61	55.5	12.0	263	US-10-724-558-28	Sequence 28, App1
62	55	11.9	266	US-09-955-493-6	Sequence 6, App1
63	55	11.9	279	US-11-098-686-10812	Sequence 10812, App
64	55	11.9	674	US-11-000-463-471	Sequence 471, App
65	55	11.9	734	US-10-995-561-770	Sequence 770, App
66	55	11.8	739	US-10-131-826A-478	Sequence 478, App
67	54.5	11.8	229	US-10-793-626-2818	Sequence 2818, App
68	54.5	11.8	305	US-11-156-084-178	Sequence 178, App
69	54.5	11.8	349	US-10-821-234-1387	Sequence 1387, App
70	54.5	11.8	497	US-11-010-239-85	Sequence 85, App1
71	54.5	11.8	729	US-10-511-538-101	Sequence 101, App
72	54.5	11.8	1151	US-10-793-626-2448	Sequence 2448, App
73	54	11.7	158	US-11-072-512-3221	Sequence 3221, App
74	54	11.7	352	US-11-098-686-10448	Sequence 10448, App
75	54	11.7	4374	US-11-128-572-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTRONI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWinn9, version 1.04

; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 47.0%; Score 217; DB 6; Length 88;
Best Local Similarity 46.6%; Pred. No. 2,3e-18;
Matches 41; Conservative 20; Mismatches 25; Indels 2; Gaps 2;

Qy 1 MARVFCYLLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMLVNEKKLMMNNA 60
Db 1 MARVFCYLLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMLVNEKKLMMNNA 60

Qy 61 DHRQLLEQEMV-NFLF-EKQDVHIEGVVP 87
Db 61 RAREYLAQOQMEQYFPGDGADA-VQGVYP 87

RESULT 2
US-11-194-246-317
; Sequence 317, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Treppod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MEI
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.051 (Mar 268,05920101)
; CURRENT FILING DATE: 2005-08-01
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/345,438
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 317
; LENGTH: 593
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 15.6%; Score 72; DB 7; Length 593;
Best Local Similarity 46.7%; Pred. No. 1.1;
Matches 14; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 32 DSISKOAVREWMKKQTMLVNEKKLMMNNA 61
Db 293 ESKSKQEMRYEAKODILNTKLTLSKKE 322

RESULT 3
US-11-072-512-2547
; Sequence 2547, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU

; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length CDNA
; FILE REFERENCE: 084335-0191
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2547
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2547

Query Match 14.4%; Score 66.5; DB 7; Length 623;
Best Local Similarity 30.8%; Pred. No. 5.2;
Matches 24; Conservative 13; Mismatches 32; Indels 9; Gaps 3;

Qy 10 LKQESGLDPOLY-----PGEI--GKRIIPDSISKQAMREWMKKQTMLVNEKKLMMNNA 61
Db 232 MKRLIEEIKFMYVTEKEFPELENNKKELHFLQKVSEPMGSHDLLESKINIEINTE 291

Qy 62 HROLLEQEMV-NFLFEGK 78
Db 292 INQLEKKMMNEPIEGK 309

RESULT 4
US-10-467-657-222
; Sequence 222, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: PIZZAZ Maria Rita
; APPLICANT: PIZZAZ Maria Rita
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWinn9, version 1.04
; SEQ ID NO 222
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-222

Query Match 14.2%; Score 65.5; DB 6; Length 285;
Best Local Similarity 29.4%; Pred. No. 2.6;
Matches 20; Conservative 14; Mismatches 21; Indels 13; Gaps 4;

Qy 8 EYLKQESGLDPOLYPGELGKRIIPDSISKQAMREWMKKQTMLVNEKKLMMNNA 65
Db 227 KYISFDGSGNNV-----SKRLSDV-----WRRCVDVLLNNLLNDRKSKYL-AVHREL 275

Qy 66 LEQEMVNF 73
Db 276 MLQEDQEF 283

RESULT 5
US-10-467-657-8230
; Sequence 8230, Application US/10467657
; Publication No. US20050260581A1

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-7

Perfect score: 461

Sequence: 1 MARIYFCEYLNKKAEGLDFO.....QENVNPLFGKDVHIGVVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21.*
1: geneeqp1980s.*
2: geneeqp1990s.*
3: geneeqp2000s.*
4: geneeqp2001s.*
5: geneeqp2002s.*
6: geneeqp2003as.*
7: geneeqp2003bs.*
8: geneeqp2004s.*
9: geneeqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	461	100.0	87	5	ABB78152 Amino aci
2	435	94.4	87	5	ABB78151 Amino aci
3	434	94.1	91	5	ABB78150 Amino aci
4	425	92.2	87	5	ABB78153 Amino aci
5	387	83.9	91	5	ABB78158 Amino aci
6	387	83.9	91	5	ABB78157 Amino aci
7	387	83.9	91	5	ABB78156 Amino aci
8	385	83.5	88	5	ABB78155 Amino aci
9	385	83.5	88	5	ABB78160 Amino aci
10	385	83.5	91	5	ABB78161 Amino aci
11	385	83.5	91	5	ABB78159 Amino aci
12	378	82.0	91	5	ABB78162 Amino aci
13	378	82.0	91	5	ABB78163 Amino aci
14	372	80.7	107	7	ABO65445 Amino aci
15	371	80.5	93	7	ADP05158 Amino aci
16	363	78.7	90	5	ABB78165 Amino aci
17	356	77.2	88	5	ABB78164 Amino aci
18	325	70.5	78	5	ABB78164 Amino aci
19	256	55.5	76	5	ABB78166 Amino aci
20	256	55.5	87	5	ABB78148 Amino aci
21	256	55.5	87	5	ABB78147 Amino aci
22	241	52.3	87	5	ABB78175 Amino aci
23	238.5	51.7	86	5	ABB78149 Amino aci
24	236	51.2	87	5	ABB78170 Amino aci

ALIGNMENTS

25	236	51.2	122	7	ABO74609 Pseudomon
26	235.5	51.1	89	9	ABE41576 L. pneumo
27	235.5	51.1	95	9	ABE38294 L. pneumo
28	235	51.0	87	5	ABB78174 Amino aci
29	230	49.9	90	5	ABB78168 Amino aci
30	229	49.7	87	5	ABB78169 Amino aci
31	227.5	49.3	90	5	ABB78167 Amino aci
32	227	49.2	88	5	ABB78171 Amino aci
33	227	49.2	88	5	ABB78172 Amino aci
34	227	49.2	88	5	ABB78173 Amino aci
35	227	49.2	88	6	ABP77219 N. gonorr
36	224	48.6	87	5	ABB78177 Amino aci
37	224	48.6	88	5	ABB78178 Amino aci
38	214.5	46.5	92	6	ADA34169 Acinetoba
39	202	43.8	87	5	ABB78176 Amino aci
40	144	31.2	110	8	ADL05173 Amino aci
41	76.5	16.6	591	2	AAV41141 Mouse mam
42	76.5	16.6	860	2	AAV41140 Mouse mam
43	76.5	16.6	1755	2	AAV41139 Mouse mam
44	73	15.8	1144	8	ADS44344 Bifidobac
45	72	15.6	506	3	ABY74371 Neisseria
46	71	15.4	503	4	ABG16577 Novel hum
47	71	15.4	883	8	ADN47233 Thermococ
48	70.5	15.3	723	7	ADB85144 Rat calci
49	70.5	15.3	723	8	ADL81552 Rat calci
50	70.5	15.3	723	8	ADL81552 Rat calci
51	70.5	15.3	723	8	ADL81552 Rat calci
52	70.5	15.3	723	8	ADL81552 Rat calci
53	70.5	15.3	959	7	ADP06594 Bacterial
54	69.5	15.1	227	3	AAAG38052 Arabidops
55	69.5	15.1	593	4	ABG19947 Novel hum
56	69	15.0	484	8	ADM90985 Human pha
57	69	15.0	507	6	ABU40210 Protein e
58	68.5	14.9	218	3	ABG45909 Arabidops
59	68.5	14.9	234	3	ABG45908 Arabidops
60	68	14.8	257	3	AAAG31203 Arabidops
61	68	14.8	297	3	AAAG31202 Arabidops
62	68	14.8	324	3	AAAG31201 Arabidops
63	67.5	14.6	283	8	ADY12704 Plant ful
64	67	14.5	474	7	ABO75727 Pseudomon
65	67	14.5	507	3	AAV74372 Neisseria
66	67	14.5	507	3	AAV74373 Neisseria
67	67	14.5	546	6	ABU38097 Protein e
68	67	14.5	1399	8	ADR75314 Bovine ac
69	67	14.5	1401	8	ADR75290 Bovine ac
70	66.5	14.4	330	4	ABU30763 Protein e
71	66.5	14.4	330	6	ADN01595 Enterobac
72	66.5	14.4	487	8	ADL81550 Rabbit ep
73	66.5	14.4	730	8	ADL81550 Rabbit ep
74	66.5	14.4	765	6	ADA20715 Artichoke
75	66.5	14.4	818	6	ADA20725 Artichoke

RESULT 1

ID ABB78152 standard; protein; 87 AA.

XX ABB78152:

XX 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;

XX hydroxyl radical; DNA damage; YggX homologue.

XX Haemophilus influenzae.

XX US2002072118-A1.

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PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnicks JA;
PI
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
CC
XX Sequence 87 AA;
SQ
Query Match 100.0%; Score 461; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 9.8e-47;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MARYFCEYLKKEABGLDFOLYPGELGKRIFPSVSKQANGEMWIKKQTMVNEKKLMNNA 60
QY 61 EHRKLLQEMVNFLEFGKDVHIEGYVP 87
DB 61 EHRKLLQEMVNFLEFGKDVHIEGYVP 87
RESULT 2
ABB78151
ID ABB78151 standard; protein; 87 AA.
XX
XX ABB78151;
AC
XX 05-NOV-2002 (first entry)
DT
XX
XX Amino acid sequence of a YggX homologue.
DB Superoxide damage; cell; YggX; Salmonella enterica serovar Typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Pasteurella multocida.
OS
XX
XX US2002072118-A1.
PN
XX 13-JUN-2002.
PD
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnicks JA;
PI
XX

```

```

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar Typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
CC
XX Sequence 87 AA;
SQ
Query Match 94.4%; Score 435; DB 5; Length 87;
Best Local Similarity 92.0%; Pred. No. 1.2e-43;
Matches 80; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 MARYFCEYLKKEABGLDFOLYPGELGKRIFPSVSKQANGEMWIKKQTMVNEKKLMNNA 60
DB 1 MARYFCEYLKKEABGLDFOLYPGELGKRIFPSVSKQANGEMWIKKQTMVNEKKLMNNA 60
QY 61 EHRKLLQEMVNFLEFGKDVHIEGYVP 87
DB 61 EHRKLLQEMVNFLEFGKDVHIEGYVP 87
RESULT 3
ABB78150
ID ABB78150 standard; protein; 91 AA.
XX
XX ABB78150;
AC
XX 05-NOV-2002 (first entry)
DT
XX
XX Amino acid sequence of a YggX homologue.
DB Superoxide damage; cell; YggX; Salmonella enterica serovar Typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
OS
XX
XX US2002072118-A1.
PN
XX 13-JUN-2002.
PD
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnicks JA;
PI
XX
XX WPI; 2002-589476/63.
DR
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502a-7

Perfect score: 461
Sequence: 1 MARVFCBYLKKRAGLDLFDQ.....QEMVNFLEGGKDVHIGVYP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	90	2	C64013
2	387	83.9	91	2	A85954
3	387	83.9	91	2	A65082
4	387	83.9	91	2	P91108
5	386	83.7	90	2	C82320
6	385	83.5	91	2	AH0879
7	363	78.7	90	2	AI0116
8	256	55.5	93	2	B84994
9	237	51.4	105	2	C82624
10	236	51.2	90	2	H83003
11	227	49.2	88	2	H81014
12	76.5	16.6	591	1	FOKVM4
13	73	15.8	1024	2	T41415
14	72.5	15.7	353	1	FOKVM4
15	68.5	14.9	1206	2	B95507
16	68	14.8	324	2	T05429
17	68	14.8	555	2	C96667
18	68	14.8	583	2	T48365
19	68	14.8	593	2	C64097
20	67.5	14.6	1119	2	T18491
21	67	14.5	328	2	T28363
22	67	14.5	485	2	A84043
23	67	14.5	507	2	A83105
24	67	14.5	507	2	C81063
25	67	14.5	546	2	A81807
26	66.5	14.4	330	1	B64561
27	66.5	14.4	394	2	B70206
28	66.5	14.4	487	1	LQBP34
29	66	14.3	258	2	S58159

30	66	14.3	548	2	A54510	63k antigen - nema
31	65.5	14.2	152	2	B70423	transcription regu
32	65.5	14.2	300	2	P84178	hypothetical prote
33	65.5	14.2	348	2	H70337	conserved hypothet
34	65.5	14.2	723	2	JC7795	epithelial calcium
35	65.5	14.2	1787	2	G97222	hypothetical prote
36	65	14.1	166	2	C95944	probable acetyltra
37	65	14.1	182	2	C69416	hypothetical prote
38	65	14.1	330	2	G91204	hypothetical prote
39	65	14.1	367	2	A86051	hypothetical prote
40	65	14.1	392	2	H90174	hypothetical prote
41	65	14.1	548	2	A28209	60k filarial antiy
42	65	14.1	548	2	B97026	probable Fe-S oxid
43	65	14.1	558	2	A85296	hypothetical prote
44	65	14.1	559	2	T05786	hypothetical prote
45	65	14.1	604	2	F64081	isomerase fuct (BC
46	64.5	14.0	165	2	A81382	shikimate kinase (
47	64.5	14.0	480	2	S38134	GLG1 protein - yea
48	64.5	14.0	1526	2	AC2239	WD-40 repeat prote
49	64.5	14.0	1645	2	A37792	spectrin beta-H ch
50	64.5	14.0	1939	2	T18372	repeat organellar
51	64	13.9	342	2	T13113	probable sogb prot
52	64	13.9	553	2	G70115	ribosomal protein
53	64	13.9	641	2	T38659	methylesterahydr
54	64	13.9	720	2	JC5131	glycosyltransferas
55	64	13.9	742	1	S58691	kinasin-related pr
56	64	13.9	946	2	T31488	hypothetical prote
57	63.5	13.8	236	2	F69866	tetrahydridipicol
58	63.5	13.8	998	2	A71080	hypothetical prote
59	63.5	13.8	1008	2	H72310	conserved hypothet
60	63.5	13.8	1321	2	JR0352	mucin MUC5B, trach
61	63	13.7	225	2	C88939	protein COSB4.8 (f
62	63	13.7	241	2	T27636	hypothetical prote
63	63	13.7	271	2	A84643	probable WRK1-type
64	63	13.7	274	2	S04610	gene 2 protein - p
65	63	13.7	502	2	A81350	probable RNA nucle
66	63	13.7	371	2	A84784	hypothetical prote
67	63	13.7	1209	2	T46027	hypothetical prote
68	63	13.7	1262	2	T33074	hypothetical prote
69	63	13.7	2672	2	A48126	translation activa
70	62.5	13.6	91	2	H90521	hypothetical prote
71	62.5	13.6	308	2	E71697	probable proteinas
72	62.5	13.6	577	1	A41289	moesin - human
73	62.5	13.6	853	2	S74609	hypothetical prote
74	62.5	13.6	1101	2	G70951	probable ATP-depen
75	62.5	13.6	1150	2	G89881	pyruvate carboxyla

ALIGNMENTS

RESULT 1

hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)

C1Species: Haemophilus influenzae

C1Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

C1Accession: C64013

R1Fleischmann, R.D.; Adams, M.D.; Clayton, R.A.; Kirkness, E.F.; Kiehlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Furumman, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A1Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A1Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A1Reference number: A64000; PMID:7542800

A1Accession: C64013

A1Status: nucleic acid sequence not shown; translation not shown

A1Molecule type: DNA

A1Cross-references: UNIPROT:P40408; UNIPARC:UPI000013B0A4; GB:U32760; GB:U42023; NID:915

C1Superfamily: fe(ii) trafficking protein Y9X

Query Match 100.0%; Score 461; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 18:23:46 ; Search time 79.9886 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502a-7

Perfect score: 461
Sequence: 1 MARYFCXYLKKEAGLDLFDQ.....QEMVNFLEGGKDVHLEGVYP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	90	1	FETP_HABIN
2	461	100.0	90	2	Q4QMD9_HABIN
3	439	95.2	91	1	FETP_MANSU
4	435	94.4	90	1	FETP_PASMU
5	425	92.2	94	1	FETP_HABDU
6	389	84.4	90	1	FETP_VIBPA
7	387	83.9	90	1	FETP_VIBVU
8	387	83.9	90	1	FETP_VIBVY
9	386	83.7	90	1	FETP_VIBCH
10	382	82.9	90	1	FETP_RCO57
11	382	82.9	90	1	FETP_RCOL1
12	382	82.9	90	1	FETP_SHIFL
13	380	82.4	90	1	FETP_SALCP
14	380	82.4	90	1	FETP_SALPA
15	380	82.4	90	1	FETP_SALTY
16	380	82.4	90	1	FETP_SALTY
17	379	82.2	90	1	FETP_PROPR
18	378	82.0	90	1	FETP_RCOL6
19	371	80.5	90	1	FETP_YERPS
20	363	78.7	90	1	FETP_YERPS
21	361	78.3	90	1	FETP_VIBP1
22	356	77.2	92	1	FETP_SHEON
23	353	76.6	90	1	FETP_EWCT
24	348	71.6	90	1	FETP_PHOTO1
25	330	71.6	90	1	FETP_IDILO
26	256	55.5	77	1	FETP_BUCAI
27	256	55.5	90	1	FETP_BORRA
28	256	55.5	90	1	FETP_BORRA
29	256	55.5	90	1	FETP_BORRA
30	244	52.9	91	1	FETP_XANAC
31	243	52.7	90	1	FETP_NITBU

32	241	52.3	90	1	FETP_XYLFT	Q87406 xyliella fae
33	241	52.3	91	1	FETP_BURMA	Q62309 burholderi
34	241	52.3	91	1	FETP_BURPS	Q63544 burholderi
35	239.5	52.0	89	1	FETP_LEGPL	Q59424 legionella
36	239	51.8	92	1	FETP_XANOR	Q59422 xanthomonas
37	237	51.4	90	1	FETP_XYLPA	Q96773 xyliella fae
38	236	51.2	90	1	FETP_PSEAR	Q94336 pseudomonas
39	236	51.2	90	2	Q4J228_AZQVI	Q4J228 azotobacter
40	235.5	51.1	89	1	FETP_LEGPA	Q52329 legionella
41	235.5	51.1	89	1	FETP_LEGPH	Q52329 legionella
42	235	51.0	92	1	FETP_XANCP	Q89229 xanthomonas
43	235	51.0	92	2	Q4UM14_XANCP	Q4UM14 xanthomonas
44	232	50.3	91	1	FETP_RALSO	Q89010 ralestonia s
45	231	50.1	91	2	Q4LS19_9BTRK	Q4LS19 burholderi
46	230	49.9	78	1	FETP_WIGBR	Q8435 wigglewort
47	230	49.9	90	1	FETP_PSRSM	Q87465 pseudomonas
48	230	49.9	90	2	Q6T7F6_PSRFL	Q6T7F6 pseudomonas
49	230	49.9	90	2	Q4ZLP3_PSRSY	Q4ZLP3 pseudomonas
50	229	49.7	80	1	FETP_PSEPK	Q88449 pseudomonas
51	227	49.2	88	1	FETP_NEIGI	Q5F553 neisseria g
52	227	49.2	88	1	FETP_NEIMA	Q5F553 neisseria m
53	227	49.2	88	1	FETP_NEIMA	Q5F553 neisseria m
54	224	48.6	90	1	FETP_COXBU	Q83406 coxiella bu
55	224	48.6	90	1	FETP_METCA	Q60637 methylococc
56	221	47.9	90	2	Q4KJ22_PSEF5	Q4KJ22 pseudomonas
57	214	46.4	87	1	FETP_BUCBP	Q89444 buchnera ap
58	214	46.4	90	1	FETP_CHRYO	Q79444 chromobacte
59	212	46.0	78	1	FETP_BUCAP	Q8425 buchnera ap
60	211.5	45.9	90	1	FETP_AC1AD	Q6T7B3 acinetobact
61	209	45.3	79	1	FETP_CANBR	Q5949 candidatus
62	192	41.6	87	1	FETP_FRATY	Q5948 franciella
63	154	33.4	92	2	Q4NMQ4_9DELT	Q4NMQ4 anaeromyxob
64	146	31.7	96	2	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
65	77.5	16.8	416	2	Q89KZ1_BRAJA	Q89KZ1 bradyrhizob
66	76.5	16.6	187	2	Q9HBF7_HUMAN	Q9HBF7 homo sapien
67	76.5	16.6	218	2	Q6SPV9_9BETR	Q6SPV9 mus musculu
68	76.5	16.6	281	2	Q6PG71_MOUSE	Q6PG71 mus musculu
69	76.5	16.6	372	2	Q85648_9BETR	Q85648 mouse mamma
70	76.5	16.6	452	2	Q7SPV8_9BETR	Q7SPV8 human betar
71	76.5	16.6	590	1	GAG_MMTVB	P10558 mouse mamma
72	76.5	16.6	590	1	GAG_MMTVC	P11284 mouse mamma
73	76.5	16.6	591	2	Q83391_9BETR	Q83391 mouse mamma
74	76.5	16.6	591	2	Q91ZT6_9BETR	Q91ZT6 exogenous m
75	76.5	16.6	591	2	Q91ZU1_9BETR	Q91ZU1 endogenous

ALIGNMENTS

RESULT 1

ID	FETP_HABIN	STANDARD	PRT	90 AA.
AC	P44048;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Pe(2+) trafficking protein.			
GN	OrderedLocusNames=H10760;			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Haemophilus.			
NC	NCBI_TaxId=727;			
NC	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=Rd / KW20 / ATCC 51907;			
RX	MEDLINE=9530630; PubMed=7542800;			
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F.,			
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,			
RA	McKenny K., Sutton G.G., Fitzhugh W., Fields C.A., Geacayre J.D.,			
RA	Scott J.D., Shetty R., Liu L.-T., Glodet A., Kelley J.M.,			
RA	Welton J.F., Phillips C.A., Spirig T., Hedblom B., Cotton M.D.,			
RA	Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,			
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,			

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RP IDENTIFICATION BY MASS SPECTROMETRY.
 RX MEDLINE=20137488; PubMed=10675023;
 RX DOI=10.1002/(SICI)1522-2683(20000101)21:2<411::AID-ELPS411>3.3.CO;2-W;
 RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
 RA Gray C., Pountoulakis M.;
 RT "Two-dimensional map of the proteome of Haemophilus influenzae";
 CC Electrophoresis 21:411-429(2000).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 acquisition and iron-requiring processes, such as synthesis and/or
 repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: U32760; AAC22419.1; -; Genomic_DNA.
 CC SRR: C64013; C64013.
 CC SMR: P44048; 1-87.
 CC TIGR: H10760; -;
 CC HAMAP: MF_00686; -; 1.
 CC InterPro: IPR007457; Y9GX.
 CC Pfam: PF04362; DUF495; 1.
 CC PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 CC ProDom: PD029191; DUF495; 1.
 CC Complete proteome; Iron.
 CC SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;
 SQ
 Query Match 100.0%; Score 461; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1,8e-39;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARYTCCEYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMWIKQTMLVNEKLMNNA 60
 DB 1 MARYTCCEYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMWIKQTMLVNEKLMNNA 60
 QY 61 EHRKLLQEMVNFLEPGKDVHIEGYVP 87
 DB 61 EHRKLLQEMVNFLEPGKDVHIEGYVP 87
 RESULT 2
 Q4QMD9_HAE18 PRELIMINARY; PRT; 90 AA.
 ID Q4QMD9; HAE18 PRELIMINARY;
 AC Q4QMD9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=NTNH10920;
 OS Haemophilus influenzae (strain 86-028NP).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OC NCBI_TaxId=281310;
 OK [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
 RA Harrison A., Dyer D.W., Gillaespy A., Ray W.C., Mungr R., Carson M.B.,
 RA Zhong H., Gibson J., Gibson M., Johnson L.S., Lewis L., Bakalatz L.O.,
 RA Munson R.S. Jr.;
 RT "Genomic sequence of an otitis media isolate of nontypeable
 RT Haemophilus influenzae: comparative study with H. influenzae serotype
 RT d, strain KW20.";
 RL J. Bacteriol. 187:4627-4636(2005).
 RL EMBL: CP000057; AAX87808.1; -; Genomic_DNA.

DR InterPro: IPR007457; Y9GX.
 DR Pfam: PF04362; DUF495; 1.
 DR PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 DR ProDom: PD029191; DUF495; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;
 Query Match 100.0%; Score 461; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1,8e-39;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARYTCCEYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMWIKQTMLVNEKLMNNA 60
 DB 1 MARYTCCEYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMWIKQTMLVNEKLMNNA 60
 QY 61 EHRKLLQEMVNFLEPGKDVHIEGYVP 87
 DB 61 EHRKLLQEMVNFLEPGKDVHIEGYVP 87
 RESULT 3
 PERP_MANSN STANDARD; PRT; 91 AA.
 ID PERP_MANSN
 AC Q65VT7;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Probable Fe(2+) trafficking protein.
 GN OrderedLocustNames=MS0316;
 OS Mannheimia succiniciproducens (strain MBE155B).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OC NCBI_TaxId=221988;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15378067; DOI=10.1038/nbt1010;
 RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
 RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
 RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
 RT succiniciproducens.";
 RT Nat. Biotechnol. 22:1275-1281(2004).
 RL
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 acquisition and iron-requiring processes, such as synthesis and/or
 repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AE016827; AAU36923.1; -; Genomic_DNA.
 CC SRR: Q65VT7; 1-88.
 CC HAMAP: MF_00686; -; 1.
 CC InterPro: IPR007457; Y9GX.
 CC Pfam: PF04362; DUF495; 1.
 CC PIRSF: PIRSF029827; Fe_traffic_Y9GX; 1.
 CC ProDom: PD029191; DUF495; 1.
 CC Complete proteome; Iron.
 CC SEQUENCE 91 AA; 10801 MW; 8190E2DA0B35AACC CRC64;
 SQ
 Query Match 95.2%; Score 439; DB 1; Length 91;
 Best Local Similarity 90.8%; Pred. No. 3,3e-37;
 Matches 79; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARYTCCEYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMWIKQTMLVNEKLMNNA 60
 DB 1 MARYTCCEYLKKEAGLDLPOLYPGELGRIIPDSVSKQAWGEMWIKQTMLVNEKLMNNA 60
 QY 61 EHRKLLQEMVNFLEPGKDVHIEGYVP 87
 DB 61 EHRKLLQEMVNFLEPGKDVHIEGYVP 87

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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502a-7

Perfect score: 461
Sequence: 1 MARVFCBYLNKRAEGLDFQ.....CEMVNLFEGKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/BCIUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	372	80.7	107	2	US-09-489-039A-11962
2	371	80.5	93	2	US-09-543-681A-5443
3	236	51.2	122	2	US-09-252-991A-23355
4	214.5	46.5	92	2	US-09-328-352-5456
5	144	31.2	110	2	US-09-540-236-2859
6	76.5	16.6	591	2	US-09-370-368-8
7	70.5	15.3	959	2	US-09-543-681A-6879
8	67.5	14.6	271	2	US-09-248-796A-19265
9	67	14.5	474	2	US-09-252-991A-24473
10	67	14.5	1401	2	US-09-750-590A-2
11	66	14.3	548	2	US-09-167-299-3
12	65.5	14.2	623	2	US-10-104-047-2547
13	65	14.1	292	2	US-09-328-352-55856
14	65	14.1	482	2	US-09-248-796A-17800
15	64.5	14.0	415	1	US-08-602-010A-10
16	64.5	14.0	415	1	US-08-680-726A-10
17	64.5	14.0	415	1	US-09-092-409-10
18	64.5	14.0	683	2	US-09-270-767-46192
19	64	13.9	217	2	US-09-543-681A-7862
20	64	13.9	680	2	US-09-298-924-4
21	64	13.9	633	2	US-09-328-352-6519
22	64	13.9	720	1	US-08-840-236-1
23	64	13.9	720	1	US-08-505-448A-1
24	63.5	13.8	586	2	US-09-270-767-44373
25	62.5	13.6	177	1	US-08-647-960-6
26	62.5	13.6	2285	2	US-09-308-375-2
27	62.5	13.6	2285	2	US-09-932-183A-2

ALIGNMENTS

28	62	13.4	337	2	US-09-270-767-41746	Sequence 41746, A
29	62	13.4	455	2	US-09-270-767-45790	Sequence 45790, A
30	62	13.4	550	2	US-09-107-532A-7201	Sequence 7201, Ap
31	62	13.4	674	2	US-08-961-083-200	Sequence 200, App
32	62	13.4	674	2	US-09-536-784-200	Sequence 200, App
33	62	13.4	674	2	US-09-765-271-200	Sequence 200, App
34	62	13.4	674	2	US-09-765-272A-200	Sequence 200, App
35	62	13.4	817	1	US-08-381-931B-2	Sequence 2, Appl
36	61.5	13.3	734	1	US-09-442-055-2	Sequence 2, Appl
37	61	13.2	191	1	US-08-468-576B-13	Sequence 13, Appl
38	61	13.2	191	1	US-08-468-576B-13	Sequence 13, Appl
39	61	13.2	191	2	US-08-468-576B-13	Sequence 13, Appl
40	61	13.2	359	1	US-09-092-770-6	Sequence 6, Appl
41	61	13.2	359	2	US-09-222-861-6	Sequence 6, Appl
42	61	13.2	359	2	US-10-265-052-6	Sequence 6, Appl
43	61	13.2	404	1	US-09-092-770-3	Sequence 3, Appl
44	61	13.2	404	2	US-09-222-861-3	Sequence 3, Appl
45	61	13.2	404	2	US-10-265-062-3	Sequence 3, Appl
46	61	13.2	407	2	US-09-949-016-11184	Sequence 11184, A
47	61	13.2	625	2	US-09-949-016-8485	Sequence 8485, Ap
48	61	13.2	625	2	US-09-949-016-8810	Sequence 8810, Ap
49	60.5	13.1	279	2	US-09-198-452A-221	Sequence 221, App
50	60.5	13.1	279	2	US-09-438-185A-205	Sequence 205, App
51	60.5	13.1	438	2	US-09-800-170-20	Sequence 20, Appl
52	60.5	13.1	496	2	US-09-800-170-20	Sequence 20, Appl
53	60.5	13.1	547	2	US-09-438-185A-214	Sequence 214, App
54	60.5	13.1	720	2	US-09-583-110-2940	Sequence 2940, Ap
55	60.5	13.1	720	2	US-09-107-433-4193	Sequence 4193, Ap
56	60.5	13.1	782	2	US-09-710-279-2352	Sequence 2352, Ap
57	60.5	13.1	794	2	US-09-134-001C-4310	Sequence 4310, Ap
58	60	13.0	243	2	US-09-270-767-31727	Sequence 31727, A
59	60	13.0	243	2	US-09-270-767-46944	Sequence 46944, A
60	60	13.0	280	2	US-09-323-998E-37	Sequence 37, Appl
61	60	13.0	319	2	US-09-710-279-2760	Sequence 2760, Ap
62	60	13.0	443	2	US-09-134-001C-3183	Sequence 3183, Ap
63	60	13.0	465	2	US-09-769-787-164	Sequence 164, App
64	60	13.0	1248	1	US-09-080-897-2	Sequence 2, Appl
65	60	13.0	1248	2	US-09-323-735-2	Sequence 3, Appl
66	60	13.0	1315	2	US-08-899-595-3	Sequence 3, Appl
67	60	13.0	2101	1	US-08-466-390-4	Sequence 4, Appl
68	60	13.0	2101	1	US-08-470-950-4	Sequence 4, Appl
69	60	13.0	2101	1	US-08-467-781-4	Sequence 4, Appl
70	60	13.0	2101	1	US-08-195-487-4	Sequence 4, Appl
71	60	13.0	2101	1	US-08-483-924-4	Sequence 4, Appl
72	60	13.0	2101	2	US-09-452-294-1	Sequence 1, Appl
73	60	13.0	2101	2	US-09-296-662-32	Sequence 32, Appl
74	60	13.0	2101	4	PCT-US93-06160-4	Sequence 4, Appl
75	60	13.0	2107	2	US-09-949-016-7646	Sequence 7646, Ap

RESULTS

US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Berton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIORITY FILING DATE: 1999-01-29
PRIORITY APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 80.7%; Score 372; DB 2; Length 107;
Best Local Similarity 74.7%; Pred. No. 1.2e-39;
Matches 65; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MARTVCEYLKKEABGLDLPOLYVGEIGKRIIPDSVSKQAWGEMIKKQTMVLNKKLMMNNA 60
DB 17 MSRTIFCTPLQREADGQDFOLYPGELGKRIYINISKEAMQWQHQTMLINKEKLSMNP 76

QY 61 EHRKLEQEMVNFLEPGKDVHIEGYVP 87
DB 77 EHRKLEQEMVNFLEPGKDVHIEGYTP 103

RESULT 2
US-09-543-681A-5443
Sequence 5443, Application US/09543681A

Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A

PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5443

LENGTH: 93
TYPE: PRT
ORGANISM: Proteus mirabilis

Query Match 80.5%; Score 371; DB 2; Length 93;
Best Local Similarity 74.7%; Pred. No. 1.3e-39;
Matches 65; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 MARTVCEYLKKEABGLDLPOLYVGEIGKRIIPDSVSKQAWGEMIKKQTMVLNKKLMMNNA 60
DB 4 MSRTIFCTPLQREADGQDFOLYPGELGKRIYINISKEAMQWQHQTMLINKEKLSMNP 63

QY 61 EHRKLEQEMVNFLEPGKDVHIEGYVP 87
DB 64 DRRKLEQEMVNFLEPGKDVHIEGYTP 90

RESULT 3
US-09-252-991A-23355
Sequence 23355, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23355

LENGTH: 122
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 51.2%; Score 236; DB 2; Length 122;
Best Local Similarity 54.5%; Pred. No. 2.9e-22;
Matches 48; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

QY 1 MARTVCEYLKKEABGLDLPOLYVGEIGKRIIPDSVSKQAWGEMIKKQTMVLNKKLMMNNA 60

DB 33 MSRTVCEYLKKEABGLDLPOLYVGEIGKRIIPDSVSKQAWGEMIKKQTMVLNKKLMMNNA 92
QY 61 EHRKLEQEMVNFLEPGKDVHIEGYVP 87
DB 93 EDRKLEQEMVNFLEPGKDVHIEGYTP 119

RESULT 4
US-09-328-352-5456
Sequence 5456, Application US/09328352

Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5456

LENGTH: 92
TYPE: PRT
ORGANISM: Acinetobacter baumannii

Query Match 46.5%; Score 214.5; DB 2; Length 92;
Best Local Similarity 46.6%; Pred. No. 1.1e-19;
Matches 41; Conservative 16; Mismatches 30; Indels 1; Gaps 1;

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DB 4 MSRTVCEYLKKEABGLDLPOLYVGEIGKRIIPDSVSKQAWGEMIKKQTMVLNKKLMMNNA 63

QY 61 EHRKLEQEMVNFLEPGKDVHIEGYVP 87
DB 64 EHRKLEQEMVNFLEPGKDVHIEGYTP 91

RESULT 5
US-09-540-236-2859
Sequence 2859, Application US/09540236

Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236

PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2859

LENGTH: 110
TYPE: PRT
ORGANISM: Moraxella catarrhalis

Query Match 31.2%; Score 144; DB 2; Length 110;
Best Local Similarity 34.9%; Pred. No. 1.3e-10;
Matches 29; Conservative 17; Mismatches 37; Indels 0; Gaps 0;

QY 5 VFCEYLKKEABGLDLPOLYVGEIGKRIIPDSVSKQAWGEMIKKQTMVLNKKLMMNNAEHRK 64
DB 25 VFCEYLKKEABGLDLPOLYVGEIGKRIIPDSVSKQAWGEMIKKQTMVLNKKLMMNNAEHRK 84

QY 65 LLEQEMVNFLEPGKDVHIEGYVP 87
DB 85 LLEQEMVNFLEPGKDVHIEGYTP 107

RESULT 6
US-09-370-368-8
Sequence 8, Application US/09370368

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502a-7

Perfect score: 461

Sequence: 1 MARVFCRYLKEAEGLDFO.....QEMVFLFGKDVHIEGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	387	83.9	91 3 US-09-955-502-11	Sequence 11, Appli
6	387	83.9	91 3 US-09-955-502-12	Sequence 12, Appli
7	387	83.9	91 3 US-09-955-502-13	Sequence 13, Appli
8	386	83.7	90 3 US-09-955-502-10	Sequence 10, Appli
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15	356	77.2	88 3 US-09-955-502-9	Sequence 9, Appli
16	325	70.5	78 3 US-09-955-502-19	Sequence 19, Appli
17	256	55.5	76 3 US-09-955-502-21	Sequence 21, Appli
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22	238.5	51.7	86 3 US-09-955-502-4	Sequence 4, Appli
23	237	51.4	89 3 US-09-955-502-22	Sequence 22, Appli
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26	229	49.7	87 3 US-09-955-502-24	Sequence 24, Appli
27	227	49.2	88 3 US-09-955-502-26	Sequence 26, Appli

ALIGNMENTS

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29	227	49.2	88 3	US-09-955-502-28	Sequence 28, Appli
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32	202	43.8	87 3	US-09-955-502-31	Sequence 31, Appli
33	76.5	16.6	591 3	US-09-827-822-8	Sequence 8, Appli
34	71	15.8	1144 4	US-10-369-493-22774	Sequence 22774, A
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45	69	15.0	507 4	US-10-282-122A-68134	Sequence 68134, A
46	68.5	14.9	2724 5	US-10-756-149-5518	Sequence 5518, Ap
47	67.5	14.6	283 4	US-10-425-114-68519	Sequence 68519, A
48	67.5	14.6	284 4	US-10-425-115-278111	Sequence 278111, A
49	67	14.5	546 4	US-10-282-122A-66021	Sequence 66021, A
50	67	14.5	853 4	US-10-437-963-168426	Sequence 168426, A
51	66.5	14.4	330 3	US-09-815-242-11319	Sequence 11319, A
52	66.5	14.4	330 4	US-10-282-122A-58687	Sequence 58687, A
53	66.5	14.4	730 4	US-10-231-913-141	Sequence 141, Appl
54	66.5	14.4	730 4	US-10-342-844-20	Sequence 20, Appli
55	66.5	14.4	765 4	US-10-078-770-84	Sequence 84, Appli
56	66.5	14.4	818 4	US-10-078-770-94	Sequence 94, Appli
57	66.5	14.4	1809 4	US-10-437-963-195972	Sequence 195972, A
58	65.5	14.2	463 4	US-10-156-761-12981	Sequence 12981, A
59	65.5	14.2	623 4	US-10-104-047-2547	Sequence 2547, Ap
60	65	14.1	451 4	US-10-263-929-173	Sequence 173, Appl
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63	64.5	14.0	292 4	US-10-425-115-249865	Sequence 249865, A
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66	64.5	14.0	497 5	US-10-917-602A-57	Sequence 57, Appli
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68	64.5	14.0	527 4	US-10-425-115-353344	Sequence 353344, A
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72	64.5	14.0	1939 5	US-10-733-923-3340	Sequence 3340, Ap
73	64.5	14.0	4097 6	US-11-097-143-237	Sequence 237, Appl
74	64	13.9	553 5	US-10-282-122A-47026	Sequence 47026, A
75	64	13.9	553 5	US-10-733-923-18350	Sequence 18350, A

RESULT 1
US-09-955-502-7
Sequence 7, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 87
TYPE: PRT
ORGANISM: Haemophilus influenzae

GenCore version 5.1.7
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Title: US-09-955-502a-7

Perfect score: 461
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Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	66.5	14.4	818	US-11-120-308-94	Sequence 94, Appl
5	65.5	14.2	623	US-11-072-512-2547	Sequence 2547, App
6	62.5	13.6	577	US-11-072-175-187	Sequence 187, Appl
7	61	13.2	342	US-11-156-084-25	Sequence 25, Appl
8	61	13.2	342	US-11-156-084-44	Sequence 44, Appl
9	61	13.2	359	US-11-087-227-8	Sequence 8, Appl
10	61	13.2	359	US-11-192-450-6	Sequence 6, Appl
11	61	13.2	369	US-11-156-084-45	Sequence 45, Appl
12	61	13.2	404	US-11-087-227-6	Sequence 6, Appl
13	61	13.2	404	US-11-192-450-3	Sequence 3, Appl
14	61	13.2	619	US-11-156-084-24	Sequence 24, Appl
15	60.5	13.1	285	US-10-467-657-222	Sequence 222, App
16	60.5	13.1	285	US-10-467-657-8230	Sequence 8230, App
17	60.5	13.1	496	US-11-069-642-20	Sequence 20, App
18	60.5	13.1	782	US-10-793-626-2352	Sequence 2352, App
19	60	13.0	319	US-10-793-626-2760	Sequence 2760, App
20	60	13.0	465	US-10-873-528-164	Sequence 164, App
21	60	13.0	2101	US-10-857-780-23	Sequence 23, Appl
22	59	12.8	834	US-10-453-372-658	Sequence 658, App
23	59	12.8	1734	US-11-192-967-6	Sequence 6, Appl
24	59	12.8	1734	US-11-193-715-6	Sequence 28, Appl
25	58.5	12.7	253	US-10-724-598-28	

26 58.5 12.7 466 6 US-10-524-647-114 Sequence 114, App
27 58.5 12.7 466 6 US-10-524-972-102 Sequence 102, App
28 58.5 12.7 729 6 US-10-511-538-101 Sequence 101, App
29 58.5 12.7 774 7 US-11-070-627-7 Sequence 7, Appl
30 58 12.6 296 7 US-11-087-227-10 Sequence 10, Appl
31 58 12.6 452 6 US-10-467-962B-14 Sequence 14, Appl
32 57.5 12.5 305 7 US-11-156-084-178 Sequence 178, App
33 57.5 12.5 635 7 US-11-098-686-10433 Sequence 10433, A
34 57.5 12.5 650 6 US-10-467-657-1948 Sequence 1948, App
35 57 12.4 336 6 US-10-453-372-640 Sequence 640, App
36 57 12.4 391 7 US-11-207-626A-16 Sequence 16, Appl
37 57 12.4 391 7 US-11-207-626A-27 Sequence 27, Appl
38 57 12.4 695 6 US-10-453-372-648 Sequence 648, App
39 57 12.4 700 6 US-10-995-561-922 Sequence 922, App
40 57 12.4 700 6 US-10-995-561-924 Sequence 924, App
41 57 12.4 775 6 US-10-453-372-656 Sequence 656, App
42 57 12.4 793 6 US-10-995-561-925 Sequence 925, App
43 57 12.4 804 6 US-10-453-372-650 Sequence 650, App
44 57 12.4 847 6 US-10-453-372-654 Sequence 654, App
45 57 12.4 857 6 US-10-453-372-652 Sequence 652, App
46 57 12.4 905 6 US-10-453-372-638 Sequence 638, App
47 57 12.4 905 6 US-10-453-372-662 Sequence 662, App
48 57 12.4 905 6 US-10-453-372-664 Sequence 664, App
49 57 12.4 963 6 US-10-995-561-923 Sequence 923, App
50 57 12.4 963 6 US-10-453-372-660 Sequence 660, App
51 57 12.4 1012 6 US-10-821-234-1387 Sequence 1387, App
52 56.5 12.3 349 6 US-10-821-234-1387 Sequence 3457, App
53 56.5 12.3 411 7 US-11-072-512-3452 Sequence 10, Appl
54 56.5 12.3 1766 7 US-11-075-185-10 Sequence 11014, A
55 55.5 12.0 250 7 US-11-098-686-11014 Sequence 718, App
56 55.5 12.0 268 6 US-10-995-561-718 Sequence 288, App
57 55.5 12.0 299 7 US-11-156-084-288 Sequence 1062, App
58 55.5 12.0 301 7 US-11-055-822-1062 Sequence 720, App
59 55.5 12.0 355 6 US-10-995-561-720 Sequence 478, App
60 55.5 12.0 739 6 US-10-131-826A-478 Sequence 6, Appl
61 55 11.9 266 5 US-09-995-493-6 Sequence 10812, A
62 55 11.9 279 7 US-11-098-686-10812 Sequence 3467, App
63 55 11.9 504 7 US-11-072-512-3467 Sequence 16, Appl
64 55 11.9 560 7 US-11-131-479-16 Sequence 220, App
65 54.5 11.8 242 7 US-11-023-562-220 Sequence 1145, App
66 54.5 11.8 1299 6 US-10-821-234-1145 Sequence 1310, App
67 54 11.7 139 6 US-10-793-626-1310 Sequence 762, App
68 54 11.7 175 5 US-09-978-360A-762 Sequence 1522, App
69 54 11.7 175 6 US-10-821-234-1522 Sequence 206, App
70 54 11.7 175 7 US-11-072-175-206 Sequence 1658, App
71 54 11.7 177 6 US-10-467-657-1658 Sequence 3198, App
72 54 11.7 254 7 US-11-072-512-3198 Sequence 4, Appl
73 54 11.7 403 6 US-11-192-450-4 Sequence 75, Appl
74 54 11.7 603 7 US-10-770-726-75 Sequence 6112, App
75 54 11.7 1122 6 US-10-467-657-6112

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwinn9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 49.2%; Score 227; DB 6; Length 88;
Best Local Similarity 50.0%; Pred. No. 1.9e-19;
Matches 44; Conservative 17; Mismatches 25; Indels 2; Gaps 2;

QY 1 MARVFCETLKKEAGLDPOLYGEIKRIPDSVSKQAMGEWIKQTMVNEKKLMMNA 60
DB 1 MARVFCVKNLEAGMKPPPLPNELGKRIFENVSQEAAMATRTQTMVNEKLSLADP 60

QY 61 EHRKLEQEMVNF-EGKDVHIEGYVP 87
DB 61 RAREVYLAQOMQOYFFPDGDADA-VGGYVP 87

RESULT 2
US-11-194-246-317
Sequence 317, Application US/11194246

Publication No. US20050272089A1
GENERAL INFORMATION:
APPLICANT: Mott, John
APPLICANT: Trepp, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
FILE REFERENCE: 00592.US1 (Mar 268,059,20101)
CURRENT APPLICATION NUMBER: US/11/194,246
PRIOR FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 14.8%; Score 68; DB 7; Length 593;
Best Local Similarity 46.7%; Pred. No. 3.6;
Matches 14; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 32 DSVSKQAMGEWIKQTMVNEKKLMMNA 61
DB 293 ESKSKQEMRYWEAKQDILNKTJLALSK 322

RESULT 3
US-11-120-308-84
Sequence 84, Application US/11120308
Publication No. US20060005277A1
GENERAL INFORMATION:
APPLICANT: Farnodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120,308
PRIOR FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 84
LENGTH: 765
TYPE: PRT
ORGANISM: Helianthus tuberosus
US-11-120-308-84

Query Match 14.4%; Score 66.5; DB 7; Length 765;
Best Local Similarity 25.0%; Pred. No. 7.4;
Matches 18; Conservative 14; Mismatches 17; Indels 23; Gaps 4;

QY 7 CEYLKGEABGLDPOLY-----PGLGK-----RIFDSVSKQAM--GEW-----I 43
DB 43 CHYTKATVDGISFDLYDAYVKAEGKPDYIARIIVEMETVDKELYPSAQWFFPAEDTVI 102

QY 44 KKQTMVNEKKL 55
DB 103 KSQAHLLDKRRV 114

RESULT 4
US-11-120-308-94
Sequence 94, Application US/11120308

Publication No. US20060005277A1
GENERAL INFORMATION:
APPLICANT: Farnodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120,308
PRIOR FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 94
LENGTH: 818
TYPE: PRT
ORGANISM: Helianthus tuberosus
US-11-120-308-94

Query Match 14.4%; Score 66.5; DB 7; Length 818;
Best Local Similarity 25.0%; Pred. No. 8;
Matches 18; Conservative 14; Mismatches 17; Indels 23; Gaps 4;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-8

Perfect score: 462

Sequence: 1 MARMVFCYLKKEAGLDFO.....AEVNFLEGGKVDHIDGYP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21.*
1: geneeqp19808.*
2: geneeqp19908.*
3: geneeqp20008.*
4: geneeqp20018.*
5: geneeqp20028.*
6: geneeqp20038.*
7: geneeqp20038.*
8: geneeqp20048.*
9: geneeqp20058.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	462	100.0	87	5	ABB78153 Amino aci
2	425	92.0	87	5	ABB78152 Amino aci
3	416	90.0	87	5	ABB78151 Amino aci
4	412	89.2	91	5	ABB78150 Amino aci
5	375	81.2	90	5	ABB78155 Amino aci
6	373	80.7	91	5	ABB78158 Amino aci
7	373	80.7	91	5	ABB78157 Amino aci
8	373	80.7	91	5	ABB78156 Amino aci
9	371	80.3	88	5	ABB78160 Amino aci
10	371	80.3	91	5	ABB78161 Amino aci
11	371	80.3	91	5	ABB78159 Amino aci
12	371	80.3	91	5	ABB78162 Amino aci
13	371	80.3	107	7	ABO65445 Amino aci
14	367	79.4	93	7	ADP05158 Amino aci
15	364	78.8	91	5	ABB78163 Amino aci
16	351	76.0	90	5	ABB78165 Amino aci
17	336	72.7	88	5	ABB78154 Amino aci
18	327	70.8	78	5	ABB78164 Amino aci
19	255	55.2	87	5	ABB78175 Amino aci
20	249	53.9	87	5	ABB78174 Amino aci
21	247	53.5	76	5	ABB78166 Amino aci
22	243	52.6	87	5	ABB78148 Amino aci
23	243	52.6	87	5	ABB78147 Amino aci
24	237	51.3	88	5	ABB78178 Amino aci

25	235.5	51.0	90	5	ABB78167 Amino aci
26	235	50.9	88	5	ABB78171 Amino aci
27	235	50.9	88	5	ABB78172 Amino aci
28	235	50.9	88	5	ABB78173 Amino aci
29	235	50.9	88	5	ABB77219 N gonorr
30	225.5	48.8	86	5	ABB78149 Amino aci
31	224.5	48.6	89	5	ABB78157 Amino aci
32	224.5	48.6	95	9	ABB78170 Amino aci
33	222	48.1	87	5	ABB78169 Amino aci
34	222	48.1	127	7	ABO74609 Pseudomon
35	221	47.8	90	5	ABB78168 Amino aci
36	219	47.4	87	5	ABB78169 Amino aci
37	211.5	45.8	92	6	ADA34169 Amino aci
38	211	45.7	87	5	ABB78176 Amino aci
39	205	44.4	87	5	ABB78177 Amino aci
40	143	31.0	110	8	ADL05173 M. catarr
41	76	16.5	217	7	ADP07577 Bacterial
42	74	16.0	1144	8	ADA44344 Bacterial
43	71	15.4	292	6	ADA34549 Actinobac
44	70	15.2	506	3	AA74371 Neisseria
45	70	15.2	975	5	ABP66068 Bifidobac
46	68.5	14.8	476	5	ABG92539 Platelet
47	68.5	14.8	476	5	ABG92539 Platelet
48	68.5	14.8	476	5	ABG92539 Platelet
49	68.5	14.8	503	2	AA22667 50 kd sub
50	68	14.7	2206	6	ABU19863 Protein e
51	67.5	14.6	507	6	ADA20715 Artichoke
52	67.5	14.6	765	6	ADA20725 Artichoke
53	67.5	14.6	818	6	ADA36587 Actinobac
54	67.5	14.6	1233	6	ABU40210 Protein e
55	67	14.5	507	6	ABU40210 Protein e
56	66.5	14.4	226	9	ABU25552 Protein e
57	66.5	14.4	234	9	ABU25552 Protein e
58	66.5	14.4	415	2	AAW22982 Canine he
59	66.5	14.4	415	2	AAW22982 Canine he
60	66.5	14.4	415	2	AAW22982 Canine he
61	66.5	14.4	415	2	AAW22982 Canine he
62	66.5	14.4	415	2	AAW22982 Canine he
63	66.5	14.4	415	2	AAW22982 Canine he
64	66.5	14.4	415	2	AAW22982 Canine he
65	66.5	14.4	415	2	AAW22982 Canine he
66	66.5	14.4	415	2	AAW22982 Canine he
67	65.5	14.2	511	6	ABU22540 Protein e
68	65.5	14.2	567	4	AAW00976 Human bon
69	65.5	14.2	591	2	AA41141 Mouse mam
70	65.5	14.2	860	2	AA41140 Mouse mam
71	65.5	14.2	1755	2	AA41139 Mouse mam
72	65	14.1	217	7	ADP07364 Bacterial
73	65	14.1	330	4	ABE57984 Drosophill
74	65	14.1	471	7	ADP62425 Human Pro
75	65	14.1	471	7	ADP62425 Human Pro

ALIGNMENTS

RESULT 1
ABB78153 standard; protein; 87 AA.

DT 05-NOV-2002 (first entry)

DR Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;

OS hydroxyl radical; DNA damage; YggX homologue.

XX Unidentified.

XX US2002072118-A1.

PD 13-JUN-2002.
 XX 18-SEP-2001; 2001US-00955502.
 XX 22-SEP-2000; 2000US-0234588P.
 PR
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALINICK J A.
 XX
 XX Downs D, Gralnick JA;
 PI
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX
 SQ Sequence 87 AA;

Query Match 100.0%; Score 462; DB 5; Length 87;
 Best Local Similarity 100.0%; Pred. No. 1.1e-46;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARWVFCETLKKEAGLDLPOLYPGELGRIFNSISKQAAEWIKKQTMVNEKCLMMNP 60
 DB 1 MARWVFCETLKKEAGLDLPOLYPGELGRIFNSISKQAAEWIKKQTMVNEKCLMMNP 60

OY 61 EHRQLLEAEWNVFLFEGKDVHIDGYVP 87
 DB 61 EHRQLLEAEWNVFLFEGKDVHIDGYVP 87

RESULT 2
 ABB78152
 ID ABB78152 standard; protein; 87 AA.
 XX
 AC ABB78152;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgxB homologue.
 XX
 DE Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
 XX hydroxyl radical; DNA damage; YgxB homologue.
 XX
 OS Haemophilus influenzae.
 XX
 OS US2002072118-A1.
 XX
 PN 13-JUN-2002.
 PD
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALINICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX
 SQ Sequence 87 AA;

Query Match 92.0%; Score 425; DB 5; Length 87;
 Best Local Similarity 90.8%; Pred. No. 2.6e-42;
 Matches 79; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 MARWVFCETLKKEAGLDLPOLYPGELGRIFNSISKQAAEWIKKQTMVNEKCLMMNP 60
 DB 1 MARWVFCETLKKEAGLDLPOLYPGELGRIFNSISKQAAEWIKKQTMVNEKCLMMNP 60

OY 61 EHRQLLEAEWNVFLFEGKDVHIDGYVP 87
 DB 61 EHRQLLEAEWNVFLFEGKDVHIDGYVP 87

RESULT 3
 ABB78151
 ID ABB78151 standard; protein; 87 AA.
 XX
 AC ABB78151;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YgxB homologue.
 XX
 DE Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
 XX hydroxyl radical; DNA damage; YgxB homologue.
 XX
 OS Pasteurella multocida.
 XX
 OS US2002072118-A1.
 XX
 PN 13-JUN-2002.
 PD
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALINICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502a-8

Perfect score: 462
Sequence: 1 MARMVFCEYLKKRABGLDFQ.....AEWVNFLEFGKVDHIDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425	92.0	90	2 C64013	hypothetical prote
2	375	81.2	90	2 C82320	conserved hypotet
3	373	80.7	91	2 A85954	hypothetical prote
4	373	80.7	91	2 A65082	hypothetical prote
5	373	80.7	91	2 F91108	hypothetical prote
6	371	80.3	91	2 AH0879	conserved hypotet
7	351	76.0	90	2 AI0116	conserved hypotet
8	247	53.5	93	2 B84994	hypothetical prote
9	246	53.2	105	2 C82624	conserved hypotet
10	235	50.9	88	2 H81014	conserved hypotet
11	222	48.1	90	2 H83003	conserved hypotet
12	222	48.1	90	2 T41415	probable leucine p
13	74	16.0	1024	2 T23047	hypothetical prote
14	71	15.4	1111	2 T23047	hypothetical prote
15	70	15.2	946	2 T11488	hypothetical prote
16	69	14.9	241	2 T27636	hypothetical prote
17	69	14.9	317	1 A31797	Spec-related prote
18	69	14.9	593	1 C64097	probable soluble 1
19	69	14.9	629	2 T28217	hypothetical prote
20	68.5	14.8	394	2 B70206	hypothetical prote
21	68.5	14.8	1526	2 AC2239	WD-40 repeat prote
22	68	14.7	225	2 C86939	protein C05E4.8 (1
23	67	14.7	2206	2 G71611	hypothetical prote
24	66.5	14.5	1119	2 T18491	hypothetical prote
25	66	14.3	1206	2 B96507	hypothetical prote
26	66	14.3	300	2 T33281	hypothetical prote
27	66	14.3	358	2 T34382	hypothetical prote
28	65.5	14.2	472	2 S74886	phycoene dehydrog
29	65.5	14.2	399	2 T31789	hypothetical prote
			591	1 F0WMM	gag polyprotein -

30	65	14.1	394	2 T22868	hypothetical prote
31	65	14.1	507	2 C81063	fumate hydratase
32	65	14.1	546	2 A81807	fumate hydratase
33	65	14.1	796	2 T43782	hypothetical prote
34	64.5	14.0	94	2 S17449	probable ligand-bl
35	64.5	14.0	416	2 S19896	plasmogen activa
36	64.5	14.0	996	2 A71080	hypothetical prote
37	64.5	14.0	1008	2 H72310	conserved hypotet
38	64.5	14.0	1150	2 G89881	pyruvate carboxyla
39	64	13.9	258	2 S58159	hypothetical prote
40	64	13.9	274	2 S04610	gene 2 protein - p
41	64	13.9	696	2 D95206	hypothetical prote
42	63.5	13.7	348	2 H70337	conserved hypotet
43	63.5	13.7	363	2 S73661	hypothetical prote
44	63.5	13.7	713	2 D71631	hypothetical prote
45	63.5	13.7	1121	2 T25715	hypothetical prote
46	63.5	13.7	1513	2 G64488	reverse gyrase (in
47	63	13.6	251	2 B90428	hypothetical prote
48	63	13.6	253	2 F85060	hypothetical prote
49	63	13.6	474	2 S16250	phycoene dehydrog
50	63	13.6	577	2 A64131	arginine-tRNA liga
51	63	13.6	961	2 T01167	hypothetical prote
52	63	13.6	2672	2 A48126	translation activa
53	62.5	13.5	236	2 F69866	tetrahydrotolpicoi
54	62.5	13.5	330	1 B64561	ketol-acid reducto
55	62.5	13.5	383	2 A49562	cartilage glycopro
56	62.5	13.5	476	2 A28439	endonuclease Scel
57	62.5	13.5	1114	2 T30299	dynein heavy chain
58	62.5	13.5	3390	1 GNVWD3	genome polyprotein
59	62	13.4	501	2 A84784	hypothetical prote
60	62	13.4	720	2 A83105	probable fumate
61	62	13.4	507	2 JC5131	glycosyltransferas
62	62	13.4	749	2 B86774	hypothetical prote
63	62	13.4	959	1 B60017	outer capsid prote
64	62	13.4	1129	2 S00097	phycochrome 4 - ga
65	61.5	13.3	330	2 S74456	regulatory protein
66	61.5	13.3	353	1 F0WAGR	gag polyprotein -
67	61.5	13.3	652	2 B59102	hypothetical prote
68	61.5	13.3	785	2 C64305	anar 5'-region hyp
69	61.5	13.3	1320	2 B59092	hypothetical prote
70	61.5	13.3	1351	2 S42167	190K protein - hum
71	61	13.2	169	2 PNO560	phycochrome - long
72	61	13.2	171	2 PNO558	phycochrome - wild
73	61	13.2	220	2 S62410	hypothetical prote
74	61	13.2	326	2 AC0832	pseudouridylylate sy
75	61	13.2	386	2 AG0081	conserved hypotet

ALIGNMENTS

RESULT 1

C64013 hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)

C/Spectrum: Haemophilus influenzae

C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

C/Accession: C64013

R/Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;

Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A/Author: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; M01D:95350630; PMID:7542800

A/Accession: C64013

A/Molecule type: DNA

A/Status: nucleic acid sequence not shown; translation not shown

A/Cross-references: UNIPROT:P44048; UNIPARC:UPI0000013B0A4; GB:U32760; GB:U42023; NID:G1E

C/Superfamily: Fe(II) trafficking protein YggX

Query Match 92.0%; Score 425; DB 2; Length 90;
Best Local Similarity 90.8%; Pred. No. 9.6e-37;

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 18:23:46 ; Search time 79.9886 Seconds

(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502a-8

Perfect score: 462

Sequence: 1 MARNVFCBYLKCBARGLDFO.....AEWVNFLEGGVHIDGVVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	94	1	FETP_HABDU
2	425	92.0	90	1	FETP_HABIN
3	425	92.0	90	2	O4QMD9_HABIE8
4	416	90.0	90	1	FETP_PASMU
5	405	87.7	91	1	FETP_MANSU
6	385	83.3	90	1	FETP_VIBCH
7	375	81.2	90	1	FETP_VIBCH
8	373	80.7	90	1	FETP_VIBCH
9	373	80.7	90	1	FETP_VIBCH
10	368	79.7	90	1	FETP_VIBCH
11	368	79.7	90	1	FETP_VIBCH
12	368	79.7	90	1	FETP_VIBCH
13	366	79.2	90	1	FETP_VIBCH
14	366	79.2	90	1	FETP_VIBCH
15	366	79.2	90	1	FETP_VIBCH
16	366	79.2	90	1	FETP_VIBCH
17	365	79.0	90	1	FETP_VIBCH
18	364	78.8	90	1	FETP_VIBCH
19	359	77.7	90	1	FETP_VIBCH
20	354	76.6	90	1	FETP_VIBCH
21	351	76.0	90	1	FETP_VIBCH
22	351	76.0	90	1	FETP_VIBCH
23	351	76.0	90	1	FETP_VIBCH
24	348	74.0	90	1	FETP_VIBCH
25	336	72.7	92	1	FETP_VIBCH
26	336	72.7	92	1	FETP_VIBCH
27	255	55.2	91	1	FETP_VIBCH
28	250	54.1	90	1	FETP_VIBCH
29	250	54.1	91	1	FETP_VIBCH
30	248	53.7	92	1	FETP_VIBCH
31	247	53.5	77	1	FETP_VIBCH

32	246	53.2	90	1	FETP_XYLR	O9PC73 xyliella fas
33	245	53.0	91	2	FETP_9BURK	O41S19 burholderi
34	243	52.6	90	1	FETP_BORPA	O7H06 bordecella
35	243	52.6	90	1	FETP_BORPA	O7H06 bordecella
36	243	52.6	90	1	FETP_BORPA	O7H06 bordecella
37	241	52.2	91	1	FETP_BORPE	O7H06 bordecella
38	241	52.2	92	1	FETP_XANCP	O8P829 xanthomonas
39	241	52.2	92	2	O4UM14_XANCP	O4UM14 xanthomonas
40	237	51.3	90	1	FETP_COXRU	O8B06 coxiella bu
41	235	50.9	88	1	FETP_NEICI	O51553 neisseria g
42	235	50.9	88	1	FETP_NEIMA	O51553 neisseria m
43	235	50.9	88	1	FETP_NEIMA	O51553 neisseria m
44	230	49.8	90	1	FETP_NITEU	O82X62 nitrosomonas
45	229	49.6	78	1	FETP_WIGBR	O82X62 nitrosomonas
46	228.5	49.5	89	1	FETP_LEBGL	O82X62 nitrosomonas
47	226	48.9	90	2	O4J228_AZOVI	O4J228 azotobacter
48	224.5	48.6	89	1	FETP_LEBPA	O5X3X9 legionella
49	224.5	48.6	89	1	FETP_LEBPA	O5X3X9 legionella
50	222	48.1	90	1	FETP_PSEAB	O5X3X9 legionella
51	221	47.8	90	1	FETP_PSEAB	O5X3X9 legionella
52	221	47.8	90	2	O4ZLF3_PSEBY	O87U15 pseudomonas
53	219	47.4	90	1	FETP_PSEBY	O87U15 pseudomonas
54	215	46.5	78	1	FETP_PSEBK	O87U15 pseudomonas
55	212	45.9	87	1	FETP_BUCAP	O8K925 pseudomonas
56	212	45.9	90	2	O6T7F6_PSEBFL	O89A44 pseudomonas
57	210	45.5	90	1	O4KUT2_PSEBFL	O89A44 pseudomonas
58	207.5	44.9	90	1	FETP_ACTAD	O6T7F6 pseudomonas
59	206	44.6	90	1	FETP_CHRVO	O4K12 pseudomonas
60	205	44.4	87	1	FETP_FRATT	O6T7F6 pseudomonas
61	205	44.4	90	1	FETP_MERCA	O6T7F6 pseudomonas
62	204	44.2	79	1	FETP_CAMP	O6T7F6 pseudomonas
63	160	34.6	92	2	O4NM04_9DEUT	O6T7F6 pseudomonas
64	145	31.4	96	2	O4FV07_9GAMM	O4FV07 psychrobact
65	80.5	17.4	1208	2	O8L609_9ARHT	O8L609 arabidopsis
66	80	17.3	265	2	O9RAH0_9NOSO	O9RAH0 nostoc sp.
67	79.5	17.2	416	2	O89K21_BRAVA	O89K21 bradyrhizob
68	76.5	16.6	655	2	O86BD5_9TURB	O86BD5 dugesia rhu
69	75.5	16.3	422	2	O74UT8_LACRO	O74UT8 lactobacilli
70	74	16.0	469	2	O4U8T5_THRAN	O4U8T5 thelaxia a
71	74	16.0	1024	2	O74889_SCHRO	O74889 schistosach
72	73.5	15.9	386	2	O6OK14_CABER	O6OK14 caenorhadi
73	73	15.8	175	2	O4UM13_THRAN	O4UM13 thelaxia a
74	73	15.8	202	2	O81J27_PLAF7	O81J27 plasmodium
75	72.5	15.7	1191	2	O81I10_PLAF7	O81I10 plasmodium

ALIGNMENTS

RESULT 1	FETP_HABDU	STANDARD;	PRT;	94 AA.
ID	FETP_HABDU			
AC	O7JKB6;			
DT	05-JUN-2004 (Rel. 44, Created)			
DT	05-JUN-2004 (Rel. 44, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	OrderedLocustNames=HD2003;			
OS	Haemophilus ducreyi.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
CC	Pasteurellaceae; Haemophilus.			
OX	NCBI_TaxID=730;			
RN				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAN=35000HP / ATCC 700724;			
RA	Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,			
RA	Johnson L., Nguyen D., Wang J., Forest C., Hood L.,			
RT	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
RL	FUNCTION: Could be a mediator in iron transactions between iron			
CC	acquisition and iron-requiring processes, such as synthesis and/or			
CC	repair of Fe-S clusters in biosynthetic enzymes (By similarity).			
CC	-1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.			

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: AE017156; AAP96716.1; -; Genomic_DNA.
CC
CC SMR: Q7YK6; 1-87.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC PIRSF: PIRSF029191; DUF495; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC KW
CC SEQUENCE 94 AA; 11039 MW; B5A232C56DE93765 CRC64;
SQ

Query Match 100.0%; Score 462; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.9e-41; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 0;

QY 1 MARVPCFYKKEAGDLPOLYPGELGKRIFNISISQAMAEWIKQTMVNEKKLMMNP 60
DB 1 MARVPCFYKKEAGDLPOLYPGELGKRIFNISISQAMAEWIKQTMVNEKKLMMNP 60
QY 61 EHRQLLEAMVNFLEGGKVHIDGYVP 87
DB 61 EHRQLLEAMVNFLEGGKVHIDGYVP 87

RESULT 2

REP_HABIN STANDARD; PRT; 90 AA.
ID REP_HABIN
AC P44048;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocNames=HI0760;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OC NCBI_TaxId=727;
OX

RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=RD / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geobaghen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).

RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RX DOI=10.1002/bsic.1522-2683(20000101)21:2<411::AID-ELPS411>3.3.CO;2-W;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae";
RT Electrophoresis 21:411-429(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL: U32760; AAC22419.1; -; Genomic_DNA.
CC PIR: C64013; C64013.
CC SMR: P44048; 1-87.
CC TIGR: H10760; -; 1.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC PIRSF: PIRSF029191; DUF495; 1.
CC ProDom: PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC KW
CC SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;
SQ

Query Match 92.0%; Score 425; DB 1; Length 90;
Best Local Similarity 90.8%; Pred. No. 3.9e-37; Indels 0; Gaps 0;
Matches 79; Conservative 4; Mismatches 4;

QY 1 MARVPCFYKKEAGDLPOLYPGELGKRIFNISISQAMAEWIKQTMVNEKKLMMNP 60
DB 1 MARVPCFYKKEAGDLPOLYPGELGKRIFNISISQAMAEWIKQTMVNEKKLMMNP 60
QY 61 EHRQLLEAMVNFLEGGKVHIDGYVP 87
DB 61 EHRQLLEAMVNFLEGGKVHIDGYVP 87

RESULT 3

Q4QMD9_HAB18 PRELIMINARY; PRT; 90 AA.
ID Q4QMD9_HAB18
AC Q4QMD9;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=NH10920;
OS Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OC NCBI_TaxId=281310;
OX

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillaespy A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gibson J., Gibson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S., Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20.";
RL J. Bacteriol. 187:4627-4636(2005).
RA EMBL: CP000057; AAX87808.1; -; Genomic_DNA.
RA InterPro: IPR007457; YggX.
RA Pfam: PF04362; DUF495; 1.
RA PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
RA ProDom: PD029191; DUF495; 1.
RA Complete proteome; Hypothetical protein.
RA KW
RA SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;
SQ

Query Match 92.0%; Score 425; DB 2; Length 90;
Best Local Similarity 90.8%; Pred. No. 3.9e-37; Indels 0; Gaps 0;
Matches 79; Conservative 4; Mismatches 4;

QY 1 MARVPCFYKKEAGDLPOLYPGELGKRIFNISISQAMAEWIKQTMVNEKKLMMNP 60
DB 1 MARVPCFYKKEAGDLPOLYPGELGKRIFNISISQAMAEWIKQTMVNEKKLMMNP 60
QY 61 EHRQLLEAMVNFLEGGKVHIDGYVP 87
DB 61 EHRQLLEAMVNFLEGGKVHIDGYVP 87

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502a-8

Perfect score: 462
Sequence: 1 MARWVFCETLKKEAGLDLFDQ.....AEWVNFLEKGVHDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5/COMB.pep:*
2: /cgn2_6/prodata/1/iaa/6/COMB.pep:*
3: /cgn2_6/prodata/1/iaa/H/COMB.pep:*
4: /cgn2_6/prodata/1/iaa/B/CUTS/COMB.pep:*
5: /cgn2_6/prodata/1/iaa/RB/COMB.pep:*
6: /cgn2_6/prodata/1/iaa/Backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	371	80.3	107	2	US-09-489-039A-11962
2	367	79.4	93	2	US-09-543-681A-5443
3	222	48.1	122	2	US-09-252-991A-23355
4	211.5	45.8	92	2	US-09-328-352-5456
5	143	31.0	110	2	US-09-540-236-2859
6	76	16.5	217	2	US-09-543-681A-7862
7	71	15.4	292	2	US-09-328-352-5836
8	68.5	14.8	476	2	US-09-316-083-3
9	68.5	14.8	476	2	US-09-328-352-7874
10	67.5	14.6	1233	2	US-09-933-700-3
11	66.5	14.4	415	1	US-08-602-010A-10
12	66.5	14.4	415	1	US-08-680-726A-10
13	66.5	14.4	415	1	US-09-092-409-10
14	66	14.3	154	2	US-09-107-532A-4611
15	65.5	14.2	591	2	US-09-370-368-8
16	65.5	14.2	683	2	US-09-270-767-46792
17	65	14.1	191	2	US-09-270-767-3362A
18	65	14.1	191	2	US-09-270-767-48841
19	65	14.1	217	2	US-09-543-681A-7649
20	65	14.1	754	1	US-08-941-262-1
21	64	13.9	360	2	US-10-037-417-67
22	64	13.9	674	2	US-08-961-083-200
23	64	13.9	674	2	US-09-536-784-200
24	64	13.9	674	2	US-09-765-271-200
25	64	13.9	674	2	US-09-765-272A-200
26	63.5	13.7	496	2	US-09-600-170-20
27	63.5	13.7	623	2	US-10-104-047-2547

28	63	13.6	359	1	US-09-092-770-6	Sequence 6, Appl1
29	63	13.6	359	2	US-09-222-851-6	Sequence 6, Appl1
30	63	13.6	359	2	US-10-265-062-6	Sequence 6, Appl1
31	63	13.6	404	1	US-09-092-770-3	Sequence 3, Appl1
32	63	13.6	404	2	US-09-222-851-3	Sequence 3, Appl1
33	63	13.6	404	2	US-10-265-062-3	Sequence 3, Appl1
34	63	13.6	407	2	US-09-949-016-11184	Sequence 11184, A
35	62.5	13.5	365	2	US-09-949-016-7947	Sequence 7947, Ap
36	62.5	13.5	365	2	US-09-949-016-6053	Sequence 6053, Ap
37	62.5	13.5	959	2	US-09-543-681A-6879	Sequence 6879, Ap
38	62	13.4	364	2	US-09-328-352-4659	Sequence 4659, Ap
39	62	13.4	474	2	US-09-252-991A-24473	Sequence 24473, A
40	62	13.4	680	2	US-09-298-924-4	Sequence 4, Appl1
41	62	13.4	720	1	US-08-840-236-1	Sequence 1, Appl1
42	62	13.4	1120	2	US-08-505-448A-1	Sequence 1, Appl1
43	62	13.4	1239	2	US-09-147-404-1	Sequence 1, Appl1
44	61.5	13.3	239	2	US-09-270-767-32538	Sequence 32538, A
45	61.5	13.3	239	2	US-09-270-767-47755	Sequence 47755, A
46	61	13.2	337	2	US-09-819-607-4	Sequence 41746, A
47	61	13.2	369	2	US-09-819-607-2	Sequence 2, Appl1
48	61	13.2	384	2	US-09-801-876B-6	Sequence 6, Appl1
49	61	13.2	384	2	US-10-254-869-6	Sequence 6, Appl1
50	61	13.2	384	2	US-10-667-442-6	Sequence 6, Appl1
51	61	13.2	399	2	US-09-819-607-4	Sequence 4, Appl1
52	61	13.2	419	2	US-09-799-875-14	Sequence 14, Appl1
53	61	13.2	482	2	US-09-248-796A-17800	Sequence 17800, A
54	61	13.2	1724	2	US-09-607-510-2	Sequence 2, Appl1
55	61	13.2	1935	2	US-09-538-092-916	Sequence 916, App
56	61	13.2	1944	2	US-09-949-016-10929	Sequence 10929, A
57	60.5	13.1	57	2	US-09-562-737-124	Sequence 124, App
58	60.5	13.1	116	2	US-09-562-737-125	Sequence 125, App
59	60.5	13.1	205	2	US-09-080-983-19	Sequence 19, Appl
60	60.5	13.1	205	2	US-09-613-486-19	Sequence 19, Appl
61	60.5	13.1	858	2	US-09-248-796A-19082	Sequence 19082, A
62	60	13.0	402	2	US-09-489-039A-9252	Sequence 9252, Ap
63	60	13.0	528	2	US-09-071-035-44	Sequence 44, Appl
64	60	13.0	528	2	US-10-206-576-44	Sequence 44, Appl
65	60	13.0	547	2	US-09-071-035-42	Sequence 42, Appl
66	60	13.0	547	2	US-10-206-576-42	Sequence 42, Appl
67	60	13.0	713	2	US-09-949-016-6674	Sequence 6674, Ap
68	60	13.0	737	2	US-09-949-016-7675	Sequence 7675, Ap
69	60	13.0	1003	2	US-09-991-181-33	Sequence 33, Appl
70	60	13.0	1003	2	US-09-990-444-33	Sequence 33, Appl
71	60	13.0	1003	2	US-09-997-333-33	Sequence 33, Appl
72	60	13.0	1003	2	US-09-992-598-33	Sequence 33, Appl
73	59.5	12.9	236	2	US-09-492-709A-342	Sequence 342, App
74	59.5	12.9	390	2	US-09-711-164-405	Sequence 405, App
75	59.5	12.9	396	2	US-09-328-352-5040	Sequence 5040, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709 2004001
CURRENT FILING DATE: 2000-01-27
PRIORITY FILING DATE: 1999-01-29
PRIORITY FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match	80.3%	Score 371;	DB 2;	Length 107;
Best Local Similarity	74.7%	Pred. No. 1.6e-40;		
Matches 65;	Conservative 13;	Mismatches 9;	Indels 0;	Gaps 0;

```

0y      1 MARWAFCEYLKKEAEGLDFOLYPGEIGRI FNSISKQAAEWIKQOTL VNEKJLMMNP 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      17 MSRTTCTFLQREADGQDFOLYPGELGRIYNEISKAAQWQHQOTL INEKLJSMNP 76

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QY 61 EHRQLLEAEWVNFLEFGKDVIHIDGYVP 87
|||:|||||:|||||:|||||
Db 77 EHRKLLLEQEMVQFLFEGKDVIHIEGYTP 103

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A

: APPLICANT: GARY BRETON
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 : TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

Query Match	79.4%;	Score 367;	DB 2;	Length 93;
Best Local Similarity	74.7%;	Pred. No. 4.5e-40;		
Matches 65;	Conservative 10;	Mismatches 12;	Indels 0;	Gaps 0

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Qy      1 MARMVEEYLKKAEGLDLFQLYPELGKRI FNSISKQAMAEWIKQTM LVEKKLNNP 600
      2 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      3 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      4 MSRTIFCTPLNKADGDLDFQLYPELGKRI FNSISKQAMQMAQTM LNEKKLTNP 630

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QY 61 EHRQLAEAMVNFLEFGKDVHIDGYR 87
 : | : | | | | | | | | | |
Db 64 DDKRLLEQEMVRFLFEGHDVHIIDGYP 90

RESULT 3
US-09-252-991A-23355
! Sequence 23355, Application US/09252991A

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/ GENERATED INFORMATION:
/
/ APPLICANT: Marc J. Rubenfield et al.
/
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/
/

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Query Match	48.1%	Score 222;	DB 2;	Length 122;
Best Local Similarity	51.1%;	Pred. No. 4.8e-21;		
Matches 45;	Conservative 14;	Mismatches 27;	Indels 2;	Gaps 2

QY 1 MARMVFC EYLKKEAEGLDQLYPGBLGKRIFNSISKQAWAEWIKKQTM LVNEKKLNMNP 60

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33 MSRTWCRKTHEELPGIDRPPYGAKEGDIYNNVSRKADWEOHQOTMLINERLNNNA 922

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Qy 61 EHRQLLEAEVNVNLFEGKD-VHIDGYVP 87
| : : | | : | | | |
Db 93 EDRKFLQGEIMDKFL-SGEDYAKADGYVP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352

APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

Query Match	45.8%	Score 211.5;	DB 2;	Length 92;
Best Local Similarly	44.3%	Pred. No. 7.7e-20;		
Matches 39;	Conservative 17;	Mismatches 31;	Indels 1;	Gaps 1;

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Qy      1 MARMWCEYLKKEAGELDFOLYPGELGRIFNSISKQAAEWIKQTMLVNEKKLMMNP    600
       :|::|||:|||||:|::|||:|||||:|::|||:|||||:|::|||:|||||:|::|||:
Db      4 MSRQVCRCRYQKQEMEGDLPAPFFGAQGGEFFENSSQAQNBWLHQRTLLINEKLNVFEP    633
```

QY 61 EHRÖLLEAEMWNFLFEKDVH-IDGYVP 87
 64 EAKKFLFEÖREKFPNNDESVEKAEGWKP 91
 Dö

RESULT 5
US-09-540-236-2859
: Sequence 2859, Application US/09540236

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

Query Match	31.0%	Score 143;	DB 2;	length 110;
Best Local Similarity	35.7%	Pred. No. 8.1e-11;		
Matches 30;	Conservative 17;	Mismatches 37;	Indels 0;	Gaps 0

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Oy      4 MYFCBYLKKKAGLDPOLYPGLGKRIFNSISKQMAEWIKKGOTMLVNEKCLNMNNZHR 6
          ||| : : | : || : || : ||| : ||| : : : :
Db     24 MYFCRKYQNLPRLPNRPFPNKAQGEIDPTISAKANNWELQTMLINEKHLSMIDPAK 8
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QY 64 QLLAEAMVNFLEGGDVHIDGYVP 87
: : : : :
Db 84 KYLNEQRKFLDNGDYEKPPAGYKP 107

RESULT 6
US-09-543-681A-7862
; Sequence 7862, Application US/09543681A

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-8

Perfect score: 462
Sequence: 1 MARWFCBYLKKRAGLDFO.....AEWVFLFRGKDVHIDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:*

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- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
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- 4: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	425	92.0	87	3	US-09-955-502-7
3	416	90.0	87	3	US-09-955-502-6
4	412	89.2	91	3	US-09-955-502-5
5	375	81.2	90	3	US-09-955-502-10
6	373	80.7	91	3	US-09-955-502-11
7	373	80.7	91	3	US-09-955-502-12
8	373	80.7	91	3	US-09-955-502-13
9	371	80.3	88	3	US-09-955-502-15
10	371	80.3	91	3	US-09-955-502-14
11	371	80.3	91	3	US-09-955-502-16
12	371	80.3	91	3	US-09-955-502-17
13	364	78.8	91	3	US-09-955-502-18
14	351	76.0	90	3	US-09-955-502-20
15	336	72.7	88	3	US-09-955-502-9
16	327	70.8	78	3	US-09-955-502-19
17	255	55.2	87	3	US-09-955-502-29
18	255	54.2	87	3	US-09-955-502-30
19	247	53.5	76	3	US-09-955-502-21
20	246	53.2	89	3	US-09-955-502-22
21	243	52.6	87	3	US-09-955-502-3
22	243	51.3	88	3	US-09-955-502-13
23	237	50.9	88	3	US-09-955-502-26
24	235	50.9	88	3	US-09-955-502-27
25	235	50.9	88	3	US-09-955-502-28
26	235	50.9	88	3	US-09-955-502-28
27	225.5	48.8	86	3	US-09-955-502-4

28 222 48.1 87 3 US-09-955-502-25 Sequence 25, Appl
29 221 47.8 90 3 US-09-955-502-23 Sequence 23, Appl
30 219 47.4 87 3 US-09-955-502-24 Sequence 24, Appl
31 211 45.7 87 3 US-09-955-502-31 Sequence 31, Appl
32 205 44.4 87 3 US-09-955-502-32 Sequence 32, Appl
33 74 16.0 1144 4 US-10-369-493-22774 Sequence 22774, A
34 68.5 14.8 476 3 US-09-774-414-3 Sequence 3, Appl
35 68.5 14.8 507 4 US-10-282-122A-4787 Sequence 4787, A
36 67.5 14.6 765 4 US-10-078-770-84 Sequence 84, Appl
37 67.5 14.6 818 4 US-10-078-770-94 Sequence 94, Appl
38 67.5 14.6 1809 4 US-10-437-963-159972 Sequence 159972, A
39 67.5 14.6 2478 4 US-10-437-963-131742 Sequence 131742, A
40 67.5 14.6 507 4 US-10-282-122A-68134 Sequence 68134, A
41 67 14.5 511 4 US-10-425-113-355492 Sequence 355492, A
42 66.5 14.4 160 4 US-10-156-275-10 Sequence 10, Appl
43 66.5 14.4 1232 4 US-10-282-122A-45194 Sequence 45194, A
44 66.5 14.3 149 4 US-10-282-122A-53476 Sequence 53476, A
45 66 14.3 150 4 US-10-282-122A-57454 Sequence 57454, A
46 65.5 14.2 511 4 US-10-282-122A-50464 Sequence 50464, A
47 65.5 14.2 591 3 US-09-827-823-8 Sequence 8, Appl
48 65.5 14.1 330 6 US-11-097-143-744 Sequence 744, Appl
49 65 14.1 449 4 US-10-231-913-110 Sequence 110, Appl
50 65 14.1 471 4 US-10-231-913-109 Sequence 109, Appl
51 65 14.1 546 4 US-10-282-122A-66021 Sequence 66021, A
52 65 14.1 745 3 US-09-881-852-1 Sequence 1, Appl
53 65 14.1 856 4 US-10-408-765A-2006 Sequence 2006, Appl
54 65 14.0 206 5 US-10-510-812-76 Sequence 76, Appl
55 64.5 14.0 500 4 US-10-437-963-170681 Sequence 170681, A
56 64.5 14.0 631 4 US-10-425-115-317990 Sequence 317990, A
57 64.5 14.0 711 4 US-10-424-599-178578 Sequence 178578, A
58 64.5 14.0 1073 3 US-09-815-242-12361 Sequence 12361, A
59 64.5 14.0 1147 3 US-09-815-242-5468 Sequence 5468, A
60 64.5 14.0 1150 4 US-10-282-122A-44391 Sequence 44391, A
61 64.5 14.0 1150 4 US-10-767-701-35066 Sequence 35066, A
62 64 13.9 235 4 US-10-103-417-67 Sequence 8, Appl
63 64 13.9 307 3 US-09-911-826A-7 Sequence 7, Appl
64 64 13.9 360 4 US-10-023-634-88 Sequence 88, Appl
65 64 13.9 360 4 US-10-037-417-67 Sequence 67, Appl
66 64 13.9 674 3 US-09-765-272-200 Sequence 200, Appl
67 64 13.9 674 6 US-11-106-648-200 Sequence 200, Appl
68 64 13.9 696 5 US-10-472-928-3656 Sequence 3656, A
69 64 13.9 1111 5 US-10-450-763-45127 Sequence 45127, A
70 64 13.9 1183 5 US-10-450-763-42869 Sequence 42869, A
71 64 13.9 1183 5 US-10-450-763-46162 Sequence 46162, A
72 64 13.9 1183 5 US-10-450-763-53544 Sequence 53544, A
73 64 13.9 1261 5 US-10-437-963-189166 Sequence 189166, A
74 63.5 13.7 115 5 US-10-739-930-9367 Sequence 9367, A
75 63.5 13.7 320 4 US-10-282-122A-46765 Sequence 46765, A

ALIGNMENTS

RESULT 1
US-09-955-502-8
Sequence 8, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.9/9559
CURRENT APPLICATION NUMBER: US/09/955.502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 87
TYPE: PRT
ORGANISM: Haemophilus ducreyi

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 5.92509 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502a-8

Perfect score: 462
Sequence: 1 MARWFCERYLKKEAGELDFQ.....AEWVFLFEGKDVHIDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Published Applications_AA_New:*
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4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	235	50.9	88	US-10-467-657-968	Sequence 968, App
2	69	14.9	593	US-11-194-246-317	Sequence 317, App
3	67.5	14.6	765	US-11-120-308-84	Sequence 84, App
4	67.5	14.6	818	US-11-120-308-94	Sequence 94, App
5	64	13.9	360	US-11-019-711-67	Sequence 67, App
6	63.5	13.7	496	US-11-069-642-20	Sequence 20, App
7	63.5	13.7	623	US-11-072-512-2547	Sequence 2547, App
8	63	13.6	359	US-11-087-227-8	Sequence 8, App
9	63	13.6	359	US-11-192-450-6	Sequence 6, App
10	63	13.6	404	US-11-087-227-6	Sequence 6, App
11	63	13.6	404	US-11-192-450-3	Sequence 3, App
12	61.5	13.3	834	US-11-098-686-10643	Sequence 658, App
13	60	13.0	140	US-11-087-327-10	Sequence 10, App
14	60	13.0	296	US-10-453-372-640	Sequence 640, App
15	59.5	12.9	336	US-11-143-980-37	Sequence 37, App
16	59.5	12.9	372	US-10-821-234-900	Sequence 900, App
17	59.5	12.9	423	US-10-453-372-648	Sequence 648, App
18	59.5	12.9	700	US-10-995-561-922	Sequence 922, App
19	59.5	12.9	700	US-10-995-561-924	Sequence 924, App
20	59.5	12.9	775	US-10-453-372-656	Sequence 656, App
21	59.5	12.9	793	US-10-995-561-925	Sequence 925, App
22	59.5	12.9	793	US-10-453-372-650	Sequence 650, App
23	59.5	12.9	804	US-10-453-372-654	Sequence 654, App
24	59.5	12.9	847	US-10-453-372-652	Sequence 652, App
25	59.5	12.9	857	US-10-453-372-652	Sequence 652, App

26 59.5 12.9 905 6 US-10-453-372-638 Sequence 638, App
27 59.5 12.9 905 6 US-10-453-372-662 Sequence 662, App
28 59.5 12.9 905 6 US-10-453-372-664 Sequence 664, App
29 59.5 12.9 963 6 US-10-995-561-923 Sequence 923, App
30 59.5 12.9 963 6 US-10-453-372-660 Sequence 660, App
31 59.5 12.9 1012 6 US-10-453-372-646 Sequence 646, App
32 58.5 12.7 253 6 US-10-724-598-28 Sequence 28, App
33 58.5 12.7 369 6 US-10-517-939-16 Sequence 16, App
34 57.5 12.4 508 7 US-11-072-512-2186 Sequence 2186, App
35 57.5 12.4 760 7 US-11-186-284-55 Sequence 55, App
36 57.5 12.4 774 7 US-11-070-627-7 Sequence 7, App
37 57 12.3 650 6 US-10-467-657-1948 Sequence 1948, App
38 56.5 12.2 349 6 US-10-821-234-1387 Sequence 1387, App
39 56.5 12.2 1734 7 US-11-192-967-6 Sequence 6, App
40 56.5 12.2 1734 7 US-11-193-715-6 Sequence 6, App
41 56.5 12.2 1822 7 US-11-169-041-193 Sequence 193, App
42 209 5 US-09-995-493-94 Sequence 94, App
43 56 12.1 342 7 US-11-156-084-25 Sequence 25, App
44 56 12.1 342 7 US-11-156-084-44 Sequence 44, App
45 56 12.1 369 7 US-11-156-084-45 Sequence 45, App
46 56 12.1 619 7 US-11-156-084-24 Sequence 24, App
47 55.5 12.0 301 7 US-11-055-822-1062 Sequence 1062, App
48 55.5 12.0 382 6 US-10-995-561-926 Sequence 926, App
49 55.5 12.0 415 6 US-10-995-561-927 Sequence 927, App
50 55.5 12.0 415 7 US-11-219-282-10 Sequence 10, App
51 55.5 12.0 1613 7 US-11-108-528-84 Sequence 84, App
52 55.5 12.0 1613 7 US-11-108-528-86 Sequence 86, App
53 55 11.9 236 7 US-11-156-084-284 Sequence 284, App
54 55 11.9 319 6 US-10-793-628-2760 Sequence 2760, App
55 55 11.9 443 6 US-10-793-628-1200 Sequence 1200, App
56 54.5 11.8 411 6 US-10-873-528-117 Sequence 117, App
57 54.5 11.8 445 7 US-11-074-176-182 Sequence 182, App
58 54.5 11.8 782 7 US-11-000-463-471 Sequence 471, App
59 54.5 11.8 864 6 US-10-793-628-2352 Sequence 2352, App
60 54 11.8 864 7 US-11-077-550-102 Sequence 102, App
61 54 11.7 254 7 US-10-821-234-1522 Sequence 1522, App
62 54 11.7 254 7 US-11-072-512-3198 Sequence 3198, App
63 54 11.7 403 7 US-11-192-450-4 Sequence 4, App
64 54 11.7 510 7 US-11-087-100-26 Sequence 26, App
65 54 11.7 510 7 US-11-087-084-26 Sequence 26, App
66 54 11.7 739 6 US-11-087-085-26 Sequence 26, App
67 54 11.7 739 6 US-10-131-826A-478 Sequence 478, App
68 54 11.7 894 7 US-11-192-219-7 Sequence 7, App
69 54 11.7 894 7 US-11-202-330-2 Sequence 2, App
70 54 11.7 1047 7 US-11-072-512-2408 Sequence 2408, App
71 54 11.7 1162 7 US-11-202-330-43 Sequence 43, App
72 54 11.7 2059 7 US-11-087-100-4 Sequence 4, App
73 54 11.7 2059 7 US-11-087-084-4 Sequence 4, App
74 54 11.7 2059 7 US-11-087-085-4 Sequence 4, App
75 54 11.7 2335 6 US-10-821-234-1610 Sequence 1610, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10-467,657
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 50.9%; Score 235; DB 6; Length 88;
Best Local Similarity 51.1%; Pred. No. 2, 4e-20;
Matches 45; Conservative 16; Mismatches 25; Indels 2; Gaps 2;

QY 1 MARWPCETLKRBAGLDPOLYPGELKRIFNISISQAAAEWIKQOTLVNEKLANMP 60
DB 1 MARWPCVTLNKEABGKPPPLPNEIKRIFENVSOEAWAATRHQOTLVNENRLSLDP 60

QY 61 EHRQLLEAMVPLF-EGKDVHIDGYVP 87
DB 61 RAREYLAQMEQYFEDGADA-VQGYVP 87

RESULT 2
US-11-194-246-317
Sequence 317, Application US/11194246
Publication No. US20050272089A1

GENERAL INFORMATION:
APPLICANT: Mott, John
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Staffan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
TITLE OF INVENTION: US
FILE REFERENCE: 00592.051 (Mar 268, 05920101)
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/11/194,246
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 14.9%; Score 69; DB 7; Length 593;
Best Local Similarity 37.5%; Pred. No. 2, 8;
Matches 18; Conservative 5; Mismatches 17; Indels 8; Gaps 1;

QY 33 SISKQAAEWIKQOTLVNEKLANMPH-----ROLLEAEWVN 72
DB 294 SISKQMRWYKQDILKTKLTALSKRGFYPLMLAATQLKQAYQLN 341

RESULT 3
US-11-120-308-84
Sequence 84, Application US/11120308
Publication No. US20060005277A1

GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120,308
CURRENT FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 84
LENGTH: 765
TYPE: PRT
ORGANISM: Helianthus tuberosus
US-11-120-308-84

Query Match 14.6%; Score 67.5; DB 7; Length 765;
Best Local Similarity 25.0%; Pred. No. 5, 6;
Matches 18; Conservative 14; Mismatches 17; Indels 23; Gaps 4;

QY 7 CEYLKKEBAGLDPOLY-----PGEIK-----RINISISKQAAAEW-----I 43
DB 43 CHYTATYDGISFDLYDAYVAERKPDYIARIVMEYDKELYSQAQWFFRAEDTVI 102

QY 44 KQOTLVNEKRL 55
DB 103 KQAHILDKRY 114

RESULT 4
US-11-120-308-94
Sequence 94, Application US/11120308
Publication No. US20060005277A1

GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Forge, Charlie
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: CDNAS Encoding Polypeptides
FILE REFERENCE: BB-1365 US NA
CURRENT APPLICATION NUMBER: US/11/120,308
CURRENT FILING DATE: 2005-05-02
PRIOR APPLICATION NUMBER: US/10/078,770
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/614,188
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,400
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/153,534
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/161,223
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/159,878
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/157,401
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: 60/143,419
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,409
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Microsoft Office 97
SEQ ID NO 94
LENGTH: 818
TYPE: PRT
ORGANISM: Helianthus tuberosus
US-11-120-308-94

Query Match 14.6%; Score 67.5; DB 7; Length 818;
Best Local Similarity 25.0%; Pred. No. 6, 1;
Matches 18; Conservative 14; Mismatches 17; Indels 23; Gaps 4;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 83.9047 Seconds

(without alignments)
460.825 Million cell updates/sec.

Title: US-09-955-502A-9

Perfect score: 466

Sequence: 1 MARTINCHINKAAGDGLDFO.....QMTSPLEKGVIEKGFVPE 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	100.0	88	5	ABB78154 Amino aci
2	356	76.4	87	5	ABB78152 Amino aci
3	347	74.5	90	5	ABB78155 Amino aci
4	346	74.2	93	7	ADP05158 Bacterial
5	345	74.0	87	5	ABB78151 Amino aci
6	344	73.8	91	5	ABB78150 Amino aci
7	336	72.1	87	5	ABB78153 Amino aci
8	336	72.1	88	5	ABB78160 Amino aci
9	336	72.1	91	5	ABB78161 Amino aci
10	336	72.1	91	5	ABB78159 Amino aci
11	336	72.1	91	5	ABB78162 Amino aci
12	332	71.2	91	5	ABB78158 Amino aci
13	332	71.2	91	5	ABB78157 Amino aci
14	332	71.2	91	5	ABB78156 Amino aci
15	332	70.2	107	7	ABO65445 Klebsiella
16	336	70.0	91	5	ABB78163 Amino aci
17	308	66.1	90	5	ABB78165 Amino aci
18	292	62.7	78	5	ABB78164 Amino aci
19	256	54.9	87	5	ABB78148 Amino aci
20	256	54.9	87	5	ABB78147 Amino aci
21	242.5	52.0	86	5	ABB78149 Amino aci
22	237	50.9	87	5	ABB78169 Amino aci
23	235	50.4	87	5	ABB78170 Amino aci
24	235	50.4	122	7	ABO74609 Pseudomon

25	230	49.4	88	5	ABB78171 Amino aci
26	230	49.4	88	5	ABB78172 Amino aci
27	230	49.4	88	5	ABB78173 Amino aci
28	230	49.4	88	6	ABP77219 N. gonorr
29	228	48.9	90	5	ABB78168 Amino aci
30	226	48.5	87	5	ABB78175 Amino aci
31	220	47.2	87	5	ABB78174 Amino aci
32	216	46.4	76	5	ABB78166 Amino aci
33	215	46.1	87	5	ABB78177 Amino aci
34	213	45.7	87	5	ABB78176 Amino aci
35	211.5	45.4	89	9	AEBA1576 L. pneumo
36	211.5	45.4	95	9	AEBA1576 L. pneumo
37	205	44.0	88	5	ABB78178 Amino aci
38	200.5	43.0	92	6	ADA34169 Acinetoba
39	186.5	40.0	90	5	ABB78167 Amino aci
40	130	27.9	110	8	ADL05173 M. catarr
41	77.5	16.6	2364	8	ABP65068 Hypoxia-1
42	77.5	16.6	2364	8	ABP65068 Hypoxia-1
43	77.5	16.6	2364	8	ABP65068 Hypoxia-1
44	75.5	16.2	1120	2	AAW81642 Human pro
45	75.5	16.2	1630	7	ADJ70625 Mouse elf
46	75.5	16.2	2154	2	AAW81639 Mouse elf
47	75.5	16.2	2154	7	ADP74491 Murine elf
48	75.5	16.2	2154	8	ADQ88363 Mouse elf
49	75.5	16.2	2154	9	ADZ85101 Full-leng
50	68.5	14.7	352	7	ADB80553 Ovarian c
51	68	14.6	315	7	ADP83528 C. reinha
52	68	14.6	315	7	ADP83527 C. reinha
53	68	14.6	344	8	ADT71540 Human CGD
54	68	14.6	359	2	AAV43175 Human cyc
55	68	14.6	359	4	AAV72464 Human cyc
56	68	14.6	359	7	ADP48690 Human cyc
57	68	14.6	359	8	ADP48690 Human cyc
58	68	14.6	404	2	AAV43173 Human cyc
59	68	14.6	404	3	AAV77483 Human cyc
60	68	14.6	404	4	AAV72462 Human cyc
61	68	14.6	404	7	ADP48687 Human cyc
62	68	14.6	404	7	ADP48687 Human cyc
63	68	14.6	404	8	ADP48687 Human cyc
64	68	14.6	404	8	ADN05983 Antipepti
65	68	14.6	404	8	ADN05983 Antipepti
66	68	14.6	404	8	ADN05983 Antipepti
67	68	14.6	404	8	ADN05983 Antipepti
68	68	14.6	404	9	ADY15468 PRO polyp
69	68	14.6	737	7	ADP83524 C. reinha
70	68	14.6	737	7	ADP83524 C. reinha
71	66.5	14.3	689	8	ADS82827 Bacterial
72	66.5	14.3	1176	6	ABR53186 Protein s
73	66.5	14.3	1176	7	ADK63224 Disease t
74	66	14.2	261	8	ADP81257 Protein o
75	66	14.2	269	8	ADP81258 Protein o
			307	5	ABB90271 Human pol

ALIGNMENTS

RESULT 1
ABB78154 standard; protein; 88 AA.
ID ABB78154;
AC ABB78154;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a Yggx homologue.
XX
XX Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; Yggx homologue.
XX
XX Unidentified.
XX
XX US2002072118-A1.
XX

PD 13-JUN-2002.
 PP 18-SEP-2001; 2001US-00955502.
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 PA Downs D, Gralnick JA;
 PI WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 88 AA;
 Query Match 100.0%; Score 466; DB 5; Length 88;
 Best Local Similarity 100.0%; Pred. No. 4.8e-49;
 Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARTVNCVHLNKEADGIDPOLYPGDLGKRIFDNISKEAWGLMOKKQTMLINEKLNMMNV 60
 DB 1 MARTVNCVHLNKEADGIDPOLYPGDLGKRIFDNISKEAWGLMOKKQTMLINEKLNMMNV 60
 QY 61 DDRKFLFAOMTSFLFEGKDVIEIGFVPE 88
 DB 61 DDRKFLFAOMTSFLFEGKDVIEIGFVPE 88
 Db
 RESULT 2
 ABB78152
 ID ABB78152 standard; protein; 87 AA.
 AC ABB78152;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.
 XX
 KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.
 XX
 OS Haemophilus influenzae.
 XX
 PN US2002072118-A1.
 PD 13-JUN-2002.
 PP 18-SEP-2001; 2001US-00955502.
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 PA Downs D, Gralnick JA;
 PI
 XX

DR WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 XX
 SQ Sequence 87 AA;
 Query Match 76.4%; Score 356; DB 5; Length 87;
 Best Local Similarity 74.7%; Pred. No. 1.4e-35;
 Matches 65; Conservative 11; Mismatches 11; Indels 0; Gaps 0;
 QY 1 MARTVNCVHLNKEADGIDPOLYPGDLGKRIFDNISKEAWGLMOKKQTMLINEKLNMMNV 60
 DB 1 MARTVNCVHLNKEADGIDPOLYPGDLGKRIFDNISKEAWGLMOKKQTMLINEKLNMMNV 60
 QY 61 DDRKFLFAOMTSFLFEGKDVIEIGFVPE 87
 DB 61 EHRKLIQEMVNFLEFGKDVHIEGYVP 87
 Db
 RESULT 3
 ABB78155
 ID ABB78155 standard; protein; 90 AA.
 AC ABB78155;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.
 XX
 KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.
 XX
 OS Vibrio cholerae.
 XX
 PN US2002072118-A1.
 PD 13-JUN-2002.
 PP 18-SEP-2001; 2001US-00955502.
 XX 22-SEP-2000; 2000US-0234588P.
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 PA Downs D, Gralnick JA;
 PI WPI; 2002-589476/63.
 XX
 XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.5846 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502a-9

Perfect score: 466
Sequence: 1 MARTVGVHMKKADGLDFQ.....QMTSFLFRGKVEIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	76.4	90	2	C64013
2	347	74.5	90	2	C82320
3	336	72.1	91	2	AH0879
4	332	71.2	91	2	A85954
5	332	71.2	91	2	A65082
6	332	71.2	91	2	F91108
7	308	66.1	90	2	A10116
8	235	50.4	90	2	H83003
9	230	49.4	88	2	H81014
10	216	46.4	93	2	B84994
11	196	42.1	105	2	C82624
12	177.5	16.6	2364	1	A44159
13	75.5	16.2	1252	2	A47213
14	70	15.0	936	2	H71728
15	68.5	14.7	412	2	S62538
16	67.5	14.5	568	2	T25859
17	67.5	14.5	1111	2	T23047
18	67	14.4	928	2	C97728
19	66.5	14.3	260	2	H82925
20	66.5	14.3	689	2	F83902
21	66.5	14.3	1123	2	T30880
22	66.5	14.3	1176	2	S40899
23	66	14.2	384	2	F64438
24	65.5	14.1	1021	2	AC2202
25	65	13.9	300	2	T15690
26	65	13.9	380	2	T18509
27	65	13.9	651	2	G69177
28	64.5	13.8	577	1	S39804
29	64.5	13.8	1119	2	T18491

30	64	13.7	365	2	C83885	hypothetical prote
31	64	13.7	578	2	T11659	hypothetical prote
32	64	13.7	964	2	T32482	hypothetical prote
33	63.5	13.6	310	2	C64370	modification methy
34	63.5	13.6	1333	2	S65812	RNA-directed DNA p
35	63.5	13.6	1492	2	T14652	protein J - Yersin
36	63.5	13.6	1545	2	T14966	phage lambda-relat
37	63	13.5	151	2	S72243	dyein heavy chain
38	63	13.5	151	2	S72245	dyein heavy chain
39	63	13.5	408	2	H64513	hypothetical prote
40	63	13.5	507	2	C81063	hypothetical prote
41	63	13.5	546	2	A81807	hypothetical prote
42	63	13.5	793	2	C72219	hypothetical prote
43	63	13.5	1638	2	D87749	DNA mismatch repa
44	63	13.5	2488	2	T42739	protein unc-73b [l
45	62.5	13.4	368	2	G71961	guanine nucleotide
46	62.5	13.4	432	2	C97258	hypothetical prote
47	62.5	13.4	481	2	T14300	sugar-binding per
48	62.5	13.4	516	2	A96753	hypothetical prote
49	62	13.3	150	2	S72244	probable chreomine
50	62	13.3	169	2	PN0560	dyein heavy chain
51	62	13.3	171	2	PN0558	phyochrome - long
52	62	13.3	179	2	B71274	probable translat
53	62	13.3	486	2	B46341	helper component p
54	62	13.3	593	2	C64097	probable soluble l
55	62	13.3	679	2	S90560	hypothetical prote
56	62	13.3	972	2	S35521	DNA topoisomerase
57	62	13.3	1006	2	T00050	hypothetical prote
58	61.5	13.2	118	2	T55515	dyein-like prote
59	61.5	13.2	237	2	A71082	hypothetical prote
60	61.5	13.2	265	2	T46013	hypothetical prote
61	61.5	13.2	423	2	H84566	probable RING zinc
62	61.5	13.2	504	2	C64398	hypothetical prote
63	61.5	13.2	583	1	A41129	radixin - mouse
64	61.5	13.2	583	1	A46127	radixin - human
65	61.5	13.2	583	1	S39805	radixin - pig
66	61.5	13.2	813	2	D64527	hypothetical prote
67	61.5	13.2	905	1	A27410	nucleotide diphosp
68	61.5	13.2	1017	2	D90550	vsaa-like (mycopla
69	61.5	13.2	1922	2	T00637	hypothetical prote
70	61	13.1	151	2	S72239	hypothetical prote
71	61	13.1	188	2	T70176	dyein-like prote
72	61	13.1	477	2	G69760	beta-glucosidase p
73	61	13.1	486	2	A46341	helper component p
74	61	13.1	583	2	T48365	hypothetical prote
75	61	13.1	847	2	G95843	conserved hypotne

ALIGNMENTS

RESULT 1

C64013 hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)

C1Species: Haemophilus influenzae

C1Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

C1Accession: C64013

R1Fleischmann, R.D.; Adams, M.D.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A1Authors: Gneim, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.

A1Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A1Reference number: A64000; MUID:95350630; PMID:7542800

A1Accession: C64013

A1Status: nucleic acid sequence not shown; translation not shown

A1Molecule type: DNA

A1Residues: 1-90 <TIGR>

A1Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:I42023; NID:915

C1Superfamily: Fe(II) trafficking protein Y93X

Query Match 76.4%; Score 356; DB 2; Length 90;
Best Local Similarity 74.7%; Pred. No. 1.9e-30;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 80.9081 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-9

Perfect score: 466
Sequence: 1 MARYNCVHNKADGLDFQ.....QWTSPLFGKDVIEIGFYPR 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	100.0	92	1	PERP_SHEON
2	362	77.7	90	1	PERP_VIBVU
3	362	77.7	90	1	PERP_VIBVY
4	361	77.5	91	1	PERP_MANSX
5	360	77.3	90	1	PERP_VIBF1
6	359	77.0	90	1	PERP_PHOPR
7	356	76.4	90	1	PERP_HABIN
8	356	76.4	90	2	Q4QMD9_HABIS
9	347	74.5	90	1	PERP_VIBCH
10	346	74.2	90	1	PERP_VIBPA
11	345	74.0	90	1	PERP_PASMU
12	341	73.2	90	1	PERP_IDILO
13	338	72.5	90	1	PERP_BRWCT
14	336	72.1	94	1	PERP_HABDU
15	331	71.0	90	1	PERP_SALCH
16	331	71.0	90	1	PERP_SALPA
17	331	71.0	90	1	PERP_SALTI
18	331	71.0	90	1	PERP_SALTY
19	330	70.8	90	1	PERP_ECOL6
20	327	70.2	90	1	PERP_ECOL5
21	327	70.2	90	1	PERP_ECOLI
22	327	70.2	90	1	PERP_SHITL
23	322	69.1	90	1	PERP_PHOUL
24	316	67.8	90	1	PERP_YERPS
25	308	66.1	90	1	PERP_YERPS
26	257	55.2	90	1	PERP_NITRU
27	256	54.9	90	1	PERP_BORRA
28	256	54.9	90	1	PERP_BORRA
29	256	54.9	90	1	PERP_BORRA
30	240	51.5	90	2	Q4J228_AZOCVI
31	237	50.9	90	1	PERP_PSEBR

32	236	50.6	91	1	PERP_RALSO	Q8Y010 ralstonia s
33	235	50.4	90	1	PERP_PSEAR	Q9H36 pseudomonas
34	230	49.4	88	1	PERP_NEIGI	Q5F53 neisseria g
35	230	49.4	88	1	PERP_NEIMA	P67615 neisseria m
36	230	49.4	88	1	PERP_NEIMB	P67616 neisseria m
37	229	49.1	90	2	Q4KJ2_PSEFS	Q4KJ2 pseudomonas
38	228	48.9	90	1	PERP_PSEBM	Q874F5 pseudomonas
39	228	48.9	90	2	Q4ZLP3_PSESY	Q4ZLP3 pseudomonas
40	227	48.7	91	2	Q4LS19_9BURK	Q4LS19 burkholderi
41	226	48.5	91	1	PERP_BURMA	Q621u9 burkholderi
42	226	48.5	91	1	PERP_BURPS	Q636j4 burkholderi
43	224	48.1	90	1	PERP_CHRYO	Q7A84 chromobacte
44	224	48.1	90	2	Q6T7F6_PSEFL	Q6T7F6 pseudomonas
45	216	46.4	77	1	PERP_BUCAI	P57618 buchnera ap
46	215.5	46.2	89	1	PERP_LEGPI	Q5W14 legionella
47	215	46.1	78	1	PERP_WIGBR	Q8A3CS wigleswort
48	215	46.1	90	1	PERP_METCA	Q608j7 methylococc
49	213	45.7	91	1	PERP_XANNC	Q8Y1h7 xanthomonas
50	211.5	45.4	89	1	PERP_LEGPA	Q5X3X9 legionella
51	211.5	45.4	89	1	PERP_LEGPH	Q5ZU80 legionella
52	208	44.6	79	1	PERP_CANRP	Q7VXG9 candidatus
53	206	44.2	92	1	PERP_XANOR	Q5GY22 xanthomonas
54	205	44.0	90	1	PERP_COXBU	Q83A06 coxiella bu
55	203	43.6	92	1	PERP_XANCP	Q8P829 xanthomonas
56	203	43.6	92	2	Q4UM14_XANCP	Q4UM14 xanthomonas
57	199	42.7	78	1	PERP_BUCAP	Q8X925 buchnera ap
58	197.5	42.4	90	1	PERP_ACTAD	Q8F6B3 acinetobact
59	196	42.1	90	1	PERP_XYLPA	Q9P673 xyella fas
60	196	42.1	90	1	PERP_XYLFT	Q87A06 xyella fas
61	185	39.7	87	1	PERP_FRATY	Q5m3h8 francisella
62	181	38.8	87	1	PERP_BUCBP	Q8N944 buchnera ap
63	148.5	31.9	92	2	Q4NMQ4_9DELT	Q4NMQ4 aneorchyob
64	131	28.1	96	2	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
65	92	19.7	507	2	Q4Y197_PLABB	Q4Y197 plasmodium
66	92	19.7	1132	2	Q4Z715_PLABB	Q4Z715 plasmodium
67	81	17.4	1096	2	Q7RTBI_PLAYO	Q7RTBI plasmodium
68	77.5	16.6	2155	2	Q81X99_HUMAN	Q81X99 homo sapien
69	77.5	16.6	2364	1	SPTB2_HUMAN	001082 homo sapien
70	76.5	16.4	546	2	Q4MPZ6_BACCR	Q4MPZ6 bacillus ce
71	75.5	16.2	2154	2	Q5QWJ7_MOUSS	Q5QWJ7 mus musculu
72	75.5	16.2	2154	2	Q5SQJ9_MOUSS	Q5SQJ9 mus musculu
73	75.5	16.2	2363	2	Q53R99_HUMAN	Q53R99 homo sapien
74	75.5	16.2	2363	2	Q5SOLA_MOUSS	Q5SOLA mus musculu
75	75.5	16.2	2377	2	Q5SERR3_HUMAN	Q5SERR3 homo sapien

ALIGNMENTS

RESULT 1	
ID PERP_SHEON	STANDARD: PRT; 92 AA.
AC Q8BEX6;	
DT 10-OCT-2003 (Rel. 42, Created)	
DT 10-OCT-2003 (Rel. 42, Last sequence update)	
DT 13-SEP-2005 (Rel. 48, Last annotation update)	
DE Probable Fe (2+) trafficking protein.	
GN OrderedLocNames=SO3369;	
OS Shewanella oneidensis.	
OC Bacteriia; Proteobacteria; Gammaproteobacteria; Alteromonadales;	
OC Shewanellaceae; Shewanella.	
OX NCBI_TaxID=70863;	
RM [1]	
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC STRAIN=MR-1;	
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;	
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos B.J., Nelson W.C.,	
RA Head T.D., Bisen J.A., Sehadri R., Ward N.L., Mehe B.A.,	
RA Clayton R.A., Meyer T., Teapin A., Scott J., Beanan M.J.,	
RA Brinkac L.M., Daugherty S.C., Deboy R.T., Dodson R.J., Durkin A.S.,	
RA Hatt D.H., Kolony J.F., Madupu R., Peterson J.D., Umayam L.A.,	
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imprial M.,	
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,	

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RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.,
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.",
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE015774; AAN56367.1; -; Genomic_DNA.
CC -----
DR TIGR; SO3369; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YgX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW SEQUENCE 92 AA; 10742 MW; 3116B2B995289B86 CRC64;

Query Match          100.0%; Score 466; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 1,1e-42;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARTVCHLNKRAADGLDPOLYPGDLGKRIFPNISKEAWGLMOKQTMLINEKLMNNV 60
OY 61 DDRKFLKLAQMTSFLPEGKQVEIEGFPVE 88
DB 61 DDRKFLKLAQMTSFLPEGKQVEIEGFPVE 88

RESULT 2
FETP_VIBVU          STANDARD; PRT; 90 AA.
ID_FETP_VIBVU
AC Q8DCC5;
DT 10-OCT-2003 (Rel. 42; Created)
DT 10-OCT-2003 (Rel. 42; Last sequence update)
DT 13-SEP-2005 (Rel. 48; Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=VVI1514;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxId=672;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CMCP6;
RA Rhoe J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RL "Complete genome sequence of Vibrio vulnificus CMCP6."
RL Submitted (DEC-2002) to the EMBL/Genbank/DBD databases.
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE016801; AAO09940.1; -; Genomic_DNA.
CC HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.

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DR Pfam; PF04362; DUF495; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
KW SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

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Best Local Similarity 77.0%; Pred. No. 2,1e-31;
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OY 61 DDRKFLKLAQMTSFLPEGKQVEIEGFPV 87
DB 61 EHRKLETEMVNFLEPGKQVEIHGTYTP 87

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ID_FETP_VIBVU
AC Q7MH14;
DT 05-JUL-2004 (Rel. 44; Created)
DT 05-JUL-2004 (Rel. 44; Last sequence update)
DT 13-SEP-2005 (Rel. 48; Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=VV2885;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxId=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC PubMed-14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen."
RL Genome Res. 13:2577-2587(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000037; BAC95649.1; -; Genomic_DNA.
CC HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YgX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
KW SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

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Best Local Similarity 77.0%; Pred. No. 2,1e-31;
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OM protein - protein search, using sw model

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353.579 Million cell updates/sec

Title: US-09-955-502a-9

Perfect score: 466

Sequence: 1 MARTVNCVHAKKADGLDFQ.....QMTFLFGKGVIEIGFVPE 88

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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6: /cgn2_6/prodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346	74.2	93	2	US-09-543-681A-5443
2	327	70.2	107	2	US-09-489-039A-11962
3	235	50.4	122	2	US-09-252-991A-23355
4	200.5	43.0	92	2	US-09-328-352-5456
5	130	27.9	110	2	US-09-540-236-2859
6	77.5	16.6	2364	2	US-09-538-092-1243
7	75.5	16.2	2154	2	US-08-841-349-4
8	75.5	16.2	2154	2	US-09-431-184A-4
9	68	14.6	359	1	US-09-092-770-6
10	68	14.6	359	2	US-09-222-851-6
11	68	14.6	359	2	US-10-265-062-6
12	68	14.6	404	1	US-09-092-770-3
13	68	14.6	404	2	US-09-222-851-3
14	68	14.6	404	2	US-10-265-062-3
15	68	14.6	407	2	US-09-949-016-11184
16	64	13.7	373	2	US-09-071-035-116
17	64	13.7	373	2	US-10-206-576-116
18	64	13.7	406	2	US-09-071-035-114
19	64	13.7	406	2	US-10-206-576-114
20	64	13.7	557	2	US-09-134-000C-4354
21	63	13.5	369	2	US-09-906-779-5
22	62.5	13.4	182	2	US-09-248-796A-17806
23	62.5	13.4	278	2	US-09-567-003C-23
24	62	13.3	309	2	US-09-248-796A-14939
25	62	13.3	525	2	US-09-540-236-2250
26	62	13.3	911	2	US-09-949-002-425
27	62	13.3	1006	2	US-09-023-905A-12

28	62	13.3	1006	2	US-09-949-002-361	Sequence 361, App
29	61.5	13.2	583	2	US-09-538-092-1071	Sequence 1071, App
30	61.5	13.2	688	2	US-09-113-750A-3	Sequence 3, App1
31	61.5	13.2	1143	2	US-09-949-016-6137	Sequence 6137, App
32	61.5	13.2	3878	2	US-09-914-259-11	Sequence 11, App1
33	61	13.1	139	2	US-09-710-279-1310	Sequence 1310, App
34	61	13.1	168	2	US-09-134-001C-5599	Sequence 5599, App
35	61	13.1	184	2	US-09-325-932A-66	Sequence 66, App1
36	61	13.1	403	1	US-09-092-770-4	Sequence 4, App1
37	61	13.1	403	2	US-09-222-851-4	Sequence 4, App1
38	61	13.1	403	2	US-10-265-062-4	Sequence 4, App1
39	61	13.1	901	2	US-09-134-001C-5351	Sequence 5351, App
40	61	13.1	1078	2	US-09-583-110-4036	Sequence 4036, App
41	61	13.1	1080	2	US-09-107-433-4883	Sequence 4883, App
42	61	13.1	1295	2	US-09-328-352-6045	Sequence 6045, App
43	60.5	13.0	526	2	US-09-071-035-84	Sequence 84, App1
44	60.5	13.0	526	2	US-10-206-576-84	Sequence 84, App1
45	60.5	13.0	546	2	US-09-071-035-82	Sequence 82, App1
46	60.5	13.0	546	2	US-10-206-576-82	Sequence 82, App1
47	60.5	13.0	586	2	US-09-040-725A-1	Sequence 1, App1
48	60	12.9	301	2	US-09-107-532A-4953	Sequence 4953, App
49	59.5	12.8	92	2	US-09-513-999C-5393	Sequence 5393, App
50	59.5	12.8	191	2	US-09-270-767-33624	Sequence 33624, App
51	59.5	12.8	191	2	US-09-270-767-48841	Sequence 48841, App
52	59.5	12.8	305	2	US-09-248-796A-18731	Sequence 18731, App
53	59.5	12.8	380	2	US-09-902-540-15247	Sequence 15247, App
54	59.5	12.8	1078	2	US-09-949-016-11185	Sequence 11185, App
55	59.5	12.8	1085	1	US-08-431-080-28	Sequence 28, App1
56	59.5	12.8	1085	1	US-08-938-534-28	Sequence 28, App1
57	59.5	12.8	1085	2	US-09-345-294-28	Sequence 28, App1
58	59	12.7	66	2	US-09-107-532A-4003	Sequence 4003, App
59	59	12.7	336	2	US-09-252-991A-28882	Sequence 28882, App
60	59	12.7	376	2	US-09-248-796A-14887	Sequence 14887, App
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69	58.5	12.6	548	2	US-09-167-299-3	Sequence 3, App1
70	58.5	12.6	867	2	US-10-104-047-3052	Sequence 3052, App
71	58	12.4	170	2	US-10-101-464A-617	Sequence 617, App
72	58	12.4	228	2	US-09-328-352-7306	Sequence 7306, App
73	58	12.4	245	2	US-09-902-540-11576	Sequence 11576, App
74	58	12.4	296	2	US-09-100-804-12	Sequence 12, App1
75	58	12.4	336	2	US-09-848-294-5	Sequence 5, App1

ALIGNMENTS

RESULT 1
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; PRIOR APPLICATION NUMBER: 2000-04-05
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Best Local Similarity 73.6%; Pred. No. 2.4e-38;
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DB 4 MSRTICTFTLNKADGLDLPOLYPGDLGKRIFDNISKEAWGLMOKQOTMLINEKLLMMNV 63
QY 61 DDRKFLAQMSTFLPEGKDYIEIGFVP 87
DB 64 DDRKFLAQMSTFLPEGKDYIEIGFVP 90

RESULT 2
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity 69.0%; Pred. No. 1e-35;
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DB 17 MSRTICTFTLNKADGLDLPOLYPGDLGKRIFDNISKEAWGLMOKQOTMLINEKLLMMNV 76
QY 61 DDRKFLAQMSTFLPEGKDYIEIGFVP 87
DB 77 EHRKILQEMVQFLPEGKDYIEIGFVP 103

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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DB 33 MSRTVCKRYHEELGDLRPPYPGAKGSDITVNSRKAWDEKQKQOTMLINEKLLMMNV 92
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DB 93 EDRKFLQEMDFL-SGEDYAKADGYVP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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QY 61 DDRKFLAQMSTFLPEGKDYIEIGFVP 88
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RESULT 5
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; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATF.
; FILE REFERENCE: 2709.2005-001
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2859

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QY 82 IEGFVP 87
DB 102 PAGYVP 107

RESULT 6
US-09-538-092-1243
; Sequence 1243, Application US/09538092

GenCore version 5.1.7
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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	356	76.4	87	3	US-09-955-502-7
3	347	74.5	90	3	US-09-955-502-10
4	345	74.0	87	3	US-09-955-502-6
5	344	73.8	91	3	US-09-955-502-5
6	336	72.1	87	3	US-09-955-502-8
7	336	72.1	88	3	US-09-955-502-15
8	336	72.1	91	3	US-09-955-502-14
9	336	72.1	91	3	US-09-955-502-16
10	336	72.1	91	3	US-09-955-502-17
11	332	71.2	91	3	US-09-955-502-11
12	332	71.2	91	3	US-09-955-502-12
13	332	71.2	91	3	US-09-955-502-13
14	326	70.0	91	3	US-09-955-502-18
15	308	66.1	90	3	US-09-955-502-20
16	292	62.7	78	3	US-09-955-502-19
17	256	54.9	87	3	US-09-955-502-2
18	256	54.9	87	3	US-09-955-502-3
19	242.5	52.0	86	3	US-09-955-502-4
20	237	50.9	87	3	US-09-955-502-24
21	235	50.4	87	3	US-09-955-502-25
22	230	49.4	88	3	US-09-955-502-26
23	230	49.4	88	3	US-09-955-502-27
24	230	49.4	88	3	US-09-955-502-28
25	228	48.9	90	3	US-09-955-502-23
26	226	48.5	87	3	US-09-955-502-29
27	226	48.5	87	3	US-09-955-502-30

28	216	46.4	76	3	US-09-955-502-21	Sequence 21, Appl
29	215	46.1	87	3	US-09-955-502-32	Sequence 32, Appl
30	213	45.7	87	3	US-09-955-502-31	Sequence 31, Appl
31	205	44.0	88	3	US-09-955-502-33	Sequence 33, Appl
32	196	42.1	89	3	US-09-955-502-22	Sequence 22, Appl
33	177.5	16.6	2364	4	US-10-170-385-15	Sequence 15, Appl
34	75.5	16.2	1630	4	US-10-408-765A-2431	Sequence 2431, Ap
35	75.5	16.2	2154	4	US-10-695-994-4	Sequence 4, Appl
36	75.5	16.2	2154	5	US-10-805-664-150	Sequence 150, Ap
37	69	14.8	921	5	US-10-732-923-3105	Sequence 3, Appl
38	68	14.6	315	5	US-10-510-628-4	Sequence 4, Appl
39	68	14.6	359	4	US-10-265-062-6	Sequence 6, Appl
40	68	14.6	359	4	US-10-755-889-324	Sequence 2938, Ap
41	68	14.6	374	5	US-10-732-923-2938	Sequence 3, Appl
42	68	14.6	404	4	US-10-265-062-3	Sequence 2938, Ap
43	68	14.6	404	5	US-10-732-923-2939	Sequence 3, Appl
44	68	14.6	737	5	US-10-510-628-2	Sequence 2, Appl
45	66.5	14.3	689	4	US-10-369-493-17280	Sequence 17280, A
46	66	14.2	307	4	US-10-264-237-2647	Sequence 2647, Ap
47	66	14.2	316	4	US-10-094-749-2195	Sequence 2195, Ap
48	66	14.2	321	4	US-10-308-279-58	Sequence 58, Appl
49	66	14.2	321	4	US-10-126-103-126	Sequence 126, Appl
50	66	14.2	321	4	US-10-431-096-126	Sequence 126, Appl
51	66	14.2	321	5	US-10-719-993-655	Sequence 655, Appl
52	66	14.2	321	5	US-10-719-993-656	Sequence 656, Appl
53	66	14.2	321	5	US-10-974-440-57	Sequence 57, Appl
54	66	14.2	344	4	US-10-050-704-281	Sequence 281, Appl
55	66	14.2	344	4	US-10-798-512-281	Sequence 281, Appl
56	66	14.2	348	4	US-10-050-704-129	Sequence 129, Appl
57	66	14.2	348	4	US-10-798-512-129	Sequence 129, Appl
58	66	14.2	355	4	US-10-424-599-264222	Sequence 264222, A
59	66	14.1	355	5	US-10-501-282-5848	Sequence 5848, Ap
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61	65.5	14.1	384	4	US-10-282-122A-63394	Sequence 63394, A
62	65.5	14.1	806	4	US-10-264-049-2841	Sequence 2841, Ap
63	65	13.9	305	4	US-10-296-115-1407	Sequence 1407, Ap
64	65	13.9	477	4	US-10-369-493-8852	Sequence 8852, Ap
65	65	13.9	483	5	US-10-732-923-19695	Sequence 19695, A
66	65	13.9	505	4	US-10-250-613-5	Sequence 5, Appl
67	65	13.9	687	5	US-10-370-715B-538	Sequence 538, Appl
68	64.5	13.8	357	4	US-10-424-599-153968	Sequence 153968, A
69	64.5	13.8	357	4	US-10-424-599-153969	Sequence 153969, A
70	64.5	13.8	393	4	US-10-282-122A-48667	Sequence 48667, A
71	64.5	13.8	593	5	US-10-450-763-50306	Sequence 50306, A
72	64.5	13.8	946	4	US-10-437-963-173299	Sequence 173299, A
73	64	13.7	81	4	US-10-050-704-278	Sequence 278, Appl
74	64	13.7	81	4	US-10-798-512-278	Sequence 278, Appl
75	64	13.7	311	4	US-10-363-829-442	Sequence 442, Appl

ALIGNMENTS

RESULT 1
US-09-955-502-9
Sequence 9, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 88
TYPE: PRT
ORGANISM: Shewanella putrefaciens

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 5.99319 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502a-9

Perfect score: 466
Sequence: 1 MARTVNCVHAKKADLDPO.....QMTSLFEGKDYIEGVPVE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

Published Applications_AA_New.*
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8: /cgn2_6/pcodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	49.4	88	US-10-467-657-968	Sequence 968, App
2	68	14.6	359	US-11-087-227-8	Sequence 8, App11
3	68	14.6	359	US-11-192-450-6	Sequence 6, App11
4	68	14.6	404	US-11-087-227-6	Sequence 6, App11
5	68	14.6	404	US-11-192-450-3	Sequence 3, App11
6	62	13.3	593	US-11-194-246-317	Sequence 317, App
7	61	13.1	139	US-10-793-626-1310	Sequence 1310, Ap
8	61	13.1	403	US-11-192-450-4	Sequence 4, App11
9	60	12.9	296	US-11-087-227-10	Sequence 10, App1
10	59.5	12.8	577	US-11-072-175-187	Sequence 187, App
11	59	12.7	750	US-11-072-512-2432	Sequence 2432, Ap
12	58.5	12.6	867	US-11-072-512-3052	Sequence 3052, Ap
13	57.5	12.3	468	US-11-167-273-1	Sequence 1, App1
14	56	12.0	539	US-10-793-626-888	Sequence 888, App
15	55.5	11.9	312	US-10-793-626-1210	Sequence 1210, Ap
16	55	11.8	266	US-09-995-493-6	Sequence 6, App11
17	55	11.8	731	US-10-613-744-10	Sequence 10, App1
18	54.5	11.7	588	US-10-793-626-3338	Sequence 3338, Ap
19	54.5	11.7	1432	US-10-510-386-218	Sequence 218, App
20	54	11.6	125	US-11-098-686-10739	Sequence 10739, A
21	54	11.6	205	US-10-498-026-83	Sequence 83, App1
22	54	11.6	304	US-11-156-084-274	Sequence 274, App
23	54	11.6	354	US-11-019-711-198	Sequence 198, App
24	54	11.6	391	US-10-623-155-110	Sequence 110, App
25	54	11.6	391	US-11-019-711-63	Sequence 63, App1

26	54	11.6	400	US-10-623-155-112	Sequence 112, App
27	54	11.6	400	US-11-019-711-12	Sequence 12, App1
28	54	11.6	400	US-11-019-711-14	Sequence 14, App1
29	54	11.6	466	US-10-524-647-114	Sequence 114, App
30	54	11.6	466	US-10-524-972-102	Sequence 102, App
31	54	11.6	508	US-11-072-512-2186	Sequence 2186, Ap
32	54	11.6	648	US-10-467-657-2802	Sequence 2802, App
33	54	11.6	829	US-10-909-769-26	Sequence 26, App
34	53.5	11.5	267	US-11-052-554A-219	Sequence 219, App
35	53.5	11.5	326	US-10-485-517-306	Sequence 306, App
36	53.5	11.5	340	US-11-165-226-128	Sequence 128, App
37	53.5	11.5	734	US-10-995-561-770	Sequence 770, App
38	53.5	11.5	756	US-11-074-176-202	Sequence 202, App
39	53.5	11.5	765	US-11-120-308-84	Sequence 84, App1
40	53.5	11.5	782	US-10-793-626-2352	Sequence 2352, Ap
41	53.5	11.5	818	US-11-120-308-94	Sequence 94, App1
42	53	11.4	177	US-10-467-657-1658	Sequence 1658, Ap
43	53	11.4	259	US-11-180-418-4	Sequence 4, App11
44	53	11.4	269	US-11-180-418-3	Sequence 3, App11
45	53	11.4	308	US-11-180-418-2	Sequence 2, App11
46	53	11.4	391	US-11-019-711-61	Sequence 61, App1
47	53	11.4	400	US-11-019-711-10	Sequence 10, App1
48	53	11.4	607	US-11-096-051-14	Sequence 14, App1
49	53	11.4	1558	US-10-329-258-14	Sequence 14, App1
50	53	11.4	2376	US-11-096-051-4	Sequence 4, App11
51	53	11.4	2715	US-11-113-424-51	Sequence 51, App1
52	53	11.4	2721	US-11-096-051-10	Sequence 10, App1
53	53	11.4	2721	US-11-096-051-10	Sequence 10, App1
54	53	11.4	2725	US-11-096-051-8	Sequence 8, App11
55	52.5	11.3	1122	US-10-467-657-6112	Sequence 6112, Ap
56	52	11.2	325	US-11-074-176-368	Sequence 368, App
57	52	11.2	359	US-10-055-877-265	Sequence 265, App
58	52	11.2	359	US-11-080-091-1	Sequence 1, App11
59	52	11.2	359	US-11-116-939-15	Sequence 15, App1
60	52	11.2	359	US-11-087-177-23	Sequence 23, App1
61	52	11.2	359	US-11-087-177-25	Sequence 25, App1
62	52	11.2	359	US-11-087-177-29	Sequence 29, App1
63	52	11.2	364	US-11-087-177-31	Sequence 31, App1
64	52	11.2	364	US-11-087-177-33	Sequence 33, App1
65	52	11.2	365	US-11-087-177-27	Sequence 27, App1
66	52	11.2	386	US-11-072-512-2777	Sequence 2777, Ap
67	52	11.2	405	US-11-072-512-3581	Sequence 3581, Ap
68	52	11.2	588	US-11-052-554A-339	Sequence 339, App
69	52	11.2	640	US-10-467-657-4930	Sequence 4930, Ap
70	52	11.2	694	US-11-072-512-2469	Sequence 2469, Ap
71	52	11.2	717	US-10-793-626-3022	Sequence 3022, Ap
72	52	11.2	842	US-10-909-769-22	Sequence 22, App1
73	52	11.2	893	US-11-072-512-3504	Sequence 3504, Ap
74	51.5	11.1	206	US-11-124-367A-316	Sequence 316, App
75	51.5	11.1	319	US-11-055-822-334	Sequence 334, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: prt
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 49.4%; Score 230; DB 6; Length 88;
Best Local Similarity 49.4%; Pred. No. 9.2e-20;
Matches 44; Conservative 19; Mismatches 24; Indels 2; Gaps 2;

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DB 1 MARMPVCVTLNKAEGCKEPPLENLGKRIIFENVSGEAWAMTRHQTMLINERLSLADP 60

QY 61 DDRKFLAQMTSFLF-EGKDVIEIGFVPE 88
DB 61 RAKEYLAQQMEQYFFGSGADA-VQGYVPQ 88

RESULT 2

US-11-087-227-8
Sequence 8, Application US/11087227
Publication No. US20050260566A1
GENERAL INFORMATION:
APPLICANT: Fischer, Timothy J.
APPLICANT: Malinowski, Douglas P.
APPLICANT: Taylor, Adriann J.
APPLICANT: Parker, Margaret R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
FILE REFERENCE: 046143/287139
CURRENT APPLICATION NUMBER: US/11/087,227
CURRENT FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: 60/556,495
PRIOR FILING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 359
TYPE: prt
ORGANISM: Homo sapiens
US-11-087-227-8

Query Match 14.6%; Score 68; DB 7; Length 359;
Best Local Similarity 27.6%; Pred. No. 1.8;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

QY 11 NKEADGLDFOLYPGDLGKRIIPDN-----ISKAWGLMOKKQTMLINEKLNMMNV 60
DB 76 HKEIGTSDFSRFTYRFRKNLFINPSPLPDLISWGCSKEVLMNMLKESRYVDKHFVLAHS 135

QY 61 DDRKFLAQMTSFLF 76
DB 136 D----LEPQMRSLILD 147

RESULT 3

US-11-192-450-6
Sequence 6, Application US/11192450
Publication No. US20050282150A1
GENERAL INFORMATION:
APPLICANT: Coates, Steven R.
APPLICANT: Baas, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: Novel Cyclin B Genes and Proteins
FILE REFERENCE: A-524
CURRENT APPLICATION NUMBER: US/11/192,450
CURRENT FILING DATE: 2005-07-28
PRIOR APPLICATION NUMBER: US/10/265,062
PRIOR FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/09/442,919
PRIOR FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 09/222,851

PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/092,770
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 359
TYPE: prt
ORGANISM: Human
US-11-192-450-6

Query Match 14.6%; Score 68; DB 7; Length 359;
Best Local Similarity 27.6%; Pred. No. 1.8;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

QY 11 NKEADGLDFOLYPGDLGKRIIPDN-----ISKAWGLMOKKQTMLINEKLNMMNV 60
DB 76 HKEIGTSDFSRFTYRFRKNLFINPSPLPDLISWGCSKEVLMNMLKESRYVDKHFVLAHS 135

QY 61 DDRKFLAQMTSFLF 76
DB 136 D----LEPQMRSLILD 147

RESULT 4

US-11-087-227-6
Sequence 6, Application US/11087227
Publication No. US20050260566A1
GENERAL INFORMATION:
APPLICANT: Fischer, Timothy J.
APPLICANT: Malinowski, Douglas P.
APPLICANT: Taylor, Adriann J.
APPLICANT: Parker, Margaret R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
FILE REFERENCE: 046143/287139
CURRENT APPLICATION NUMBER: US/11/087,227
CURRENT FILING DATE: 2005-03-23
PRIOR APPLICATION NUMBER: 60/556,495
PRIOR FILING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 404
TYPE: prt
ORGANISM: Homo sapiens
US-11-087-227-6

Query Match 14.6%; Score 68; DB 7; Length 404;
Best Local Similarity 27.6%; Pred. No. 2.1;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

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DB 76 HKEIGTSDFSRFTYRFRKNLFINPSPLPDLISWGCSKEVLMNMLKESRYVDKHFVLAHS 135

QY 61 DDRKFLAQMTSFLF 76
DB 136 D----LEPQMRSLILD 147

RESULT 5

US-11-192-450-3
Sequence 3, Application US/11192450
Publication No. US20050282150A1
GENERAL INFORMATION:
APPLICANT: Coates, Steven R.
APPLICANT: Baas, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: Novel Cyclin B Genes and Proteins
FILE REFERENCE: A-524
CURRENT APPLICATION NUMBER: US/11/192,450
CURRENT FILING DATE: 2005-07-28

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 85.816 Seconds
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460.825 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 2443163

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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- 5: geneseqp2002s:*
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- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	399	82.3	91	5	ABb78150 Amino aci
7	389	80.2	91	5	ABb78161 Amino aci
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9	389	80.2	91	5	ABb78162 Amino aci
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11	387	79.8	93	7	ABb78152 Amino aci
12	386	79.6	87	5	ABb78151 Amino aci
13	375	77.3	87	5	ABb78153 Amino aci
14	375	77.3	87	5	ABb78154 Amino aci
15	375	77.3	91	5	ABb78163 Amino aci
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18	347	71.5	88	5	ABb78154 Amino aci
19	249	51.3	87	5	ABb78148 Amino aci
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21	241	49.7	88	5	ABb78178 Amino aci
22	240	49.5	88	5	ABb78171 Amino aci
23	240	49.5	88	5	ABb78172 Amino aci
24	240	49.5	88	5	ABb78173 Amino aci

25	240	49.5	88	6	ABb77219 N. gonorr
26	235	48.5	86	5	ABb78149 Amino aci
27	231	47.6	76	5	ABb78166 Amino aci
28	231	47.6	122	7	ABb74609 Pseudomon
29	228	47.0	87	5	ABb78169 Amino aci
30	228	47.0	90	5	ABb78168 Amino aci
31	226	46.6	87	5	ABb78175 Amino aci
32	224.5	46.3	89	5	ABb78157 Amino aci
33	224.5	46.3	95	9	ABb78294 L. pneumo
34	223	46.0	87	5	ABb78170 Amino aci
35	220	45.4	87	5	ABb78174 Amino aci
36	218.5	45.1	92	6	ADb34169 Acinetoba
37	217.5	44.8	90	5	ABb78167 Amino aci
38	215	44.3	87	5	ABb78177 Amino aci
39	204	42.1	87	5	ABb78176 Amino aci
40	154	31.8	110	8	ADb05173 M. catarr
41	92	19.0	506	3	AAy74371 Neisseria
42	87	17.9	507	3	AAy74372 Neisseria
43	87	17.9	507	3	AAy74373 Neisseria
44	87	17.9	546	6	ABb38097 Protein e
45	84	17.3	507	6	ABb40210 Protein e
46	76.5	15.8	525	8	ADb04564 M. catarr
47	75.5	15.6	507	6	ABb41973 Protein e
48	75	15.5	474	7	ABb075727 Pseudomon
49	73.5	15.2	406	6	ABb35111 Protein e
50	72	14.8	309	8	ADb46828 Thermococ
51	72	14.8	311	7	ADb26256 Hyperther
52	71.5	14.7	3390	4	AAb07989 Wild-type
53	71.5	14.7	3390	4	AAb07990 Wild-type
54	71.5	14.7	3390	8	ADb93316 DEN3 (Sle
55	71	14.6	118	8	ADb28311 Human KPP
56	71	14.6	211	8	ADb48383 Human KPP
57	71	14.6	315	7	ADb168481 Human bea
58	71	14.6	411	8	ADb51530 Human lip
59	71	14.6	488	8	ADb83531 Human dia
60	71	14.6	495	8	ADb51529 Human lip
61	71	14.6	504	8	ADb51531 Human lip
62	71	14.6	504	8	ADb83533 Human dia
63	71	14.6	515	7	ADb10046 Human NOV
64	71	14.6	518	8	ADb51528 Human lip
65	71	14.6	518	8	ADb52961 Calciun/C
66	71	14.6	518	8	ADb17989 Human can
67	71	14.6	518	8	ADb47349 Human can
68	71	14.6	525	4	AAb25814 Human pro
69	71	14.6	525	4	AAb79441 Human pro
70	71	14.6	527	7	ADb56673 Rat Prote
71	71	14.6	527	7	ADb61790 Rat Prote
72	71	14.6	527	7	ADb61788 Rat Prote
73	71	14.6	527	8	ADb51527 Human lip
74	71	14.6	549	8	ADb83534 Human dia
75	71	14.6	556	7	ADb99066 Human KPP

ALIGNMENTS

RESULT 1	ABb78155	standard; protein; 90 AA.
ID	ABb78155	
AC	ABb78155;	
XX	05-NOV-2002	(first entry)
DE	Amino acid sequence of a YggX homologue.	
XX	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX	Vibrio cholerae.	
OS		
XX		
PN	US2002072118-A1.	
XX		

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX CC cell. The method comprises engineering the cell to produce more than the
XX CC native amount of YggX protein (a protein identified from *Salmonella*
XX CC enterica serovar typhimurium) or its homolog, where the cells are
XX CC rendered more resistant to superoxide damage. YggX reduces the oxidation
XX CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX CC clusters. The resulting decrease in free-iron levels generates fewer
XX CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 90 AA;

Query Match 100.0%; Score 485; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 8.7e-52;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVFCRLQKADGLDLPOLYPGELGKRIIPDNICKKMAWAQOTKOTMLINEKLNMDP 60
DB 1 MARTVFCRLQKADGLDLPOLYPGELGKRIIPDNICKKMAWAQOTKOTMLINEKLNMDP 60
QY 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPPAK 90
DB 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPPAK 90

RESULT 2
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
XX ABO65445;
XX
XX 29-JUL-2004 (first entry)
XX
XX Klebsiella pneumoniae polypeptide seqid 11962.
XX DE Klebsiella pneumoniae polypeptide seqid 11962.
XX
XX Recombinant expression vector; transcription regulatory element;
XX KM Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX Klebsiella pneumoniae.
XX OS
XX
XX US6610836-B1.
XX PN
XX 26-AUG-2003.
XX PD
XX 27-JAN-2000; 2000US-00489039.
XX PF
XX 29-JAN-1999; 99US-0117747P.
XX PR
XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA
XX Breton GL, Osborne M;
XX PI
XX WPI; 2003-895346/82.
XX DR

DR N-PSDB; ACH98996.
XX
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
XX PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
XX
XX Disclosure; SEQ ID NO 11962; 932pp; English.
XX
XX

The invention describes a new isolated nucleic acid encoding a Klebsiella
XX CC pneumoniae polypeptide. Also described are: a recombinant expression
XX CC vector comprising the nucleic acid, operably linked to a transcription
XX CC regulatory element; and a cell comprising the recombinant expression
XX CC vector. The nucleic acid is useful for preparing a vaccine composition
XX CC against Klebsiella pneumoniae. This is the amino acid sequence of a
XX CC Klebsiella pneumoniae polypeptide of the invention
XX

SQ Sequence 107 AA;

Query Match 84.3%; Score 409; DB 7; Length 107;
Best Local Similarity 83.3%; Pred. No. 2.7e-42;
Matches 75; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MARTVFCRLQKADGLDLPOLYPGELGKRIIPDNICKKMAWAQOTKOTMLINEKLNMDP 60
DB 17 MSRTIFCTFLQKADGQDFOLYPGELGKRIYVISEKMAWAQOTKOTMLINEKLNMDP 76
QY 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPPAK 90
DB 77 EHRKLEQEMVNFLEFGKDVHIIEGYTPPEK 106

RESULT 3
ABB78158
ID ABB78158 standard; protein; 91 AA.
XX
XX ABB78158;
XX

DT 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX DE

XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX KM
XX

XX Unidentified.
XX OS

XX US2002072118-A1.
XX PN

XX 13-JUN-2002.
XX PD

XX 18-SEP-2001; 2001US-00955502.
XX PF

XX 22-SEP-2000; 2000US-0234588P.
XX PR

XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX

XX Downs D, Gralnick JA;
XX PI

XX WPI; 2002-589476/63.
XX DR

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX

XX Example; Fig 1A; 16pp; English.
XX PS

XX The specification describes a method for reducing superoxide damage to a
XX CC cell. The method comprises engineering the cell to produce more than the
XX CC native amount of YggX protein (a protein identified from *Salmonella*
XX CC enterica serovar typhimurium) or its homolog, where the cells are
XX CC rendered more resistant to superoxide damage. YggX reduces the oxidation
XX CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX CC clusters. The resulting decrease in free-iron levels generates fewer
XX CC

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:05:33 ; Search time 13.8933 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502a-10

Perfect score: 485
Sequence: 1 MARYFCRIQKADGLDFO.....VNFLEGEVHIEGYTPAK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485	100.0	90	2	C82320
2	402	82.9	91	2	A65854
3	402	82.9	91	2	A65082
4	402	82.9	91	2	F91108
5	394	81.2	90	2	C64013
6	389	80.2	91	2	AH0879
7	366	75.5	90	2	AT0116
8	240	49.5	88	2	H81014
9	231	47.6	90	2	H83003
10	231	47.6	93	2	E84994
11	228	47.0	105	2	C82624
12	87	17.9	507	2	C81063
13	87	17.9	546	2	A81807
14	76	15.7	604	2	S66993
15	75	15.5	507	2	A83105
16	73.5	15.2	91	2	H90521
17	71.5	14.7	3390	1	GNW023
18	71	14.6	518	1	B46619
19	71	14.6	527	1	A31908
20	71	14.6	556	2	UC5636
21	70	14.4	542	1	A45025
22	69.5	14.3	204	1	MNN339
23	69.5	14.3	996	2	A71080
24	68.5	14.3	1008	2	H72310
25	68.5	14.1	166	2	F70562
26	68	14.0	379	2	T24654
27	68	14.0	478	1	A30355
28	68	14.0	478	1	S04365
29	68	14.0	543	2	T16015

30	68	14.0	549	2	T16016	hypothetical prote
31	68	14.0	4116	2	T13719	calo protein - fru
32	67	13.8	533	1	A34366	Ca2+/calmodulin-de
33	67	13.8	542	1	A26464	Ca2+/calmodulin-de
34	67	13.8	589	2	S68470	Ca2+/calmodulin-de
35	67	13.8	743	2	S19437	hypothetical prote
36	67	13.8	768	2	S43567	R01H10.7 protein (
37	67	13.8	996	2	JE0237	apolipoprotein E r
38	66.5	13.7	472	2	S74886	phycoene dehydroge
39	66.5	13.7	3391	1	GNWV26	genome polypotein
40	66.5	13.7	3391	1	GNWV26	genome polypotein
41	66.5	13.7	3391	2	US0219	polyprotein - deng
42	66	13.6	306	2	A97249	Zn-binding lipopro
43	66	13.6	518	1	S43845	Ca2+/calmodulin-de
44	66	13.6	583	2	T48365	hypothetical prote
45	65.5	13.5	635	2	S75668	DNA primase (EC 2.
46	65.5	13.5	1418	2	T37264	phospholipase C (B
47	65	13.4	389	2	S73910	slow myosin heavy
48	65	13.4	1931	2	A59234	genome polypotein
49	65	13.4	3396	1	A42551	translation elonga
50	64.5	13.3	401	2	C70159	hypothetical prote
51	64.5	13.3	683	2	AC2256	hypothetical prote
52	64.5	13.3	1206	2	E96507	genome polypotein
53	64.5	13.3	3391	1	GNWV16	TNP2-like transpos
54	64	13.2	304	2	H96496	xylian endo-1,3-bet
55	64	13.2	387	2	JC2484	ehltimate kinase/3
56	64	13.2	492	2	B72389	probable fumarate
57	64	13.2	505	2	C82216	farneyyl-pyrophosp
58	63.5	13.1	347	2	S71436	moesin - human
59	63.5	13.1	577	1	A41289	hypothetical prote
60	63.5	13.1	1010	2	F75134	hypothetical prote
61	63	13.0	253	2	F85060	hypothetical prote
62	63	13.0	265	2	C86516	hypothetical prote
63	63	13.0	265	2	D72105	KDO-transferrase 2,
64	63	13.0	336	2	T04196	RNA-binding protei
65	63	13.0	504	2	F64143	hypothetical prote
66	63	13.0	599	2	T23470	probable GTPase/GP
67	63	13.0	593	2	C64097	probable soluble 1
68	63	13.0	629	2	T28217	hypothetical prote
69	63	13.0	909	1	QRXLL1	LDL receptor 1 pre
70	63	13.0	909	1	QRXLL2	LDL receptor 2 pre
71	63	13.0	1148	2	T13347	Cdn protein - fru1
72	62.5	12.9	305	2	A75211	asparaginase (EC 3
73	62.5	12.9	577	1	S39804	moesin - pig
74	62.5	12.9	1119	2	T18491	hypothetical prote
75	62	12.8	330	2	S74456	regulatory protein

ALIGNMENTS

RESULT 1
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serog
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: C82320
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Drygoli, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10953301
A:Accession: C82320
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <HEI>
A:Cross-references: UNIPARC:UPI00000C2CCF; GB:AB004132; GB:AB003852; NID:99654871; PIDN:f
A:Experimental source: serogroup O1, strain N16961, biotype El Tor
C:gene: VC0451
A:Map position: 1
C:Superfamily: fe(ii) trafficking protein Yggx

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 82.7469 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502a-10
Perfect score: 485
Sequence: 1 MARVFCRLQKADGDFQ.....VNFLFKGKVIHIGYTPPAK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprotl:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485	100.0	90	1	Q9KUR4 vibrio chol
2	442	91.1	90	1	PERP_VIBCH
3	442	91.1	90	1	PERP_VIBVU
4	432	89.1	90	1	PERP_VIBBY
5	407	83.9	90	1	PERP_VIBPA
6	406	83.7	90	1	PERP_PHOPR
7	397	81.9	90	1	PERP_VIBP1
8	397	81.9	90	1	PERP_ECOLI
9	397	81.9	90	1	PERP_SHIRL
10	394	81.2	90	1	PERP_HABIN
11	394	81.2	90	2	Q4QMD9_HAB18
12	393	81.0	90	1	PERP_ECOL6
13	385	79.4	91	1	PERP_MANSN
14	384	79.2	90	1	PERP_SALCH
15	384	79.2	90	1	PERP_SALPA
16	384	79.2	90	1	PERP_SALTI
17	384	79.2	90	1	PERP_SALTY
18	383	79.0	90	1	PERP_PASNU
19	381	78.6	90	1	PERP_ERWCT
20	375	77.3	94	1	PERP_HABDU
21	374	77.1	90	1	PERP_YERPS
22	368	75.9	90	1	PERP_PHOHL
23	366	75.5	90	1	PERP_YERPE
24	353	72.8	90	1	PERP_IDILIO
25	347	71.5	92	1	PERP_SHEON
26	257	53.0	90	1	PERP_BORBR
27	257	53.0	90	1	PERP_BORPA
28	257	53.0	90	1	PERP_BORPB
29	247	50.9	91	1	PERP_XANAC
30	246	50.7	90	1	PERP_NITRU
31	244	50.3	92	1	PERP_XANOR

32	241	49.7	90	1	PERP_COXBU	Q83d06 coxiella bu
33	240	49.5	88	1	PERP_NEIG1	Q55533 neisseria g
34	240	49.5	88	1	PERP_NEIMA	P67615 neisseria m
35	240	49.5	88	1	PERP_NEIMB	P67616 neisseria m
36	240	49.5	90	1	PERP_PSEBK	O88r49 pseudomonas
37	238	49.1	91	1	PERP_BURMA	O62i09 burkholderi
38	238	49.1	91	1	PERP_BURPS	O638j4 burkholderi
39	237	48.9	92	1	PERP_XANCP	O89829 xanthomonas
40	237	48.9	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
41	235	48.5	91	2	Q4LS19_9BURK	Q4LS19 burkholderi
42	231	47.6	77	1	PERP_BUCAI	P57618 buchnera ap
43	231	47.6	90	1	PERP_PSEBK	O9nu36 pseudomonas
44	230	47.4	90	2	Q4KJ72_PSEBK	Q4KJ72 pseudomonas
45	228	47.0	90	1	PERP_PSEBK	O87uf5 pseudomonas
46	228	47.0	90	1	PERP_XYLPA	O9pc073 xyella fas
47	228	47.0	90	2	Q4ZLF3_PSEBK	Q4ZLF3 pseudomonas
48	227	46.8	91	1	PERP_RALBO	O87010 ralstonia s
49	224.5	46.3	89	1	PERP_LEGPA	O53x99 legioneella
50	224.5	46.3	89	1	PERP_LEGPH	O52u80 legioneella
51	223	46.0	90	1	PERP_XYLPT	O87d06 xyella fas
52	223	46.0	90	2	Q4J228_AZCOVI	Q4J228 azotobacter
53	222	45.8	90	1	PERP_MENCA	O60a17 methylococc
54	221.5	45.7	89	1	PERP_LEGFL	O5wvc4 legioneella
55	218.5	45.1	90	1	PERP_ACIAD	O6f1b3 actinobact
56	218	44.9	90	2	O6T7F6_PSEBK	O6T7F6 pseudomonas
57	217	44.7	78	1	PERP_WIGBR	O843cs wigglewort
58	214	44.1	90	1	PERP_CHRYO	O7v9r3 chromobacte
59	208	42.9	78	1	PERP_BUCAP	O8k925 buchnera ap
60	208	42.9	87	1	PERP_PRAAT	O5nhj8 francisella
61	201	41.4	79	1	PERP_CANBP	O7v9r3 candidatus
62	186	38.4	87	1	PERP_BUCBP	Q8n444 buchnera ap
63	168.5	34.7	92	2	Q4NMQ4_9DELT	Q4NMQ4 anemomyxob
64	158	32.6	96	2	Q4FVJ7_9GAMB	Q4FVJ7 psychrobact
65	90.5	18.7	514	2	O6A1Z9_DESPS	O6A1Z9 deusulotale
66	87	17.9	507	2	Q9JYB3_NEIMB	O9JYB3 neisseria m
67	87	17.9	546	2	Q9JTB3_NEIMA	O9JTB3 neisseria m
68	85	17.5	508	2	Q7NSFO_CHRYO	O7NSFO chromobacte
69	84	17.3	507	2	Q88PF3_PSEBK	Q88PF3 pseudomonas
70	84	17.3	855	2	Q416M2_GIBZE	Q416M2 gibberella
71	82	16.9	526	2	Q4PC82_USUTMA	Q4PC82 usutlilgo ma
72	78.5	16.2	345	2	O55821_9FLAV	O55821 rocio virus
73	77	15.9	482	2	Q5NUY1_9BURK	Q5NUY1 ralstonia m
74	76.5	15.8	996	2	Q9C925_ARATH	Q9C925 arabidopsis
75	76	15.7	604	2	Q12166_YEAST	Q12166 saccharomyc

ALIGNMENTS

RESULT 1
ID PERP_VIBCH STRAND: PRT: 90 AA.
AC Q9KUR4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLOCNames=VC0451;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisele J.A., Nelson W.C., Clayton R.A., Gilm M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamatheyan U.J., Baas S., Qin H., Dracoi I.,
RA Sellera P., McDonald L.A., Uitterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;

```

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
CC -|- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
CC -|- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL; AE004132; AAF93624.1; -; Genomic_DNA.
DR TIGR; VC0451; -.
DR HAMAP; MF_00686; -, 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR Prodom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10647 MW; 972331B2600B3184 CRC64;

Query Match 100.0%; Score 485; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARYTCRLQKADGLDPOLYPGELGKRIFDNICKKAAWQOTKQTLINCKLNMNDP 60
DB 1 MARYTCRLQKADGLDPOLYPGELGKRIFDNICKKAAWQOTKQTLINCKLNMNDP 60
OY 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPPAK 90
DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPPAK 90

RESULT 2
FETP_VIBVU STANDARD; PRT; 90 AA.
ID FETP_VIBVU
AC Q8DC5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=VV11514;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
CC -|- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
CC -|- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR HAMAP; AB016801; AA009940.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -, 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR Prodom; PD029191; DUF495; 1.

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KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

Query Match 91.1%; Score 442; DB 1; Length 90;
Best Local Similarity 91.1%; Pred. No. 5.6e-39;
Matches 82; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 MARYTCRLQKADGLDPOLYPGELGKRIFDNICKKAAWQOTKQTLINCKLNMNDP 60
DB 1 MSRTVFCARLNKADGLDPOLYPGELGKRIFDNISKEAWGQHKQTLINCKLNMNDP 60
OY 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPPAK 90
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RESULT 3
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ID FETP_VIBVU
AC Q7MH14;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=VV2885;
OS Vibrio vulnificus (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen."
RL Genome Res. 13:2577-2587(2003).
CC -|- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (by similarity).
CC -|- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; BA000037; BAC95649.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -, 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR Prodom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

Query Match 91.1%; Score 442; DB 1; Length 90;
Best Local Similarity 91.1%; Pred. No. 5.6e-39;
Matches 82; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 MARYTCRLQKADGLDPOLYPGELGKRIFDNICKKAAWQOTKQTLINCKLNMNDP 60
DB 1 MSRTVFCARLNKADGLDPOLYPGELGKRIFDNISKEAWGQHKQTLINCKLNMNDP 60
OY 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPPAK 90
DB 61 EHRKLEQEMVNFLEPGKEVHIIEGYTPPAK 90

RESULT 4
FETP_VIBBA

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:09:58 ; Search time 21.0443 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-10

Perfect score: 485
Sequence: 1 MARIPTCTRLQKADGLDFQ.....VNLFEGKEVHIGYTPPAK 90

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents AA.*
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4: /cgn2_6/ptodata/1/iaa/PTCUS.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	409	84.3	107	2	US-09-489-039A-11962
2	387	79.8	93	2	US-09-543-681A-5443
3	231	47.6	122	2	US-09-252-991A-23355
4	218.5	45.1	92	2	US-09-328-352-5456
5	154	31.8	110	2	US-09-540-236-2859
6	76.5	15.8	525	2	US-09-540-236-2250
7	75	15.5	474	2	US-09-252-991A-24473
8	71	14.6	556	2	US-09-800-960-4
9	71	14.6	556	2	US-10-096-960-4
10	71	14.6	565	2	US-09-800-960-2
11	71	14.6	565	2	US-10-096-960-2
12	69	14.2	57	2	US-09-562-737-124
13	68	14.0	73	2	US-09-513-999C-5376
14	68	14.0	217	2	US-09-543-681A-7862
15	68	14.0	292	2	US-09-328-352-5836
16	67	13.8	116	2	US-09-563-737-125
17	67	13.8	516	2	US-09-820-7808-2
18	67	13.8	542	2	US-09-820-7808-4
19	66	13.6	584	1	US-08-415-593-41
20	65.5	13.5	898	2	US-09-949-016-10987
21	64.5	13.3	311	2	US-09-248-796A-26397
22	64	13.2	388	1	US-08-282-197C-56
23	64	13.2	713	2	US-09-949-016-6674
24	64	13.2	737	2	US-09-949-016-7675
25	64	13.2	1676	2	US-09-949-016-7610
26	63	13.0	279	2	US-09-198-452A-221
27	63	13.0	279	2	US-09-438-185A-205

28	63	13.0	325	2	US-09-134-000C-4346	Sequence 4346, Ap
29	63	13.0	546	1	US-08-533-669A-2	Sequence 2, Appl
30	63	13.0	546	2	US-09-183-861-2	Sequence 2, Appl
31	63	13.0	546	2	US-09-022-765-2	Sequence 2, Appl
32	63	13.0	546	2	US-09-551-974A-2	Sequence 2, Appl
33	63	13.0	546	2	US-09-565-501A-2	Sequence 2, Appl
34	63	13.0	546	2	US-09-639-206A-2	Sequence 2, Appl
35	63	13.0	546	2	US-09-874-923-2	Sequence 2, Appl
36	63	13.0	546	2	US-08-798-841-2	Sequence 2, Appl
37	63	13.0	982	2	US-09-551-974A-95	Sequence 2, Appl
38	63	13.0	982	2	US-09-565-501A-95	Sequence 2, Appl
39	63	13.0	982	2	US-09-639-206A-95	Sequence 2, Appl
40	63	13.0	982	2	US-09-874-923-95	Sequence 2, Appl
41	63	13.0	1427	2	US-09-551-974A-97	Sequence 95, Appl
42	63	13.0	1427	2	US-09-565-501A-97	Sequence 95, Appl
43	63	13.0	1427	2	US-09-639-206A-97	Sequence 97, Appl
44	63	13.0	1427	2	US-09-874-923-97	Sequence 97, Appl
45	63	13.0	1641	2	US-09-551-974A-96	Sequence 96, Appl
46	63	13.0	1641	2	US-09-565-501A-96	Sequence 96, Appl
47	63	13.0	1641	2	US-09-639-206A-96	Sequence 96, Appl
48	63	13.0	1641	2	US-09-874-923-96	Sequence 96, Appl
49	62.5	12.9	798	2	US-09-328-352-8094	Sequence 8094, Ap
50	62.5	12.9	92	2	US-09-861-451A-12	Sequence 12, Appl
51	61.5	12.7	355	2	US-09-513-999C-5393	Sequence 5393, Ap
52	61.5	12.7	355	2	US-09-442-348A-107	Sequence 107, Appl
53	61.5	12.7	358	2	US-09-949-016-11528	Sequence 11528, A
54	61.5	12.7	911	2	US-09-949-002-425	Sequence 425, Appl
55	61.5	12.7	1006	2	US-09-023-905A-12	Sequence 12, Appl
56	61.5	12.7	1006	2	US-09-949-002-361	Sequence 361, Appl
57	61	12.6	548	2	US-09-167-299-3	Sequence 3, Appl
58	61	12.6	579	2	US-09-949-016-10483	Sequence 10483, A
59	61	12.6	583	2	US-09-538-092-1071	Sequence 1071, Ap
60	61	12.6	1871	2	US-09-964-956-42	Sequence 42, Appl
61	60.5	12.5	921	2	US-09-248-796A-14950	Sequence 14950, A
62	60	12.4	293	2	US-09-695-458-23	Sequence 23, Appl
63	60	12.4	307	2	US-09-023-905A-36	Sequence 36, Appl
64	60	12.4	318	2	US-09-695-458-22	Sequence 22, Appl
65	59.5	12.3	378	2	US-09-248-796A-18526	Sequence 18526, A
66	59.5	12.3	780	2	US-10-148-806-35	Sequence 35, Appl
67	59	12.2	402	2	US-09-489-039A-9252	Sequence 9252, Ap
68	59	12.2	680	2	US-09-298-924-4	Sequence 4, Appl
69	59	12.2	720	1	US-08-840-236-1	Sequence 1, Appl
70	59	12.2	720	1	US-08-505-448A-1	Sequence 1, Appl
71	59	12.2	817	1	US-08-381-931B-2	Sequence 2, Appl
72	59	12.2	1091	2	US-09-328-352-5758	Sequence 5758, Ap
73	58.5	12.1	136	2	US-09-252-991A-22070	Sequence 22070, A
74	58.5	12.1	359	2	US-09-902-540-13907	Sequence 13907, A
75	58.5	12.1	455	2	US-09-270-767-45790	Sequence 45790, A

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity 83.3%; Pred. No. 1.5e-44;
Matches 75; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MARTVFCRLQKADGDLDPOLYPGELGKRIFDNICKKAWAQWOTKQTMLINEKTLNMMDP 60
Db 17 MSRTIFCTFLQKADGDLDPOLYPGELGKRIFDNICKKAWAQWOTKQTMLINEKTLNMMDP 76

Qy 61 EHRKLEQEMVNFLEPGKEVHIEGYTPPAK 90
Db 77 EHRKLEQEMVNFLEPGKEVHIEGYTPPEK 106

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 1999-04-09
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 79.8%; Score 387; DB 2; Length 93;
Best Local Similarity 78.9%; Pred. No. 8.1e-42;
Matches 71; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

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Qy 61 EHRKLEQEMVNFLEPGKEVHIEGYTPPAK 90
Db 64 DDRKLEQEMVNFLEPGKHVIDGYTPPEK 93

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Best Local Similarity 48.3%; Pred. No. 1e-21;
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Qy 61 EHRKLEQEMVNFLEPGKEVHIEGYTPPA 89
Db 93 EDRKFLQEMDNFLSGEDYAKADGYVPPS 121

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562938
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Qy 61 EHRKLEQEMVNFLEPGKEVHIEGYTP 87
Db 64 EAKKFLQEMDNFLSGEDYAKADGYVPPS 91

RESULT 5
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; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

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Qy 65 EHRKLEQEMVNFLEPGKEVHIEGYTP 87
Db 85 EHRKLEQEMVNFLEPGKEVHIEGYTP 107

RESULT 6
US-09-540-236-2250
; Sequence 2250, Application US/09540236

GenCore version 5.1.7
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Title: US-09-955-502a-10

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	402	82.9	91	3	US-09-955-502-13	Sequence 13, Appl
5	399	82.3	91	3	US-09-955-502-5	Sequence 5, Appl
6	389	80.2	91	3	US-09-955-502-14	Sequence 14, Appl
7	389	80.2	91	3	US-09-955-502-16	Sequence 16, Appl
8	389	80.2	91	3	US-09-955-502-17	Sequence 17, Appl
9	387	79.8	88	3	US-09-955-502-15	Sequence 15, Appl
10	386	79.6	87	3	US-09-955-502-7	Sequence 7, Appl
11	375	77.3	87	3	US-09-955-502-6	Sequence 6, Appl
12	375	77.3	87	3	US-09-955-502-8	Sequence 8, Appl
13	375	77.3	87	3	US-09-955-502-18	Sequence 18, Appl
14	366	75.5	90	3	US-09-955-502-20	Sequence 20, Appl
15	350	72.2	78	3	US-09-955-502-19	Sequence 19, Appl
16	347	71.5	88	3	US-09-955-502-9	Sequence 9, Appl
17	249	51.3	87	3	US-09-955-502-2	Sequence 2, Appl
18	249	51.3	87	3	US-09-955-502-3	Sequence 3, Appl
19	241	49.7	88	3	US-09-955-502-33	Sequence 33, Appl
20	240	49.5	88	3	US-09-955-502-26	Sequence 26, Appl
21	240	49.5	88	3	US-09-955-502-27	Sequence 27, Appl
22	240	49.5	88	3	US-09-955-502-28	Sequence 28, Appl
23	235	48.5	86	3	US-09-955-502-4	Sequence 4, Appl
24	231	47.6	76	3	US-09-955-502-21	Sequence 21, Appl
25	228	47.0	87	3	US-09-955-502-24	Sequence 24, Appl
26	228	47.0	89	3	US-09-955-502-22	Sequence 22, Appl
27	228	47.0	90	3	US-09-955-502-23	Sequence 23, Appl

28	226	46.6	87	3	US-09-955-502-29	Sequence 29, Appl
29	226	46.6	87	3	US-09-955-502-30	Sequence 30, Appl
30	223	46.0	87	3	US-09-955-502-25	Sequence 25, Appl
31	215	44.3	87	3	US-09-955-502-32	Sequence 32, Appl
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35	75.5	15.6	507	4	US-10-282-122A-69897	Sequence 69897, A
36	74	15.3	921	5	US-10-732-923-3305	Sequence 3305, Ap
37	73.5	15.2	406	4	US-10-282-122A-63035	Sequence 63035, A
38	71.5	14.7	3390	5	US-10-719-547-22	Sequence 22, Appl
39	71.5	14.7	3390	5	US-10-871-775-33	Sequence 33, Appl
40	71	14.6	315	4	US-10-408-765A-287	Sequence 287, Appl
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43	71	14.6	527	5	US-10-487-090-16	Sequence 16, Appl
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45	71	14.6	556	4	US-10-623-505-4	Sequence 4, Appl
46	71	14.6	556	5	US-10-491-467-19	Sequence 19, Appl
47	71	14.6	565	4	US-10-096-960-2	Sequence 2, Appl
48	71	14.6	565	4	US-10-623-505-2	Sequence 2, Appl
49	71	14.6	588	4	US-10-311-034-22	Sequence 22, Appl
50	70.5	14.5	222	4	US-10-425-115-333235	Sequence 333335, A
51	69	14.2	57	4	US-10-211-962-124	Sequence 124, App
52	69	14.2	212	4	US-10-156-761-12946	Sequence 12946, A
53	69	14.2	511	4	US-10-282-122A-50464	Sequence 50464, A
54	69	14.2	856	4	US-10-408-765A-2006	Sequence 2006, Ap
55	68.5	14.1	166	5	US-10-482-706-269	Sequence 269, App
56	68	14.0	321	4	US-10-664-421-74	Sequence 74, Appl
57	68	14.0	321	5	US-10-941-635-74	Sequence 74, Appl
58	68	14.0	336	5	US-10-723-860-1754	Sequence 1754, Ap
59	68	14.0	379	4	US-10-369-493-5262	Sequence 5262, Ap
60	68	14.0	479	5	US-10-487-090-17	Sequence 17, Appl
61	68	14.0	489	4	US-10-649-400-2	Sequence 2, Appl
62	68	14.0	527	5	US-10-723-860-1920	Sequence 1920, Ap
63	68	14.0	543	4	US-10-369-493-5403	Sequence 5403, Ap
64	68	14.0	549	4	US-10-369-493-5404	Sequence 5404, Ap
65	68	14.0	699	5	US-10-643-795A-141	Sequence 141, App
66	68	14.0	699	5	US-10-482-029-295	Sequence 295, App
67	68	14.0	699	5	US-10-948-518-111	Sequence 111, App
68	68	14.0	5322	6	US-11-097-143-35058	Sequence 35058, A
69	67.5	13.9	535	4	US-10-282-122A-56172	Sequence 56172, A
70	67	13.8	116	4	US-10-211-962-125	Sequence 125, Appl
71	67	13.8	280	5	US-10-635-398-12	Sequence 12, Appl
72	67	13.8	372	3	US-09-764-876-876	Sequence 876, App
73	67	13.8	499	4	US-10-087-192-1500	Sequence 1500, Ap
74	67	13.8	503	5	US-10-635-398-16	Sequence 16, Appl
75	67	13.8	506	5	US-10-635-398-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-955-502-10
Sequence 10, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Dowm, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIORITY FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 90
TYPE: PRT
ORGANISM: Vibrio cholerae

US-09-955-502-10

Query Match	100.0%;	Score 485;	DB 3;	Length 90;
Best Local Similarity	100.0%;	Pred. No. 1.7e-48;		
Matches 90; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MARTVETRLQKADGDLFQLYPGELGRIFDNICKAAHQWQTQTMLINEKLNMDP 600
.
1 MARTVETRLQKADGDLFQLYPGELGRIFDNICKAAHQWQTQTMLINEKLNMDP 600
Db

Qy		61 EHRKLLQEWMVNFLEFGKEVHIIEGYTPAK 90
Db		61 EHRKLLQEWMVNFLEFGKEVHIIEGYTPAK 90

RESULT 2

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US-09-955-502-11
? Sequence 11, Application US/09955502
? Patent No. US20020072118A1
? GENERAL INFORMATION:
? APPLICANT: Downs, Diana M.
? APPLICANT: Gralnick, Jeff A.
? TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
? TITLE OF INVENTION: Oxygen-Labile Proteins
? FILE REFERENCE: 960296, 97559
? CURRENT APPLICATION NUMBER: US/09/955, 502
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: 60/234,588
? PRIOR FILING DATE: 2000-09-22
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 11
? LENGTH: 91
? TYPE: PRT
? ORGANISM: Escherichia coli K-12 MG1655
US-09-955-502-11

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Query Match	82.9%;	Score 402;	DB 3;	Length 91;
Best Local Similarity	83.3%;	Pred. No. 7.9e-39;		
Matches 75; Conservative	7;	Mismatches 8;	Indels 0;	Gaps 0;

QY 1 MARTVFCTRLQKADGDLFQLYGELGKRIFDNICKEAAMQQTQMTMLINEKLLNMDP 600

Db 1 MSRTIFCTFLQREAGQDFQLYGELGKRIYNLSKEAAMQMQHQKQMTMLINEKLLNWNNA 600

QY 61 EHRKLLQEMVNFLEFGKEVHIIEGYTPAK 90
Db 61 EHRKLLQEMVNFLEFGKEVHIIEGYTPAK 90

RESULT 3

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US-09-955-502-12
? Sequence 12, Application US/09955502
? Patent No. US20020072118A1
? GENERAL INFORMATION:
? APPLICANT: Downs, Diana M.
? APPLICANT: Gralnick, Jeff A.
? TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
? TITLE OF INVENTION: Oxygen-Labile Proteins
? FILE REFERENCE: 960296.97559
? CURRENT APPLICATION NUMBER: US/09/955,502
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: 60/234,588
? PRIOR FILING DATE: 2000-09-22
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 12
? LENGTH: 91
? TYPE: PRT
? ORGANISM: Escherichia coli O157:H7EDL933
? US-09-955-502-12

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Query Match 82.9%; Score 402; DB 3; Length 91,

Best Local Similarity - 83.3%; Pred. NO. 7.9e-39;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Dy
1 MARVYFCTRLQKEADGLDFOLYPGELGKRI FNI CKEAQAQWQKQTMLINEKKLNMDP 60

Dd
1 MSRTLFCTFLQREAGQDFOLYPGELGKRI YNEISKEAQAQWQHQTMLINEKKLNMDNA 60

2Y 61 EHRKLLQEQMVNFLPEGKEVHIEGYTPPAK 90
 |||||
 Db 61 EHRKLLQEQMVNFLPEGKEVHIEGYTPEDK 90

RESULT 4

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US-09-955-502-13
? Sequence 13, Application US/09955502
? Patent No. US20020072118A1
? GENERAL INFORMATION:
? APPLICANT: Downs, Diana M.
? APPLICANT: Gralnick, Jeff A.
? TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
? TITLE OF INVENTION: Oxygen-Labile Proteins
? FILE REFERENCE: 960296, 97559
? CURRENT APPLICATION NUMBER: US/09/955,502
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: 60/234,588
? PRIOR FILING DATE: 2000-09-22
? NUMBER OF SEQ ID NOS: 33
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 13
? LENGTH: 91
? TYPE: PRF
? ORGANISM: Escherichia coli O157:H7
? US-09-955-502-13

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Query Match	82.9%;	Score 402;	DB 3;	Length 91;
Best Local Similarity	83.3%;	Pred. No. 7.9e-39;		
Matches 75; Conservative	7;	Mismatches 8;	Indels 0;	Gaps 0;

QY 1 MARYTFCSTRQK EADGLDFQLYPGELGKRIFDNICKEAQAQWQKTKQTMLINEKKUNMDP 60

Db 1 MSRTIFCTPLQRBAGQDFQLYPGELGKRIYNEISKEAQAQWQHKQTMLINEKKUNMNA 60

QY 61 EHRKLTQEMVNFLEFGKVAHIEGYTPPAK 90
DB 61 EHRKLTQEMVNFLEFGKVAHIEGYTPEDK 90

RESULT 5

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US-09-955-502-5
/ Sequence 5, Application US/09955502
/ Patent No. US20020072118A1
/ GENERAL INFORMATION:
/ APPLICANT: Downs, Diana M.
/ APPLICANT: Gralnick, Jeff A.
/ TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
/ TITLE OF INVENTION: Oxygen-Labile Proteins
/ FILE REFERENCE: 960296, 97559
/ CURRENT APPLICATION NUMBER: US/09/955,502
/ CURRENT FILING DATE: 2001-09-18
/ PRIOR APPLICATION NUMBER: 60/234,588
/ PRIOR FILING DATE: 2000-09-22
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 91
/ TYPE: PRT
/ ORGANISM: Actinobacillus actinomycetemcomitans
/ US-09-955-502-5

```

Query Match	82.3%;	Score 399;	DB 3;	Length 91;
Best Local Similarity	81.8%;	Pred. No. 1.8e-38;		
Matches 72; Conservative	9;	Mismatches 7;	Indels 0;	Gaps 0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 6.1294 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502a-10

Perfect score: 485

Sequence: 1 MARYFCRLQKADGLDFO.....VNFLEGRKHIEGYTPAK 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications_AA_New:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	68.5	14.1	179	US-10-467-657-6542
3	68	14.0	695	US-10-453-372-648
4	68	14.0	775	US-10-453-372-656
5	68	14.0	834	US-10-453-372-658
6	67	13.8	700	US-10-995-561-922
7	67	13.8	700	US-10-995-561-924
8	66	13.6	336	US-10-453-372-640
9	66	13.6	793	US-10-995-561-925
10	66	13.6	804	US-10-453-372-650
11	66	13.6	847	US-10-453-372-654
12	66	13.6	857	US-10-453-372-652
13	66	13.6	905	US-10-453-372-638
14	66	13.6	905	US-10-453-372-662
15	66	13.6	905	US-10-453-372-664
16	66	13.6	963	US-10-995-561-923
17	66	13.6	963	US-10-453-372-660
18	66	13.6	1012	US-10-453-372-646
19	63.5	13.1	577	US-11-072-175-187
20	63	13.0	266	US-09-995-493-6
21	63	13.0	593	US-11-194-246-317
22	61	12.6	1871	US-10-877-346-42
23	61	12.6	3433	US-10-714-781A-67
24	57.5	11.9	242	US-11-022-562-220
25	57.5	11.9	278	US-11-098-686-10664

26 57 11.8 667 6 US-10-793-626-198 Sequence 198, App

27 56 11.5 177 6 US-10-467-657-1658 Sequence 1658, Ap

28 56 11.5 359 7 US-11-087-227-8 Sequence 8, Appl

29 56 11.5 359 7 US-11-192-450-6 Sequence 6, Appl

30 56 11.5 404 7 US-11-087-227-6 Sequence 6, Appl

31 56 11.5 404 7 US-11-192-450-3 Sequence 3, Appl

32 56 11.5 1122 6 US-10-995-561-705 Sequence 705, App

33 56 11.5 1129 6 US-10-995-561-706 Sequence 706, App

34 55.5 11.4 397 7 US-11-098-686-10901 Sequence 10901, A

35 55 11.3 198 7 US-11-182-016-43 Sequence 43, Appl

36 55 11.3 235 7 US-11-098-686-11270 Sequence 11270, A

37 55 11.3 1813 6 US-10-495-083-10 Sequence 10, Appl

38 54.5 11.2 349 6 US-10-821-233-1387 Sequence 1387, Ap

39 54.5 11.2 752 7 US-11-072-512-3003 Sequence 3003, Ap

40 54.5 11.2 765 7 US-11-120-308-84 Sequence 84, Appl

41 54.5 11.2 818 7 US-11-120-308-94 Sequence 94, Appl

42 54 11.1 305 7 US-11-156-084-178 Sequence 178, App

43 54 11.1 319 6 US-10-793-626-2760 Sequence 2760, Ap

44 54 11.1 1194 7 US-11-098-686-10270 Sequence 10270, A

45 54 11.1 1678 7 US-11-124-367A-340 Sequence 340, App

46 54 11.1 1678 7 US-11-124-367A-341 Sequence 341, App

47 53.5 11.0 58 6 US-10-957-887B-82 Sequence 82, Appl

48 53.5 11.0 243 7 US-11-214-796-2 Sequence 2, Appl

49 53.5 11.0 286 7 US-11-082-389-88 Sequence 88, Appl

50 53.5 11.0 455 6 US-10-714-887-212 Sequence 212, App

51 53.5 11.0 508 6 US-10-934-944-174 Sequence 174, App

52 53.5 11.0 516 7 US-11-135-604-2 Sequence 2, Appl

53 53.5 11.0 532 7 US-11-135-604-4 Sequence 4, Appl

54 53.5 11.0 537 7 US-11-135-604-6 Sequence 6, Appl

55 53.5 11.0 657 7 US-11-072-512-2529 Sequence 2529, Ap

56 53.5 11.0 731 6 US-10-613-744-10 Sequence 10, Appl

57 53.5 11.0 767 7 US-11-055-557-2 Sequence 2, Appl

58 53.5 11.0 767 7 US-11-055-557-14 Sequence 14, Appl

59 53.5 11.0 1613 7 US-11-108-528-86 Sequence 86, Appl

60 53.5 11.0 1613 7 US-11-108-528-86 Sequence 86, Appl

61 53 10.9 478 6 US-11-165-067A-21 Sequence 21, Appl

62 53 10.9 478 6 US-10-821-234-915 Sequence 915, App

63 53 10.9 521 6 US-10-934-944-216 Sequence 216, App

64 53 10.9 521 6 US-10-934-944-264 Sequence 264, App

65 53 10.9 600 7 US-11-072-512-3845 Sequence 3845, Ap

66 53 10.9 2665 7 US-11-124-368A-214 Sequence 214, App

67 53 10.9 2668 7 US-11-124-368A-215 Sequence 215, App

68 52.5 10.8 508 7 US-11-072-512-2186 Sequence 2186, Ap

69 52.5 10.8 678 7 US-11-072-512-3832 Sequence 3832, Ap

70 52.5 10.8 723 5 US-09-934-948-2 Sequence 2, Appl

71 52.5 10.8 723 5 US-09-934-948-6 Sequence 6, Appl

72 52.5 10.8 1432 6 US-10-510-386-218 Sequence 218, App

73 52 10.7 708 7 US-11-196-475-76 Sequence 76, Appl

74 52 10.7 783 7 US-11-192-219-7 Sequence 7, Appl

75 52 10.7 894 7 US-11-202-330-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-10-467-657-968

Sequence 968, Application US/10467657

Publicacion No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: Seqwin99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: prt
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 49.5%; Score 240; DB 6; Length 88;
Best Local Similarity 50.6%; Pred. No. 6,9e-22;
Matches 44; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

Qy 1 MARYFCTRLQKADGLDFOLYPGLGKRIFDNICKEANAQKQTMLINEKLNMDP 60
Db 1 MARWFCVAKLNKEABGMKPPPLPNELGKRIFENVSGEAWAATRHQTMLINEKLNMDP 60

Qy 61 EHRKLEQEMVNFLEFGKEVHIEGYTP 87
Db 61 RAREYLAQMQEYFFGDGADAVGVYP 87

RESULT 2
US-10-467-657-6542

Sequence 6542, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 6542
LENGTH: 179
TYPE: prt
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6542

Query Match 14.1%; Score 68.5; DB 6; Length 179;
Best Local Similarity 34.1%; Pred. No. 0.46; Mismatches 14; Indels 5; Gaps 1;
Matches 15; Conservative 10;

Qy 40 AQWQTKQTMLINEKLNMDPEHRKLEQEMVNFLEFGKEVHIE 83
Db 2 ASWKTGVDVLLNGKILITGRDAHAKRL-----VNMUDKGEELPVD 40

RESULT 3
US-10-453-372-648

Sequence 648, Application US/10453372
Publication No. US20060003323A1
GENERAL INFORMATION:
APPLICANT: Alsbrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476

PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 648
LENGTH: 695
TYPE: prt
ORGANISM: Homo sapiens
US-10-453-372-648

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Best Local Similarity 32.7%; Pred. No. 2.8; Mismatches 20; Indels 6; Gaps 2;
Matches 17; Conservative 9;

Qy 39 WAQWTKQTMLINEKLNMDPEHRKLEQEMVNFLEFGKEVHIEGYTPPAK 90
Db 639 WNNWKRK-----NTRKSMNFDNVPVRYKTEEEDEDEHIGRTAQI-GHYVYPAR 684

RESULT 4
US-10-453-372-656

Sequence 656, Application US/10453372
Publication No. US20060003323A1
GENERAL INFORMATION:
APPLICANT: Alsbrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 656
LENGTH: 775
TYPE: prt
ORGANISM: Homo sapiens
US-10-453-372-656

Query Match 14.0%; Score 68; DB 6; Length 775;
Best Local Similarity 32.7%; Pred. No. 3.2; Mismatches 20; Indels 6; Gaps 2;
Matches 17; Conservative 9;

Qy 39 WAQWTKQTMLINEKLNMDPEHRKLEQEMVNFLEFGKEVHIEGYTPPAK 90
Db 719 WNNWKRK-----NTRKSMNFDNVPVRYKTEEEDEDEHIGRTAQI-GHYVYPAR 764

GenCore version 5.1.7
Copyright (c) 1993 - 2006 BioCeleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 86.765 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502a-11

Perfect score: 486

Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLFGKVEHIGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
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3	486	100.0	91 5	ABB78156 Amino aci
4	469	96.5	91 5	ABB78161 Amino aci
5	469	96.5	91 5	ABB78159 Amino aci
6	469	96.5	91 5	ABB78162 Amino aci
7	455	93.6	91 5	ABB78163 Amino aci
8	453	93.2	88 5	ABB78160 Amino aci
9	450	92.6	107 7	ABO65445 Amino aci
10	402	82.7	90 5	ABB78155 Amino aci
11	396	81.5	90 5	ABB78165 Amino aci
12	395	81.3	78 5	ABB78164 Amino aci
13	389	80.0	93 7	ADP05158 Bacterial
14	388	79.8	91 5	ABB78150 Amino aci
15	387	79.6	87 5	ABB78152 Amino aci
16	379	78.0	87 5	ABB78151 Amino aci
17	373	76.7	87 5	ABB78153 Amino aci
18	332	68.3	88 5	ABB78154 Amino aci
19	265	54.5	87 5	ABB78166 Amino aci
20	255	52.5	87 5	ABB78148 Amino aci
21	255	52.5	87 5	ABB78147 Amino aci
22	241	49.6	86 5	ABB78149 Amino aci
23	231.5	47.6	89 9	AEB41576 L. pneumo
24	231.5	47.6	95 9	AEB38294 L. pneumo

ALIGNMENTS

25	231	47.5	87 5	ABB78170 Amino aci
26	231	47.5	122 7	ABO74609 Pseudomon
27	227	46.7	88 5	ABB78178 Amino aci
28	227	46.7	90 5	ABB78168 Amino aci
29	225	46.3	87 5	ABB78169 Amino aci
30	216.5	44.5	90 5	ABB78167 Amino aci
31	213	43.8	88 5	ABB78171 Amino aci
32	213	43.8	88 5	ABB78172 Amino aci
33	213	43.8	88 5	ABB78173 Amino aci
34	213	43.8	88 5	ABB77219 N. gonorr
35	206	42.4	87 5	ABB78175 Amino aci
36	200	41.2	87 5	ABB78177 Amino aci
37	200	41.2	87 5	ABB78174 Amino aci
38	200	41.2	87 5	ABB78176 Amino aci
39	199.5	41.0	92 6	ADA34169 Amino aci
40	131	27.0	110 8	ADU05173 M. catarr
41	83	17.1	506 3	AAV74371 Neisseria
42	83	17.1	1647 4	ABG10750 Novel hum
43	81	16.7	507 6	ABU40210 Protein e
44	78	16.0	507 3	AAV74372 Neisseria
45	78	16.0	507 3	AAV74373 Neisseria
46	78	16.0	546 6	ABU38097 Protein e
47	76	15.6	548 4	AAE04737 Brugia ma
48	75	15.4	309 8	ADN46828 Thermococ
49	74.5	15.3	632 8	ADS29711 Bacterial
50	72	14.8	474 7	ABO75727 Pseudomon
51	71.5	14.7	679 9	ADZ85056 Partial P
52	71	14.6	311 7	ADM26256 Hypertther
53	70.5	14.5	285 4	AAE92683 Human pro
54	70.5	14.5	414 6	ABU11747 Human MD
55	70.5	14.5	614 9	ADX06837 Cyclin-de
56	70.5	14.5	614 9	ADY16108 PRO polyp
57	70.5	14.5	764 5	ABB77432 Human tum
58	70.5	14.5	764 7	ADC99062 Human KRP
59	70.5	14.5	817 4	AAH38657 Human KRP
60	70.5	14.5	863 4	AAH38656 Human pol
61	70.5	14.5	1135 8	ADS10706 Human the
62	70.5	14.5	1181 8	ADS10708 Human the
63	70.5	14.5	1186 8	ADS10709 Human the
64	70.5	14.5	1188 8	ADH45460 Human mol
65	70.5	14.5	1206 5	ADH48860 NOV61 pro
66	70.5	14.5	1214 7	ADK65785 Angiogene
67	69.5	14.3	374 4	AAH39682 Human pol
68	69.5	14.3	389 4	AAH41468 Human pol
69	69.5	14.3	481 5	AAU93169 Arabidops
70	69.5	14.3	481 7	ADD30148 plant yie
71	69.5	14.3	481 7	ADB31497 plant yie
72	69.5	14.3	481 8	ADL41933 plant tra
73	69.5	14.3	485 5	ABB08477 Human lat
74	69.5	14.3	488 4	AAH94458 Human pro
75	69.5	14.3	488 4	AAH67252 Amino aci

RESULT 1
ABB78158 standard; protein; 91 AA.

ABB78158; 05-NOV-2002 (first entry)

Amino acid sequence of a YggX homologue.

Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.

Unidentified.

US2002072118-A1.

```
PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnack JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 91 AA;

Query Match          100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTFCFLQREAGQDFOLYPGELGKRIYNEISKEMAWQOHQOTMLINEKLNMMNA 60
DB 1 MSRTTFCFLQREAGQDFOLYPGELGKRIYNEISKEMAWQOHQOTMLINEKLNMMNA 60
QY 61 EHRKLLQEQMVNPLFEGKEVHIIEGYTPEDKK 91
DB 61 EHRKLLQEQMVNPLFEGKEVHIIEGYTPEDKK 91

RESULT 2
ABB78157
ID ABB78157 standard; protein; 91 AA.
XX
XX ABB78157;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnack JA;
XX
```

```
DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from Salmonella
XX enterica serovar typhimurium) or its homolog, where the cells are
XX rendered more resistant to superoxide damage. YggX reduces the oxidation
XX of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX clusters. The resulting decrease in free-iron levels generates fewer
XX hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 91 AA;

Query Match          100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTFCFLQREAGQDFOLYPGELGKRIYNEISKEMAWQOHQOTMLINEKLNMMNA 60
DB 1 MSRTTFCFLQREAGQDFOLYPGELGKRIYNEISKEMAWQOHQOTMLINEKLNMMNA 60
QY 61 EHRKLLQEQMVNPLFEGKEVHIIEGYTPEDKK 91
DB 61 EHRKLLQEQMVNPLFEGKEVHIIEGYTPEDKK 91

RESULT 3
ABB78156
ID ABB78156 standard; protein; 91 AA.
XX
XX ABB78156;
XX
XX 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX
XX Escherichia coli.
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnack JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX cell, comprises engineering the cell to produce more YggX protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX cell. The method comprises engineering the cell to produce more than the
XX native amount of YggX protein (a protein identified from Salmonella
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 14.0477 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502a-11

Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLFGKVEHIEGYTPEDRK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	486	100.0	91	2 A85954	hypothetical prote
2	486	100.0	91	2 A65082	hypothetical prote
3	486	100.0	91	2 F91108	hypothetical prote
4	469	96.5	91	2 AH0879	conserved hypotet
5	402	82.7	90	2 C82320	conserved hypotet
6	396	81.5	90	2 A10116	conserved hypotet
7	387	79.6	90	2 C64013	hypothetical prote
8	265	54.5	93	2 E84994	hypothetical prote
9	231	47.5	90	2 H83003	conserved hypotet
10	226	46.5	105	2 C82624	conserved hypotet
11	213	43.8	88	2 H81014	conserved hypotet
12	78	16.0	507	2 C81063	conserved hypotet
13	78	16.0	546	2 A81807	conserved hypotet
14	76	15.6	548	2 A54510	conserved hypotet
15	75.5	15.5	1638	2 D87749	conserved hypotet
16	75.5	15.5	2488	2 T42739	conserved hypotet
17	74.5	15.3	683	2 AC2256	conserved hypotet
18	72	14.8	265	2 T46013	hypothetical prote
19	72	14.8	447	2 T16527	hypothetical prote
20	72	14.8	507	2 A83105	hypothetical prote
21	72	14.8	511	2 A99574	hypothetical prote
22	69	14.2	258	2 A97991	hypothetical prote
23	69	14.2	258	2 E95121	hypothetical prote
24	69	14.2	258	2 A28209	hypothetical prote
25	69	14.2	1119	2 T15842	hypothetical prote
26	68	14.0	2672	2 A48126	hypothetical prote
27	67.5	13.9	209	2 T64172	hypothetical prote
28	67	13.8	235	2 G65212	hypothetical prote
29	67	13.8	324	2 T05429	hypothetical prote

30	67	13.8	433	2 A70465	probable GTP bindi
31	67	13.8	447	2 JC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2 T40058	probable chromatin
33	66.5	13.7	1260	2 T04440	hypothetical prote
34	66	13.6	593	2 C64097	hypothetical prote
35	66	13.6	689	2 F83902	probable soluble 1
36	65.5	13.5	173	2 H86869	beta-galactosidase
37	65.5	13.5	305	2 A75211	hypothetical prote
38	65.5	13.5	323	2 A90536	asparaginase (EC 3
39	65.5	13.5	365	2 B54128	lipoprotein (impor
40	65.5	13.5	821	2 A12417	Fc-binding protein
41	65	13.4	251	2 E90428	hypothetical prote
42	65	13.4	330	2 S74456	regulatory protein
43	65	13.4	445	2 XUHUMB	alpha-1,3-mannosyl
44	65	13.4	456	2 G71152	hypothetical prote
45	65	13.4	1008	2 H85055	probable transpos
46	65	13.4	1141	2 T29185	hypothetical prote
47	65	13.4	1230	2 S56850	SMC1 protein homol
48	64.5	13.3	245	2 AG2300	hypothetical prote
49	64.5	13.3	305	2 A71247	probable L-asparag
50	64.5	13.3	495	2 AH0985	probable zinc-prot
51	64.5	13.3	859	2 T29630	hypothetical prote
52	64	13.2	220	2 S62410	hypothetical prote
53	64	13.2	438	2 T37786	probable RNA-bind
54	64	13.2	447	1 A38561	alpha-1,3-mannosyl
55	64	13.2	583	2 T48365	hypothetical prote
56	64	13.2	604	2 S66993	hypothetical prote
57	64	13.2	990	2 T43445	hypothetical prote
58	64	13.2	1051	2 S27002	phospholipase C (B
59	64	13.2	1234	2 S52099	phospholipase C be
60	64	13.2	1394	2 I38994	phospholipase C-be
61	63.5	13.1	91	2 H90521	hypothetical prote
62	63.5	13.1	243	2 T29635	hypothetical prote
63	63.5	13.1	460	2 T00639	hypothetical prote
64	63.5	13.1	591	1 F0WVMM	gag polyprotein -
65	63	13.0	880	2 AB0179	probable ATPase ch
66	63	13.0	1251	2 A56677	neuronal cell cycl
67	63	13.0	1327	2 T14594	guanine nucleoti
68	63	13.0	1611	1 MMTMPV	183k protein - pep
69	62.5	12.9	483	1 STSSET	glutamate-CrNA lig
70	62.5	12.9	551	2 B84106	hypothetical prote
71	62.5	12.9	555	2 C96667	unknown protein, 7
72	62.5	12.9	617	2 B71071	probable prolyl en
73	62.5	12.9	964	1 T04325	probable ATP-depen
74	62.5	12.9	1417	2 T00661	hypothetical prote
75	62	12.8	169	2 PNO560	phytochrome - long

ALIGNMENTS

RESULT 1
A85954 hypothetical protein Y9GX [imported] - Escherichia coli (strain O157:H7, substrain EDL9)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #ext_change 05-Oct-2004
C:Accession: A85954
R:Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, B.J.; Davis, N.W.; Lam, A.; DiMallanca, E.; Potamouzis, K.; Apodaca
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Residue: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE005174; NID:G12517511; 1
C:Genetics:
A:Gene: Y9GX
C:Superfamily: fe(II) trafficking protein Y9GX
Query Match 100.0%; Score 486; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

Qy 61 EHRKLLBQEMVNFLEGGKVHIEGYTPEDKK 91
Db 61 EHRKLLBQEMVNFLEGGKVHIEGYTPEDKK 91

RESULT 2

hypothetical protein b2962 - Escherichia coli (strain K-12)

Query Match	100.0%;	Score 486;	DB 2;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 1.6e-41;		
Matches	91;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy 1 MSRTTCTFLQREAEQDFQLYPGEIGKRIYNEISKEAQAQWQHQTMLINEKULNMNA 600
|||||
Db 1 MSRTTCTFLQREAEQDFQLYPGEIGKRIYNEISKEAQAQWQHQTMLINEKULNMNA 600

Qy	Db
61 EHRKLTQEMVNFLEGGKEVHIIEGYTPEDKK 91	61 EHRKLTQEMVNFLEGGKEVHIIEGYTPEDKK 91

RESULT 3

hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1591108)

Query Match	100.0%	Score 486;	DB 2;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 1.6e-41;		
Matches 91; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy

1 MSRTICTFLQREAGGDFQLYGGELGRINYEISKEAAMQWQHQTMLINEKLLNMNA 600
Db

1 MSRTICTFLQREAGGDFQLYGGELGRINYEISKEAAMQWQHQTMLINEKLLNMNA 600

Oy 61 EHRKLTGEQVNFLEPGKEVHIIGYTPEDKK 91
|||||
Db 61 EHRKLTGEQVNFLEPGKEVHIIGYTPEDKK 91

RESULT 4

conserved hypothetical protein STY3266 [imported] - *Salmonella enterica* subsp. *enterica*

Query Match	96.5%	Score	469	DB 2	Length	91	
Best Local Similarity	94.5%	Pred. No.	7.9e-40				
Matches	86	Conservative	5	Mismatches	0	Gaps	0

```
0y 1 MSRTTCTCTGOREAGGDFOLYPGELKRIYNEISKZMAQOWHQMTLNEKLNMMNA 600
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSRTTCTCTYORDAEGGDFOLYPGELKRIYNEISKZMAQOWHQMTLNEKLNMMNA 600
```

```
QY      61 EHRKLLQEMVNFLEEGKEVHIIEGYTPEDKK 91
      |||||:||||:|||||
Db      61 EHRKLLQEMVNFLEEGKDVIHIEGYTPEDKK 91
```

RESULT 5

conserved hypothetical protein VC0451 [Imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

A.Gene: VC0451
A.Map position: 1
C.Superfamily: fe(II) trafficking protein ysgx

Query Match	82.7%	Score 402	DB 2	Length 90
Best Local Similarly	83.3%	Pred. No. 3.6e-33		
Matches 75	Conservative 7	Mismatches 8	Indels 0	Gaps 0

Db 1 MARIPTRLQKADGLDLYPGEIGRIIFDNI CKKAWAQMQTKOTMLINEKUNMDP 600

Qy 61 EHRKLLIQEMVNFLEGGKSVHIEGYTPEDK 90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 83.6663 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502a-11
Perfect score: 486
Sequence: 1 MSRTFTCTPLQREAGQDFQ.....NFLPFGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	481	99.0	90	1	FERP_ECO57
2	481	99.0	90	1	FERP_ECO57
3	481	99.0	90	1	FERP_ECO57
4	477	98.1	90	1	FERP_ECO57
5	464	95.5	90	1	FERP_ECO57
6	464	95.5	90	1	FERP_ECO57
7	464	95.5	90	1	FERP_ECO57
8	464	95.5	90	1	FERP_ECO57
9	411	84.6	90	1	FERP_ECO57
10	404	83.1	90	1	FERP_ECO57
11	402	82.7	90	1	FERP_ECO57
12	402	82.7	90	1	FERP_ECO57
13	402	82.7	90	1	FERP_ECO57
14	399	82.1	90	1	FERP_ECO57
15	396	81.5	90	1	FERP_ECO57
16	389	80.0	90	1	FERP_ECO57
17	387	79.6	90	1	FERP_ECO57
18	387	79.6	90	1	FERP_ECO57
19	382	78.6	90	1	FERP_ECO57
20	381	78.4	90	1	FERP_ECO57
21	379	78.0	90	1	FERP_ECO57
22	373	76.7	90	1	FERP_ECO57
23	366	75.3	90	1	FERP_ECO57
24	335	68.9	90	1	FERP_ECO57
25	332	68.3	90	1	FERP_ECO57
26	265	54.5	90	1	FERP_ECO57
27	255	52.5	90	1	FERP_ECO57
28	255	52.5	90	1	FERP_ECO57
29	247	50.8	90	1	FERP_ECO57
30	247	50.8	90	1	FERP_ECO57
31	235	48.4	90	1	FERP_ECO57

32	231.5	47.6	89	1	FERP_LEGPA	05x3x9 legionella
33	231.5	47.6	89	1	FERP_LEGPA	05x3x9 legionella
34	231	47.5	90	1	FERP_LEGPA	05x3x9 pseudomonas
35	231	47.5	91	1	FERP_XANAC	08p1h7 xanthomonas
36	228.5	47.0	89	1	FERP_LEGPA	05wvc4 legionella
37	227	46.7	90	1	FERP_COXBU	083d06 coxiella bu
38	227	46.7	90	1	FERP_PSESM	087uf5 pseudomonas
39	227	46.7	90	2	Q4ZLP3_PSESY	04zlp3 pseudomonas
40	226	46.5	90	1	FERP_XYLPA	09pc73 xyloella fas
41	225	46.3	90	1	FERP_PSEPK	088r49 pseudomonas
42	225	46.3	92	1	FERP_XANOR	059t22 xanthomonas
43	223	45.9	90	2	Q4U228_AZCVI	04j528 azotobacter
44	222	45.7	90	1	FERP_XYLPA	087d06 xyloella fas
45	222	45.7	92	1	FERP_XANCP	08p219 xanthomonas
46	222	45.7	92	2	Q4UW14_XANCP	04uw14 xanthomonas
47	220	45.3	90	1	FERP_NITRU	082xf2 nitrosomonas
48	215	44.2	90	2	Q6T7F6_PSEFL	06t7f6 pseudomonas
49	214	44.0	87	1	FERP_BUCBP	089444 buchnera ap
50	213	43.8	88	1	FERP_NEIGI	05f553 neisseria g
51	213	43.8	88	1	FERP_NEIMA	067615 neisseria m
52	213	43.8	88	1	FERP_NEIMA	067615 neisseria m
53	212	43.6	79	1	FERP_CANBP	07vrg9 candidatus
54	212	43.6	90	2	Q4KJ2_PSEFS	04kj2 pseudomonas
55	211	43.4	90	1	FERP_CHRYO	07n8t9 chromobacter
56	207	42.6	91	2	Q4LS19_9BURK	04ls19 burkholderi
57	206	42.4	91	1	FERP_BURMA	063j14 burkholderi
58	206	42.4	91	1	FERP_BURMA	063j14 burkholderi
59	206	42.4	91	1	FERP_RALSO	08y010 ralstonia s
60	200	41.2	87	1	FERP_METCA	060aj7 methylococc
61	199	40.9	87	1	FERP_FRATY	05njf8 franciella
62	194.5	40.0	90	1	FERP_ACIDA	06fdb3 acinetobact
63	144	29.6	96	2	Q4FVJ7_9GAMM	04fvj7 psychrobact
64	142	29.2	92	2	Q4WMO4_9DELT	04wmo4 anaeromyxob
65	90.5	18.6	482	2	Q5NUV1_9BURK	05nuv1 ralstonia m
66	85.5	16.6	514	2	Q6A1Z9_DSPPS	06a1z9 desulfotale
67	81	16.7	507	2	Q88P3_PSEPK	088p3 pseudomonas
68	81	16.7	508	2	Q7NSFO_CHRYO	07nsfo chromobacter
69	80	16.5	486	2	Q7WX51_ALCEU	07wx51 alcaligenes
70	78.5	16.2	760	2	Q4YR2_PLACB	04yr2 plasmidium
71	78	16.0	507	2	Q9UYB3_NEIMA	09uyb3 neisseria m
72	78	16.0	546	2	Q9UTB3_NEIMA	09utb3 neisseria m
73	78	16.0	2248	2	Q4UB40_THEAN	04ub40 theileria a
74	77.5	15.9	337	2	Q8IAR8_BACCR	08iar8 bacillus ce
75	77.5	15.9	1123	2	Q7RJ10_PLAYO	07rj10 plasmidium

ALIGNMENTS

RESULT 1
ID FERP_ECO57 STANDARD; PRT; 90 AA.
AC POA8P4; P52065; (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y99X; OrderedLocusNames=z4307, ECs3838;
GN Bacterichia coli O157:H7.
OC Bacterichia; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Bacterichia.
OK NCBI_Taxid=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
RC MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G., Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamotis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.,
RT "Genome sequence of enterohaemorrhagic Bacterichia coli O157:H7.";

RL Nature 409:529-533(2001).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC.

RA MEDLINE=21156231; PubMed=1158796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

RA Kubara S., Shiba T., Hattori M., Shingawa H.;

RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*

RT O157:H7 and genomic comparison with a laboratory strain K-12.";

RL Nucleic Acids Res. 8:11-22(2001).

CC -1- FUNCTION: Could be a mediator in iron transactions between iron

CC acquisition and iron-requiring processes, such as synthesis and/or

CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).

CC -1- SUBUNIT: Monomer (By similarity).

CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL, AB005174; AAG58093.1; -; Genomic DNA.

CC EMBL, BA000007; BAB37261.1; -; Genomic DNA.

CC PIR, A85954; A85954.

CC PIR, P91108; P91108.

CC HAMAP, MF_00686; -, 1.

CC InterPro, IPR007457; Y9gX.

CC Pfam, PF04362; DUF495; 1.

CC PIRSF, PIRSF029827; Fe traffic_Y9gX; 1.

CC ProDom, PD029191; DUF495; 1.

CC Complete proteome; Iron.

CC INIT_MET 0

CC By similarity.

CC SEQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;

Best Local Similarity 100.0%; Pred. No. 4,5e-41;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTICTFLQREAGQDFQLYPGLGKRIYNEISKAMQWQHOKQTMLINEKKNMNAE 61

DB 1 SRTICTFLQREAGQDFQLYPGLGKRIYNEISKAMQWQHOKQTMLINEKKNMNAE 60

QY 62 HKRLAEQENVNPLFEKGVHISGYTPEDKX 91

DB 61 HKRLAEQENVNPLFEKGVHISGYTPEDKX 90

RESULT 2

PEPT_ECOLI STANDARD; PRT; 90 AA.

AC P0ABP3; P52065;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Probable Fe(2+) trafficking protein.

GN Name=Y9gX; OrderedLocNames=b2962;

OS *Escherichia coli*.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; *Escherichia*.

OC NCBI_TaxID=562;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glaser J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of *Escherichia coli* K-12.";

RL Science 277:1453-1474(1997).

RN [2]

RP PARTIAL PROTEIN SEQUENCE OF 1-12.

RC STRAIN=K12 / EMG2;

RX MEDLINE=97443975; PubMed=9298646;

RA Link A.J., Rodison K., Church G.M.;

RT "Comparing the predicted and observed properties of proteins encoded

RT in the genome of *Escherichia coli* K-12.";

RL Electrophoresis 18:1259-1313(1997).

RN [3]

RP PROTEIN SEQUENCE OF 1-10.

RC STRAIN=K12;

RX MEDLINE=99085675; PubMed=9668784;

RA Wasinger V.C., Humphrey-Smith I.;

RT "Small genes/gene-products in *Escherichia coli* K-12.";

RL FEWS Microbiol. Lett. 169:375-382(1998).

RN [4]

RP IDENTIFICATION BY MASS SPECTROMETRY.

RX MEDLINE=99420866; PubMed=10493123;

RX DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;

RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;

RT "Enrichment of low abundance proteins of *Escherichia coli* by

RT hydroxyapatite chromatography";

RL Electrophoresis 20:2181-2195(1999).

RN [5]

RP INDUCTION, AND FUNCTION.

RC STRAIN=K12 / GC4468;

RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;

RA Pomposiello P.J., Koutsolioutou A., Carrasco D., Demple B.;

RT "SoxRS-regulated expression and genetic analysis of the y9gX gene of

RT *Escherichia coli*.";

RL J. Bacteriol. 185:6624-6632(2003).

RN [6]

RP STRUCTURE BY NMR, AND FUNCTION.

RX PubMed=15883188; DOI=10.1110/ps.051358105;

RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;

RT "The solution structure of the oxidative stress-related protein Y9gX

RT from *Escherichia coli*.";

RL Protein Sci. 14:1673-1678(2005).

CC -1- FUNCTION: Could be a mediator in iron transactions between iron

CC acquisition and iron-requiring processes, such as synthesis and/or

CC repair of Fe-S clusters in biosynthetic enzymes. Necessary to

CC maintain high levels of aconitase under oxidative stress.

CC -1- SUBUNIT: Monomer (Probable).

CC -1- INDUCTION: By oxidative stress and soxS.

CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL, U28377; AAA69129.1; -; Genomic DNA.

CC EMBL, U00096; AAC75999.1; -; Genomic DNA.

CC PIR, A65082; A65082.

CC PDB, 1YHD; NMR, A-1-90.

CC SWISS-2DPAGE; P0ABP3; COLI.

CC Echobase; EB2809; -.

CC EcoGene; EG12984; Y9gX.

CC HAMAP, MF_00686; -, 1.

CC InterPro, IPR007457; Y9gX.

CC Pfam, PF04362; DUF495; 1.

CC PIRSF, PIRSF029827; Fe traffic_Y9gX; 1.

CC ProDom, PD029191; DUF495; 1.

CC 3D-structure; Complete proteome; Direct protein sequencing; Iron.

CC INIT_MET 0

CC By similarity.

CC SEQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;

Best Local Similarity 100.0%; Pred. No. 4,5e-41;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTICTFLQREAGQDFQLYPGLGKRIYNEISKAMQWQHOKQTMLINEKKNMNAE 61

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:09:58 ; Search time 21.2781 Seconds
(without alignments)
353.579 Million cell updates/sec

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Perfect score: 486
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	92.6	107	2	US-09-489-039A-11962
2	389	80.0	93	2	US-09-543-681A-5443
3	231	47.5	122	2	US-09-252-991A-23355
4	199.5	41.0	92	2	US-09-328-352-5456
5	131	27.0	110	2	US-09-540-236-2859
6	76	15.6	548	2	US-09-167-229-3
7	72	14.8	474	2	US-09-252-991A-24473
8	70.5	14.5	1214	2	US-10-164-595-24
9	67.5	13.9	184	1	US-09-325-932A-66
10	67.5	13.9	546	1	US-08-533-669A-2
11	67.5	13.9	546	2	US-09-183-861-2
12	67.5	13.9	546	2	US-09-022-765-2
13	67.5	13.9	546	2	US-09-551-974A-2
14	67.5	13.9	546	2	US-09-565-501A-2
15	67.5	13.9	546	2	US-09-639-206A-2
16	67.5	13.9	546	2	US-09-874-923-2
17	67.5	13.9	546	2	US-08-798-841-2
18	67.5	13.9	982	2	US-09-551-974A-95
19	67.5	13.9	982	2	US-09-565-501A-95
20	67.5	13.9	982	2	US-09-639-206A-95
21	67.5	13.9	982	2	US-09-874-923-95
22	67.5	13.9	1427	2	US-09-551-974A-97
23	67.5	13.9	1427	2	US-09-565-501A-97
24	67.5	13.9	1427	2	US-09-639-206A-97
25	67.5	13.9	1427	2	US-09-874-923-97
26	67.5	13.9	1641	2	US-09-551-974A-96
27	67.5	13.9	1641	2	US-09-565-501A-96

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 20040001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

28	67.5	13.9	1641	2	US-09-639-206A-96	Sequence 96, Appl
29	67.5	13.9	1641	2	US-09-874-923-96	Sequence 96, Appl
30	65.5	13.5	395	2	US-09-914-098-46	Sequence 46, Appl
31	65	13.4	292	2	US-09-328-352-5836	Sequence 5836, Ap
32	64.5	13.3	209	2	US-09-252-991A-20905	Sequence 20905, A
33	64	13.2	227	2	US-09-270-767-58283	Sequence 58283, A
34	64	13.2	280	2	US-09-323-998E-37	Sequence 37, Appl
35	64	13.2	448	2	US-09-270-767-42959	Sequence 42959, A
36	64	13.2	534	2	US-09-312-762A-5	Sequence 5, Appl
37	63.5	13.1	534	2	US-09-370-368-8	Sequence 8, Appl
38	63	13.0	525	2	US-09-540-226-2250	Sequence 2250, Ap
39	63	13.0	569	2	US-09-107-532A-6689	Sequence 6689, Ap
40	62.5	12.9	325	2	US-09-134-000C-4346	Sequence 4346, Ap
41	62.5	12.9	544	2	US-09-248-796A-42911	Sequence 12, Appl
42	62.5	12.9	798	2	US-09-861-451A-12	Sequence 12, Appl
43	62	12.8	959	2	US-09-543-681A-6879	Sequence 6879, Ap
44	62	12.8	1394	2	US-09-248-796A-19555	Sequence 19555, A
45	62	12.8	1501	2	US-09-710-279-2850	Sequence 2850, Ap
46	62	12.8	1529	2	US-09-134-001C-3945	Sequence 3945, Ap
47	61.5	12.7	57	2	US-09-562-737-124	Sequence 124, App
48	61.5	12.7	116	2	US-09-562-737-125	Sequence 125, App
49	61.5	12.7	311	2	US-09-248-796A-26397	Sequence 26397, A
50	61.5	12.7	419	2	US-09-543-681A-7295	Sequence 7295, Ap
51	61.5	12.7	680	2	US-09-298-924-4	Sequence 4, Appl
52	61.5	12.7	720	1	US-08-840-236-1	Sequence 1, Appl
53	61.5	12.7	720	1	US-08-505-448A-1	Sequence 1, Appl
54	61	12.6	308	2	US-09-198-452A-1004	Sequence 1004, Ap
55	61	12.6	444	2	US-09-861-451A-16	Sequence 16, Appl
56	61	12.6	480	2	US-09-438-185A-934	Sequence 934, App
57	60.5	12.4	139	2	US-09-513-999C-4802	Sequence 4802, Ap
58	60.5	12.4	258	2	US-09-513-999C-4800	Sequence 4800, Ap
59	60.5	12.4	264	2	US-09-949-016-6012	Sequence 6012, Ap
60	60.5	12.4	276	2	US-09-949-016-6012	Sequence 11703, A
61	60.5	12.4	404	2	US-09-914-098-48	Sequence 48, Appl
62	60.5	12.4	640	2	US-09-873-404-2	Sequence 2, Appl
63	60.5	12.4	640	2	US-10-243-735-2	Sequence 2, Appl
64	60.5	12.4	1076	2	US-09-171-991-7	Sequence 41085, A
65	60	12.3	98	2	US-09-270-767-41085	Sequence 56301, A
66	60	12.3	98	2	US-09-270-767-66301	Sequence 61671, A
67	60	12.3	184	2	US-09-270-767-61671	Sequence 19465, A
68	60	12.3	271	2	US-09-248-796A-19265	Sequence 221, App
69	60	12.3	279	2	US-09-198-452A-205	Sequence 205, App
70	60	12.3	331	2	US-09-438-185A-205	Sequence 6400, Ap
71	60	12.3	331	2	US-09-328-352-6400	Sequence 41746, A
72	60	12.3	337	2	US-09-270-767-41746	Sequence 46116, A
73	60	12.3	389	2	US-09-270-767-46116	Sequence 8705, Ap
74	60	12.3	410	2	US-09-949-016-8705	Sequence 32, Appl
75	60	12.3	411	2	US-09-886-319A-32	

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Best Local Similarity 91.2%; Pred. No. 1e-48;
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Qy 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 91
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RESULT 2

US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 1999-04-09
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 80.0%; Score 389; DB 2; Length 93;
Best Local Similarity 80.0%; Pred. No. 3.8e-41;
Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MSRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQOHKQTMLINEKLMNNA 60
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Qy 61 EHRKLEQEMVNFLEPGKEVHIEGYTPEDK 90
Db 64 DDRKLEQEMVNFLEPGKEVHIEGYTPEDK 93

RESULT 3

US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 1998-07-27
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Best Local Similarity 51.7%; Pred. No. 3.6e-21;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

Qy 1 MSRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQOHKQTMLINEKLMNNA 60

Db 33 MSRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQOHKQTMLINEKLMNNA 92

Qy 61 EHRKLEQEMVNFLEPGKEVHIEGYTP 87
Db 93 EHRKLEQEMVNFLEPGKEVHIEGYTP 119

RESULT 4

US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 41.0%; Score 199.5; DB 2; Length 92;
Best Local Similarity 42.7%; Pred. No. 2.2e-17;
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Qy 61 EHRKLEQEMVNFLEPGKEVHIEGYTP 88
Db 64 EHRKLEQEMVNFLEPGKEVHIEGYTP 92

RESULT 5

US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-09-540-236-2859

Query Match 27.0%; Score 131; DB 2; Length 110;
Best Local Similarity 34.9%; Pred. No. 1.1e-08;
Matches 29; Conservative 13; Mismatches 41; Indels 0; Gaps 0;

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Qy 65 LLEQEMVNFLEPGKEVHIEGYTP 87
Db 85 YLNEQREKFLDNGDYKPDAGYTP 107

RESULT 6

US-09-167-299-3
; Sequence 3, Application US/09167299

GenCore version 5.1.7
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	313	67.9	91	1	Q8Y010 raietonia s
5	304	65.9	91	2	Q4LS19 burkholderi
6	300	65.1	91	1	Q638J4 burkholderi
7	300	65.1	91	1	Q638J4 burkholderi
8	297	64.4	90	1	Q7NAR4 chromobacte
9	290	62.9	88	1	Q5F553 neisseria g
10	290	62.9	88	1	Q5F553 neisseria g
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12	286	62.0	90	1	Q68XIF nltrososoma
13	260	56.4	90	1	Q68XIF methylococc
14	256	55.5	90	1	Q4OMD9 haemophilus
15	256	55.5	90	2	Q4OMD9 haemophilus
16	256	55.5	91	1	Q68XIF methylococc
17	256	55.5	92	1	Q68XIF methylococc
18	255	55.3	90	1	Q68XIF methylococc
19	254	55.1	90	1	Q68XIF methylococc
20	252	54.7	90	1	Q68XIF methylococc
21	251	54.4	90	1	Q68XIF methylococc
22	250	54.2	90	1	Q68XIF methylococc
23	250	54.2	90	1	Q68XIF methylococc
24	250	54.2	90	1	Q68XIF methylococc
25	250	54.2	90	1	Q68XIF methylococc
26	250	54.2	90	1	Q68XIF methylococc
27	249	54.0	89	1	Q68XIF methylococc
28	249	54.0	89	1	Q68XIF methylococc
29	249	54.0	89	1	Q68XIF methylococc
30	248	53.8	89	1	Q68XIF methylococc
31	247	53.6	90	1	Q68XIF methylococc

32	246	53.4	90	1	Q68XIF methylococc
33	246	53.4	90	1	Q68XIF methylococc
34	244	52.9	90	1	Q68XIF methylococc
35	244	52.9	90	1	Q68XIF methylococc
36	244	52.9	90	1	Q68XIF methylococc
37	244	52.9	90	1	Q68XIF methylococc
38	243	52.7	94	1	Q68XIF methylococc
39	240	52.1	90	1	Q68XIF methylococc
40	239	51.8	90	1	Q68XIF methylococc
41	239	51.8	90	2	Q68XIF methylococc
42	234	50.8	90	1	Q68XIF methylococc
43	231.5	50.2	91	1	Q68XIF methylococc
44	231	50.1	91	1	Q68XIF methylococc
45	230	49.9	90	1	Q68XIF methylococc
46	226	48.4	90	1	Q68XIF methylococc
47	223	48.4	92	1	Q68XIF methylococc
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49	222	48.2	92	1	Q68XIF methylococc
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55	214	46.4	90	2	Q68XIF methylococc
56	213	46.2	79	1	Q68XIF methylococc
57	212	46.0	90	1	Q68XIF methylococc
58	205	44.5	90	1	Q68XIF methylococc
59	200	43.4	77	1	Q68XIF methylococc
60	193	41.9	78	1	Q68XIF methylococc
61	184	39.9	87	1	Q68XIF methylococc
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67	77	16.7	2410	2	Q68XIF methylococc
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69	76.5	16.6	207	1	Q68XIF methylococc
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74	76.5	16.6	749	2	Q68XIF methylococc
75	75.5	16.4	116	2	Q68XIF methylococc

ALIGNMENTS

Result ID	Query Match	Length	ID	Description
1	461	100.0	90	1
2	461	100.0	90	1
3	461	100.0	90	1
4	313	67.9	91	1
5	304	65.9	91	2
6	300	65.1	91	1
7	300	65.1	91	1
8	297	64.4	90	1
9	290	62.9	88	1
10	290	62.9	88	1
11	290	62.9	88	1
12	286	62.0	90	1
13	260	56.4	90	1
14	256	55.5	90	1
15	256	55.5	90	2
16	256	55.5	91	1
17	256	55.5	92	1
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19	254	55.1	90	1
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28	249	54.0	89	1
29	249	54.0	89	1
30	248	53.8	89	1
31	247	53.6	90	1

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RA Rabbinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transacations between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: BX640447; CAE33897.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC PRODOM: PD029191; DUF495; 1.
CC Complete proteome: Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,6e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSRIYVCYKLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNERNLNLADA 60
Db 1 MSRIYVCYKLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNERNLNLADA 60
Oy 61 PAKRYLQOQMERFLFEDGTVAAGYVP 87
Db 61 PAKRYLQOQMERFLFEDGTVAAGYVP 87

RESULT 2
FETP BORPA STANDARD; PRT; 90 AA.
ID FETP BORPA STANDARD; PRT; 90 AA.
AC Q7W9Q2;
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BP11703;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OK NCBI_TaxID=519;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Alkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabbinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
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CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
CC EMBL: BX640448; CAE37004.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.
CC Pfam: PF04362; DUF495; 1.
CC PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
CC PRODOM: PD029191; DUF495; 1.
CC Complete proteome: Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,6e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSRIYVCYKLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNERNLNLADA 60
Db 1 MSRIYVCYKLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNERNLNLADA 60
Oy 61 PAKRYLQOQMERFLFEDGTVAAGYVP 87
Db 61 PAKRYLQOQMERFLFEDGTVAAGYVP 87

RESULT 3
FETP BORPE STANDARD; PRT; 90 AA.
ID FETP BORPE STANDARD; PRT; 90 AA.
AC Q7WVC4;
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BP2336;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OK NCBI_TaxID=520;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Alkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabbinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
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CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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CC removed.
CC -----
CC EMBL: BX640419; CAE42609.1; -; Genomic_DNA.
CC HAMAP: MF_00686; -; 1.
CC InterPro: IPR007457; YggX.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-2

Perfect score: 461

Sequence: 1 MSRLVNCYKLRKRAEGDLP.....QMERFLPDGTVAQGVVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	243	52.7	107	2	US-09-489-039A-11962
2	242	52.5	93	2	US-09-543-681A-5443
3	240	52.1	122	2	US-09-252-991A-23355
4	230.5	50.0	92	2	US-09-328-352-5456
5	164	35.6	110	2	US-09-540-236-2859
6	72.5	15.7	303	2	US-09-902-540-13601
7	70.5	15.3	200	2	US-09-710-279-1186
8	70.5	15.3	200	2	US-09-710-279-1186
9	70.5	15.3	208	2	US-09-134-001C-3785
10	67.5	14.6	504	1	US-08-441-139-18
11	67.5	14.6	521	1	US-08-557-122A-32
12	67.5	14.6	522	2	US-09-262-666-32
13	67.5	14.6	530	1	US-09-368-588-2
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17	67	14.5	391	2	US-09-964-899-13
18	66.5	14.4	591	2	US-09-370-368-8
19	66	14.3	366	2	US-09-058-260-26
20	65	14.1	366	2	US-08-928-213B-59
21	64.5	14.0	805	1	US-08-045-806-2
22	64.5	14.0	856	2	US-08-366-051B-2
23	64	13.9	856	2	US-09-252-991A-17850
24	64	13.9	1493	2	US-09-713-273A-20
25	63.5	13.8	219	2	US-08-928-213B-61
26	63.5	13.8	498	2	US-09-058-260-16
27	63.5	13.8	503	1	US-08-781-802-2

ALIGNMENTS

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31	63.5	13.8	503	2	US-09-058-260-2	Sequence 2, Appl
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33	63.5	13.8	503	2	US-09-058-260-12	Sequence 12, Appl
34	63.5	13.8	503	2	US-09-058-260-28	Sequence 28, Appl
35	63.5	13.8	503	2	US-09-058-260-28	Sequence 28, Appl
36	63.5	13.8	503	2	US-09-058-260-30	Sequence 30, Appl
37	63	13.7	1242	2	US-09-107-532A-5241	Sequence 5241, Ap
38	63	13.7	581	2	US-09-713-773A-12	Sequence 12, Appl
39	63	13.7	2532	2	US-09-215-694-10	Sequence 10, Appl
40	62.5	13.6	666	2	US-09-270-767-62249	Sequence 10, Appl
41	62.5	13.6	721	2	US-09-270-767-46645	Sequence 46645, A
42	62.5	13.6	839	2	US-09-489-039A-13252	Sequence 13252, A
43	62	13.4	862	1	US-08-685-118-2	Sequence 2, Appl
44	62	13.4	862	1	US-08-914-520-2	Sequence 2, Appl
45	62	13.4	862	1	US-08-914-520-2	Sequence 2, Appl
46	62	13.4	862	1	US-08-914-520-2	Sequence 2, Appl
47	62	13.4	862	1	US-08-914-520-2	Sequence 2, Appl
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49	61.5	13.3	979	2	US-09-949-016-7758	Sequence 4, Appl
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54	61.5	13.3	1464	2	US-09-713-273A-21	Sequence 21, Appl
55	61.5	13.3	1464	2	US-10-038-224-2	Sequence 2, Appl
56	61	13.2	1464	2	US-09-746-390-2	Sequence 2, Appl
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61	61	13.2	1245	1	US-08-611-928-8	Sequence 8, Appl
62	61	13.2	1245	1	US-09-173-891-8	Sequence 8, Appl
63	60.5	13.1	81	2	US-09-716-964B-87	Sequence 87, Appl
64	60.5	13.1	314	2	US-10-290-579A-138	Sequence 138, App
65	60	13.0	563	2	US-09-252-991A-18752	Sequence 18752, A
66	60	13.0	713	2	US-09-949-016-10801	Sequence 10801, A
67	59.5	12.9	447	2	US-09-540-236-3595	Sequence 3595, Ap
68	59.5	12.9	623	2	US-10-104-047-33195	Sequence 33195, A
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70	59	12.8	226	2	US-10-104-047-33195	Sequence 33195, A
71	59	12.8	265	2	US-09-710-279-17820	Sequence 3820, Ap
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73	59	12.8	371	2	US-10-104-047-3421	Sequence 3421, Ap
74	59	12.8	437	2	US-09-134-001C-53442	Sequence 5342, Ap
75	59	12.8	520	2	US-09-328-352-7451	Sequence 7451, Ap

RESULT 1

US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502a-2

Perfect score: 461

Sequence: 1 MSRIIVCYKLRKRAGLDP.....QOMERFLPEDGTVEAGYVP 87

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : Published_Applications_AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	87	3	US-09-955-502-2
2	461	100.0	87	3	US-09-955-502-3
3	443.5	96.2	86	3	US-09-955-502-4
4	300	65.1	87	3	US-09-955-502-29
5	300	65.1	87	3	US-09-955-502-30
6	290	62.9	88	3	US-09-955-502-26
7	290	62.9	88	3	US-09-955-502-27
8	290	62.9	88	3	US-09-955-502-28
9	275	59.7	87	3	US-09-955-502-31
10	260	56.4	87	3	US-09-955-502-32
11	260	56.4	91	3	US-09-955-502-5
12	256	55.5	87	3	US-09-955-502-7
13	256	55.5	88	3	US-09-955-502-9
14	255	55.3	91	3	US-09-955-502-11
15	255	55.3	91	3	US-09-955-502-12
16	255	55.3	91	3	US-09-955-502-13
17	251	54.4	87	3	US-09-955-502-6
18	249	54.0	88	3	US-09-955-502-15
19	249	54.0	90	3	US-09-955-502-10
20	249	54.0	91	3	US-09-955-502-14
21	249	54.0	91	3	US-09-955-502-16
22	243	52.7	87	3	US-09-955-502-8
23	243	52.7	87	3	US-09-955-502-18
24	240	52.1	87	3	US-09-955-502-25
25	230	49.9	88	3	US-09-955-502-33
26	226	49.0	90	3	US-09-955-502-20

ALIGNMENTS

RESULT 1
US-09-955-502-2
Sequence 2, Appl1 Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 87
TYPE: PRT
ORGANISM: Bordetella pertussis

US-09-955-502-2

Query Match 100.0%; Score 461; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIYCVLKRBAEGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNNENRLNLADA 60
DB 1 MSRIYCVLKRBAEGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNNENRLNLADA 60

QY 61 RARKYLQOQMERFLPEDGTVEAGGYVP 87
DB 61 RARKYLQOQMERFLPEDGTVEAGGYVP 87

RESULT 2

US-09-955-502-3
Sequence 3, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 87
TYPE: PRT
ORGANISM: Bordetella parapertussis

US-09-955-502-3

Query Match 100.0%; Score 461; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.9e-45;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIYCVLKRBAEGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNNENRLNLADA 60
DB 1 MSRIYCVLKRBAEGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNNENRLNLADA 60

QY 61 RARKYLQOQMERFLPEDGTVEAGGYVP 87
DB 61 RARKYLQOQMERFLPEDGTVEAGGYVP 87

RESULT 3

US-09-955-502-4
Sequence 4, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 86
TYPE: PRT
ORGANISM: Bordetella bronchiseptica

US-09-955-502-4

Query Match 96.2%; Score 443.5; DB 3; Length 86;

Best Local Similarity 98.9%; Pred. No. 2e-43;
Matches 86; Conservative 0; Mismatches 1; Indels 1;

QY 1 MSRIYCVLKRBAEGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNNENRLNLADA 60
DB 1 MSRIYCVLKRBAEGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNNENRLNLADA 60

QY 61 RARKYLQOQMERFLPEDGTVEAGGYVP 87
DB 61 RARKYLQOQMERFLPEDGTVEAGGYVP 86

RESULT 4

US-09-955-502-29
Sequence 29, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia mallei

US-09-955-502-29

Query Match 65.1%; Score 300; DB 3; Length 87;
Best Local Similarity 57.5%; Pred. No. 8.1e-27;
Matches 50; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

QY 1 MSRIYCVLKRBAEGLDPPYPGELGTRIMQOISKEAMEBWKQIQTRLVNNENRLNLADA 60
DB 1 MARKTHCKLKGKBAEGLDPPYPGELGKRLYESVSKOMQWLKQITLNNENRLNLADA 60

QY 61 RARKYLQOQMERFLPEDGTVEAGGYVP 87
DB 61 RARKYLQOQMERFLPEDGTVEAGGYVP 87

RESULT 5

US-09-955-502-30
Sequence 30, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296, 97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 87
TYPE: PRT
ORGANISM: Burkholderia pseudomallei

US-09-955-502-30

Query Match 65.1%; Score 300; DB 3; Length 87;
Best Local Similarity 57.5%; Pred. No. 8.1e-27;
Matches 50; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 5.92509 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502A-2

Perfect score: 461

Sequence: 1 MSRTVNCVKLRKREGLDPP.....QQMERFLPEDTVEAQQGVVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	62.9	88	6	US-10-467-657-968
2	70.5	15.3	200	6	US-10-793-626-1186
3	70.5	15.3	200	6	US-10-793-626-1186
4	67	14.5	1320	7	US-11-098-686-10831
5	64.5	14.0	567	7	US-11-033-039-1279
6	64.5	14.0	805	7	US-11-108-539-2
7	62.5	13.6	483	7	US-11-137-465-40
8	61.5	13.3	832	7	US-11-098-686-10182
9	60	13.0	240	7	US-11-044-111-10
10	59.5	12.9	623	7	US-11-072-512-3378
11	59	12.8	226	7	US-11-072-512-3820
12	59	12.8	265	6	US-10-793-626-174
13	59	12.8	371	7	US-11-072-512-3421
14	59	12.8	805	6	US-10-927-641-77
15	58.5	12.7	662	7	US-11-072-175-184
16	58	12.6	919	6	US-10-821-234-951
17	57.5	12.5	104	7	US-11-120-308-74
18	57.5	12.5	398	6	US-10-793-626-44
19	57.5	12.5	398	6	US-10-793-626-1498
20	57.5	12.5	897	6	US-10-821-234-1523
21	57	12.4	212	7	US-11-044-111-6
22	57	12.4	212	7	US-11-044-111-6
23	57	12.4	239	7	US-11-044-111-5
24	57	12.4	239	7	US-11-044-111-25
25	57	12.4	240	7	US-11-044-111-9

26	57	12.4	464	6	US-10-959-322-5
27	57	12.4	809	7	US-11-072-512-3367
28	57	12.4	1056	7	US-11-044-111-22
29	56	12.1	183	7	US-11-072-512-3180
30	56	12.1	702	7	US-11-072-512-2154
31	56	12.1	1076	6	US-10-467-657-7916
32	55.5	12.0	237	6	US-10-467-657-570
33	55.5	12.0	497	7	US-11-010-239-85
34	55.5	12.0	522	7	US-11-072-512-3665
35	55.5	12.0	563	7	US-11-040-218-23
36	55.5	12.0	625	7	US-11-072-512-3210
37	55.5	12.0	3353	7	US-11-037-243-64
38	55	11.9	519	7	US-11-099-691-10
39	54.5	11.8	356	7	US-11-143-986-8
40	54.5	11.8	356	7	US-11-143-986-9
41	54.5	11.8	1275	6	US-10-724-598-49
42	54.5	11.8	1340	7	US-11-070-575-6
43	54.5	11.8	1344	7	US-11-091-643-20
44	54.5	11.8	1659	7	US-11-072-175-205
45	54.5	11.8	2080	7	US-11-124-367A-364
46	54.5	11.8	2542	7	US-11-124-367A-363
47	54	11.7	331	7	US-11-098-686-10431
48	53.5	11.6	372	6	US-10-467-657-2318
49	53.5	11.6	599	7	US-11-109-157A-3
50	53.5	11.6	1373	7	US-11-098-686-11150
51	53.5	11.6	1686	7	US-11-109-157A-1
52	53.5	11.6	1686	7	US-11-226-701-2
53	53.5	11.6	2250	6	US-10-922-232B-57
54	53.5	11.6	2630	7	US-11-186-731-2
55	53.5	11.6	4060	6	US-10-922-232B-55
56	53.5	11.6	6738	6	US-10-922-232B-56
57	53.5	11.6	7968	7	US-11-186-731-5
58	53	11.5	200	7	US-11-194-246-402
59	53	11.5	240	7	US-11-007-282-8
60	53	11.5	240	7	US-11-007-282-13
61	53	11.5	240	7	US-11-007-282-14
62	53	11.5	258	7	US-11-007-282-6
63	53	11.5	342	7	US-11-156-084-25
64	53	11.5	342	7	US-11-156-084-44
65	53	11.5	369	7	US-11-156-084-45
66	53	11.5	384	7	US-11-098-686-10752
67	53	11.5	453	7	US-11-072-512-3394
68	53	11.5	618	6	US-10-454-437-396
69	53	11.5	619	7	US-11-156-084-24
70	53	11.5	784	6	US-10-517-939-324
71	52.5	11.4	237	6	US-10-793-626-1714
72	52.5	11.4	143	7	US-11-044-111-11
73	52.5	11.4	362	6	US-10-517-939-68
74	52.5	11.4	471	6	US-10-770-726-68
75	52.5	11.4	471	7	US-11-152-366-31

ALIGNMENTS

RESULT 1

US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; TITLE OF INVENTION: MONACI Elisabetta
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

ALIGNMENTS

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; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match          62.9%; Score 290; DB 6; Length 88;
Best Local Similarity 60.9%; Pred. No. 3.5e-27;
Matches 53; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MSRVNCKLKREAGLDPPYPGELGTRIMQOISKEAWEW--KQIQ-TRLVNNRLNLADARAKY----- 65
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MARVFCVKLNKEAGMKFPPLNELGKRIFFENVSQEAAWTRHTQMLINENRLSLADP 60
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 RARKYLOQOMERFLFEDGTVEAQGVP 87
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 RAREYLAQOMEQYFFGDGADAVQGYVP 87
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 2
US-10-793-626-1186
; Sequence 1186, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1186
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1186

Query Match          15.3%; Score 70.5; DB 6; Length 200;
Best Local Similarity 26.3%; Pred. No. 0.38;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;

Qy 17 LDPP-PYPGELGTRIMQOISKEAWEW--KQIQ-TRLVNNRLNLADARAKY----- 65
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 109 MDIPLLYENEL-----QDTVDVWVVVYTSIQIDRLMERNNLSLEDAKARVYSQISDK 163
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 66 -----LQOQMERFLFEDGTVEAQ 83
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 164 KSRMADHVINDGLKLEKQNLQKLEEGYIQSE 198
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 3
US-10-793-626-2390
; Sequence 2390, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2390
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2390

Query Match          15.3%; Score 70.5; DB 6; Length 200;
Best Local Similarity 26.3%; Pred. No. 0.38;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;

Qy 17 LDPP-PYPGELGTRIMQOISKEAWEW--KQIQ-TRLVNNRLNLADARAKY----- 65
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 109 MDIPLLYENEL-----QDTVDVWVVVYTSIQIDRLMERNNLSLEDAKARVYSQISDK 163
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 66 -----LQOQMERFLFEDGTVEAQ 83
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 164 KSRMADHVINDGLKLEKQNLQKLEEGYIQSE 198
   :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 4
US-11-098-686-10831
; Sequence 10831, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10831
; LENGTH: 1320
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10831

Query Match          14.5%; Score 67; DB 7; Length 1320;
Best Local Similarity 31.5%; Pred. No. 9.4;
Matches 23; Conservative 11; Mismatches 25; Indels 14; Gaps 3;

Qy 5 VNCVKLKREAGLDPPYPGELGTRIMQOISKEAWEW--KQIQ-TRLVNNRLNLADARAKY----- 61
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Qy 62 ARKYLOQOQMERFL 74
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Db 272 AR-----MERAL 278
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RESULT 5
US-11-033-039-1279
; Sequence 1279, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KBY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-3
Perfect score: 461
Sequence: 1 MSRLVNCVKLRKREAGLDPP.....QOMERFLFDGTVEAQGYVP 87

Scoring table:
BLOSUM62
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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	87	5	ABB78148
2	461	100.0	87	5	ABB78147
3	443.5	96.2	86	5	ABB78149
4	300	65.1	87	5	ABB78175
5	294	63.8	87	5	ABB78174
6	290	62.9	88	5	ABB78171
7	290	62.9	88	5	ABB78172
8	290	62.9	88	5	ABB78173
9	290	62.9	88	6	ABP77219
10	275	59.7	87	5	ABB78176
11	260	56.4	87	5	ABB78177
12	260	56.4	91	5	ABB78150
13	256	55.5	87	5	ABB78152
14	256	55.5	88	5	ABB78154
15	255	55.3	91	5	ABB78158
16	255	55.3	91	5	ABB78157
17	255	55.3	91	5	ABB78156
18	251	54.0	87	5	ABB78151
19	249	54.0	88	5	ABB78160
20	249	54.0	89	9	ABE41576
21	249	54.0	90	5	ABB78155
22	249	54.0	91	5	ABB78161
23	249	54.0	91	5	ABB78159
24	249	54.0	91	5	ABB78162

ALIGNMENTS

RESULT 1

ABB78148
ID ABB78148 standard; protein; 87 AA.

XX AC ABB78148;

XX AC ABB78148;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;

XX hydroxyl radical; DNA damage; YggX homologue.

OS Bordetella parapertussis.

XX US2002072118-A1.

25	249	54.0	95	9	ABB38294
26	243	52.7	87	5	ABB78153
27	243	52.7	107	7	ABO65445
28	242	52.5	91	5	ABB78163
29	242	52.5	93	7	ADF05158
30	240	52.1	87	5	ABB78170
31	240	52.1	122	7	ABO74609
32	230.5	50.0	92	6	ADA34169
33	230	49.9	88	5	ABB78178
34	226	49.0	90	5	ABB78165
35	222	48.2	78	5	ABB78164
36	222	48.2	87	5	ABB78169
37	218	47.3	90	5	ABB78168
38	200	43.4	76	5	ABB78166
39	197.5	42.8	90	5	ABB78167
40	164	35.6	110	8	ADL05173
41	76.5	16.6	207	6	ABM73508
42	76.5	16.6	207	9	ADV16859
43	76.5	16.6	207	9	ADM94758
44	76.5	16.6	749	5	ABB54524
45	72.5	15.7	303	9	ABM94402
46	70.5	15.3	200	4	AA82648
47	70.5	15.3	200	4	AA82046
48	70.5	15.3	208	5	ABP38940
49	70.5	15.3	208	8	ADS06726
50	70.5	15.3	308	6	ABM70179
51	69.5	15.1	1233	8	ADQ66727
52	69	15.0	124	9	ADX40209
53	69	15.0	527	6	ADB06106
54	69	15.0	528	6	ADB06108
55	68.5	14.9	529	5	AAE26857
56	68.5	14.9	720	7	ADF29270
57	68.5	14.9	720	7	ADG32479
58	67.5	14.6	522	2	AAW69726
59	67.5	14.6	522	9	ABE13006
60	67.5	14.6	522	9	ABE50108
61	67.5	14.6	522	2	AAE26174
62	67.5	14.6	530	9	ABE13007
63	67.5	14.6	530	9	ABE50109
64	67.5	14.6	714	8	ADN20031
65	67	14.5	381	5	AAO20498
66	67	14.5	389	4	AAAM0170
67	67	14.5	593	6	ABR39276
68	67	14.5	678	5	ABBA47819
69	66.5	14.4	591	2	AAV41141
70	66.5	14.4	860	2	AAV41140
71	66.5	14.4	1755	2	AAV41139
72	66	14.3	229	3	AAAB41703
73	66	14.3	318	5	ABG77906
74	66	14.3	503	2	AAW85085
75	66	14.3	856	6	ABR39820

Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
hydroxyl radical; DNA damage; YggX homologue.

Bordetella parapertussis.

US2002072118-A1.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-3
Perfect score: 461
Sequence: 1 MSRTVCVKLRKRAAGLDFP.....QWERFLFEDGTVEAGGVVP 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	62.9	88	2	H81014
2	256	55.5	90	2	C64013
3	255	55.3	91	2	A65954
4	255	55.3	91	2	A65082
5	255	55.3	91	2	P91108
6	249	54.0	90	2	C62320
7	249	54.0	91	2	AH0879
8	240	52.1	90	2	H83003
9	226	49.0	90	2	A10116
10	205	44.5	105	2	C82624
11	200	43.4	93	2	B84994
12	176.5	16.6	207	2	B89952
13	176.5	16.6	749	2	B86774
14	71.5	15.0	855	2	A45713
15	69	15.0	429	2	A62501
16	68.5	14.9	241	2	S19999
17	68	14.8	134	2	T37027
18	67.5	14.6	312	2	H82399
19	67.5	14.6	522	1	ISBYS
20	67.5	14.6	714	2	S77385
21	67	14.5	389	2	T14751
22	67	14.5	678	2	AB1130
23	66.5	14.4	591	1	POMVM
24	66	14.3	318	2	S77153
25	66	14.3	1276	2	T09204
26	65.5	14.2	164	2	B75293
27	65	14.1	238	1	LKRT52
28	65	14.1	323	2	JT0755
29	65	14.1	323	2	A86184

30	65	14.1	393	2	S03576	DNA-directed RNA p
31	64.5	14.0	228	2	C26599	ciathrin light cha
32	64.5	14.0	229	2	B31775	protein kinase-lik
33	64.5	14.0	393	2	T49257	hemagglutinin prec
34	64.5	14.0	560	1	HMI17	hypothetical prote
35	64.5	14.0	622	2	T23804	aryl hydrocarbon r
36	64.5	14.0	805	2	A46266	spectrum beta chai
37	64.5	14.0	2291	1	A46147	fatty-acid synthas
38	64.5	14.0	3063	2	S55505	hypothetical prote
39	64	13.9	133	2	G75385	protein SPE-11 - C
40	64	13.9	299	2	T29546	signal recognition
41	64	13.9	451	2	B64312	hypothetical prote
42	64	13.9	1068	2	S73091	gag polyprotein -
43	63.5	13.8	353	1	POMGR	hemagglutinin prec
44	63.5	13.8	563	1	A45539	aryl hydrocarbon r
45	63.5	13.8	853	2	S58375	aryl hydrocarbon r
46	63.5	13.8	920	2	UC7313	WD-repeat protein
47	63	13.7	506	2	T50211	hypothetical prote
48	63	13.7	569	2	T47358	hypothetical prote
49	62.5	13.6	388	2	T38810	hemagglutinin prec
50	62.5	13.6	563	1	HMI1V	probable transket
51	62.5	13.6	694	2	A95866	dynein heavy chain
52	62.5	13.6	897	2	G02529	hypothetical prote
53	62.5	13.6	1675	2	S70770	hypothetical prote
54	62	13.4	337	2	AG2423	hypothetical prote
55	62	13.4	416	2	C47017	probable transcrip
56	62	13.4	416	2	AF2017	RNA polymerase sig
57	62	13.4	563	2	T17316	hypothetical prote
58	62	13.4	563	2	T46183	zinc proteinase (E
59	62	13.4	1291	2	T09273	probable tail-host
60	61.5	13.3	188	2	C87216	probable hemagglut
61	61.5	13.3	283	4	POHUR1	retrovirus-related
62	61.5	13.3	310	2	B64311	hypothetical prote
63	61.5	13.3	320	2	S69347	transcription init
64	61.5	13.3	1464	2	T07050	hypothetical prote
65	61.5	13.3	4644	1	A38905	dynein heavy chain
66	61	13.2	143	2	D70003	general stress pro
67	61	13.2	320	2	S11879	ethylene-forming e
68	61	13.2	321	2	T02754	probable 1-antibio
69	61	13.2	372	2	B81952	probable type II r
70	61	13.2	504	1	C4RTD5	cytochrome P450 2D
71	61	13.2	678	2	A81490	penicillin-binding
72	61	13.2	865	2	B84718	hypothetical prote
73	61	13.2	1138	2	T24635	hypothetical prote
74	61	13.2	1245	2	T18211	delta endotoxin -
75	60.5	13.1	138	2	T10309	hypothetical prote

ALIGNMENTS

RESULT 1
H81014
Conserved hypothetical protein NMB2021 [Imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014, F81958
R/Retelin, H.; Saundere, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Piazza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000, MUID:2015755, PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TEF>
A/Cross-references: UNIPARC:UP100000C4E7F; GB:A800552; GB:A8002098; NID:972227279; PIDN:
A/Experimental source: serogroup B, strain MC58
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagele, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 79.9886 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502a-3

Perfect score: 461
Sequence: 1 MSRIIVCVKIKREARGLDFP.....QMERFLPDGTVEAGQVVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	90	1	FETP BORR
2	461	100.0	90	1	FETP BORR
3	461	100.0	90	1	FETP BORR
4	313	67.9	91	1	FETP_RALSO
5	304	65.9	91	2	Q4LS19_9BURK
6	300	65.1	91	1	FETP BURR
7	300	65.1	91	1	FETP BURR
8	297	64.4	90	1	FETP CHRYO
9	290	62.9	88	1	FETP_NEIGI
10	290	62.9	88	1	FETP_NEIGI
11	290	62.9	88	1	FETP_NEIGI
12	286	62.0	90	1	FETP_NEIGI
13	260	56.4	90	1	FETP_NEIGI
14	256	55.5	90	1	FETP_NEIGI
15	256	55.5	90	2	Q4QMD9_HAREI
16	256	55.5	91	1	FETP_MANSN
17	256	55.5	92	1	FETP_MANSN
18	255	55.3	90	1	FETP_VIBR
19	254	55.1	90	1	FETP_VIBR
20	252	54.7	90	1	FETP_VIBR
21	251	54.4	90	1	FETP_VIBR
22	250	54.2	90	1	FETP_VIBR
23	250	54.2	90	1	FETP_VIBR
24	250	54.2	90	1	FETP_VIBR
25	250	54.2	90	1	FETP_VIBR
26	250	54.2	90	1	FETP_VIBR
27	249	54.0	89	1	FETP_VIBR
28	249	54.0	89	1	FETP_VIBR
29	249	54.0	89	1	FETP_VIBR
30	248	53.8	89	1	FETP_VIBR
31	247	53.6	90	1	FETP_VIBR

32	246	53.4	90	1	FETP_ECOL6	O8fe19 escherichia
33	246	53.4	90	1	FETP_ECOL6	O7n711 photobacter
34	244	52.9	90	1	FETP_SALCH	O57k04 salmonella
35	244	52.9	90	1	FETP_SALCH	O5pmn1 salmonella
36	244	52.9	90	1	FETP_SALCH	O5pmn1 salmonella
37	244	52.9	90	1	FETP_SALCH	O5pmn1 salmonella
38	243	52.7	94	1	FETP_HABPU	O7vkb6 haemophilus
39	240	52.1	90	1	FETP_PSEAR	O9nu36 pseudomonas
40	239	51.8	90	1	FETP_BRMCT	O6d8j9 erwinia car
41	239	51.8	90	2	Q4J228_AZOV1	O4j228 azotobacter
42	234	50.8	90	1	FETP_YERPS	O666m3 yersinia ps
43	231.5	50.2	90	1	FETP_ACTIAD	O6f1b3 actinobact
44	231	50.1	91	1	FETP_XANAC	O8p1j7 xanthobact
45	230	49.9	90	1	FETP_COXBU	O8d3d6 coxiella bu
46	226	49.0	90	1	FETP_YERBP	O8zhe7 yersinia pe
47	223	48.4	92	1	FETP_XANOR	O5gy22 xanthomonas
48	222	48.2	90	1	FETP_PSEBK	O8p829 pseudomonas
49	222	48.2	92	1	FETP_XANCP	O8p829 pseudomonas
50	222	48.2	92	2	Q4UW14_XANCP	O4uw14 xanthomonas
51	220	47.7	78	1	FETP_BUCAP	O8k925 buchnera ap
52	218	47.3	90	1	FETP_PSESM	O8j7u5 pseudomonas
53	218	47.3	90	2	Q4ZLF3_PSEST	O4z1p3 pseudomonas
54	214	46.4	90	2	O6T7F6_PSEFL	O6t7f6 pseudomonas
55	214	46.4	90	2	Q4KJ72_PSEF5	O4kj72 pseudomonas
56	213	46.2	79	1	FETP_CANBF	O7vrg9 candidatus
57	212	46.0	90	1	FETP_XYLFT	O8rd06 xyloella fas
58	205	44.5	90	1	FETP_PSESM	O8p829 pseudomonas
59	200	43.4	77	1	FETP_BUCAI	O8k925 buchnera ap
60	193	41.9	78	1	FETP_WIGBR	O8d3c5 wiggleswort
61	184	39.9	87	1	FETP_FRAIT	O5nhj8 francisella
62	178	38.6	92	2	Q4NMQ4_9DELT	O4nmq4 anaeromyxob
63	175	38.0	96	2	Q4FVJ7_9GAMW	O4fvj7 psychrobact
64	157	34.1	87	1	FETP_BUCBP	O8p829 pseudomonas
65	157	34.1	87	1	FETP_BUCBP	O8p829 pseudomonas
66	77	16.7	330	2	O5DA35_SCHUA	O5daf3 human immun
67	77	16.7	67	2	O5A249_EMENT	O5a249 aspergillus
68	76.5	16.6	207	1	COAE_STAM	O63830 staphylococ
69	76.5	16.6	207	1	COAE_STAM	O63831 staphylococ
70	76.5	16.6	207	1	COAE_STAM	O63831 staphylococ
71	76.5	16.6	207	1	COAE_STAM	O63831 staphylococ
72	76.5	16.6	207	1	COAE_STAM	O63831 staphylococ
73	76.5	16.6	207	2	O5HPF5_STAMC	O5hpf5 staphylococ
74	76.5	16.6	749	2	O9CGA2_LACLA	O9cga2 lactococcus
75	75.5	16.4	116	2	Q6WS71_9HIV1	O6ws71 human immun

ALIGNMENTS

RESULT 1
FETP BORR STANDARD; PRT; 90 AA.
ID FETP BORR
AC Q7WH06;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Pe(2+) trafficking protein.
GN OrderedLocustNames=BB3405;
OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxId=518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatina M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.J., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdano-Farraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achtmann M., Atkin R., Baker S., Baeson D., Baeson N., Cherevach I.,
Chillingworth T., Collins A., Cronin A., Davis P., Doggett J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagsis K.,
Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,

```
RA Rabbittowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Urein L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.",
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL: BX640447; CAB3897.1; -; Genomic_DNA.
DR HAMAP: MF_00686; -; 1.
DR InterPro: IPR007457; YggX.
DR Pfam: PF04362; DUF495; 1.
DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR PRODOM: PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIYVCVKLRKREAGLDPPYPGELGTRIMWQISKEAMEWKOIOTRLVNNENLNLAADA 60
DB 1 MSRIYVCVKLRKREAGLDPPYPGELGTRIMWQISKEAMEWKOIOTRLVNNENLNLAADA 60

QY 61 PAKRYLQOQMERFLFEDGTVEAGGYVP 87
DB 61 PAKRYLQOQMERFLFEDGTVEAGGYVP 87

RESULT 2
FETP BORPA STANDARD; PRT; 90 AA.
ID FETP BORPA
AC Q7W9Q2;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS OrderedLocustNames=BP1703;
GN Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;

RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STAIN=12822 / ATCC BAA-587;
RC MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatina M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jørgels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabbittowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Urein L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.",
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
```

```
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL: BX640428; CAB37004.1; -; Genomic_DNA.
DR HAMAP: MF_00686; -; 1.
DR InterPro: IPR007457; YggX.
DR Pfam: PF04362; DUF495; 1.
DR PIRSF: PIRSF029827; Fe_traffic_YggX; 1.
DR PRODOM: PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIYVCVKLRKREAGLDPPYPGELGTRIMWQISKEAMEWKOIOTRLVNNENLNLAADA 60
DB 1 MSRIYVCVKLRKREAGLDPPYPGELGTRIMWQISKEAMEWKOIOTRLVNNENLNLAADA 60

QY 61 PAKRYLQOQMERFLFEDGTVEAGGYVP 87
DB 61 PAKRYLQOQMERFLFEDGTVEAGGYVP 87

RESULT 3
FETP BORPE STANDARD; PRT; 90 AA.
ID FETP BORPE
AC Q7W9Q4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS OrderedLocustNames=BP2336;
GN Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;

RA NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RC MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatina M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jørgels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabbittowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Urein L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.",
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR EMBL: BX640418; CAB42609.1; -; Genomic_DNA.
DR HAMAP: MF_00686; -; 1.
DR InterPro: IPR007457; YggX.
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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502a-3

Perfect score: 461

Sequence: 1 MSRIYVCVLRRAEGLDFP.....QOMERFLPEDGTVEAGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	240	52.1	122	2	US-09-252-991A-23355
4	230.5	50.0	92	2	US-09-328-352-5456
5	164	35.6	110	2	US-09-540-236-2859
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8	70.5	15.3	200	2	US-09-710-279-1186
9	70.5	15.3	200	2	US-09-710-279-1186
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19	66.5	14.4	591	2	US-09-370-368-8
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22	64.5	14.0	805	1	US-08-045-806-2
23	64	13.9	856	1	US-08-366-051B-2
24	63.5	13.8	1493	2	US-09-252-991A-17850
25	63.5	13.8	219	2	US-09-713-273A-20
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31 63.5 13.8 503 2 US-09-058-260-2 Sequence 2, Appl1

32 63.5 13.8 503 2 US-09-058-260-10 Sequence 10, Appl1

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34 63.5 13.8 503 2 US-09-058-260-28 Sequence 28, Appl1

35 63.5 13.8 503 2 US-09-058-260-30 Sequence 30, Appl1

36 63.5 13.8 1242 2 US-09-107-532A-5241 Sequence 5241, Ap

37 63 13.7 581 2 US-09-713-273A-12 Sequence 12, Appl1

38 63 13.7 2532 2 US-09-215-694-10 Sequence 10, Appl1

39 63 13.7 2532 2 US-10-109-310-10 Sequence 10, Appl1

40 62.5 13.6 666 2 US-09-270-767-62249 Sequence 62249, A

41 62.5 13.6 721 2 US-09-270-767-46645 Sequence 46645, A

42 62.5 13.6 839 2 US-09-489-039A-13252 Sequence 13252, A

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57 61 13.2 312 2 US-09-605-703B-2656 Sequence 2656, Ap

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62 61 13.2 1245 2 US-09-716-964B-87 Sequence 87, Appl1

63 60.5 13.1 81 2 US-10-290-579A-138 Sequence 138, App

64 60.5 13.1 314 2 US-09-252-991A-18752 Sequence 18752, A

65 60 13.0 563 2 US-09-540-236-3595 Sequence 3595, Ap

66 60 13.0 713 2 US-09-540-236-3595 Sequence 3595, Ap

67 59.5 12.9 447 2 US-09-902-540-13195 Sequence 13195, A

68 59.5 12.9 623 2 US-10-104-047-3378 Sequence 4, Appl1

69 59.5 12.9 5037 2 US-09-424-783-4 Sequence 3820, Ap

70 59 12.8 226 2 US-10-104-047-3820 Sequence 174, App

71 59 12.8 265 2 US-09-710-279-1782 Sequence 14939, A

72 59 12.8 309 2 US-09-248-796A-14939 Sequence 3421, Ap

73 59 12.8 371 2 US-10-104-047-3421 Sequence 5342, Ap

74 59 12.8 437 2 US-09-134-001C-5342 Sequence 7451, Ap

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RESULT 1

US-09-489-039A-11962

Sequence 11962, Appl1

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117, 747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 11962

LENGTH: 107

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-3
Perfect score: 461
Sequence: 1 MSRLVNCVKLRBAEGLDFP.....QMERPLPEQGTVAQGVVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	290	62.9	88	US-09-955-502-26	Sequence 26, Appli
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9	275	59.7	87	US-09-955-502-31	Sequence 31, Appli
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22	249	54.0	91	US-09-955-502-17	Sequence 17, Appli
23	243	52.7	87	US-09-955-502-8	Sequence 8, Appli
24	242	52.5	91	US-09-955-502-18	Sequence 18, Appli
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26	230	49.9	88	US-09-955-502-33	Sequence 33, Appli
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US-09-955-502-2
Sequence 2, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955.502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 87
TYPE: PRT
ORGANISM: Bordetella pertussis

US-09-955-502-2

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Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSRIIVNCVKLRBAEGDPPYPGELGTRIMQOISKEAMBEWKQIOTRLVNERNLNLADA 60

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Db 61 RARKYLOQOMERFLFEDGTVEAOGYVP 87

RESULT 2
US-09-955-502-3

; Sequence 3, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3

; LENGTH: 87
; TYPE: PRT
; ORGANISM: Bordetella parapertussis

US-09-955-502-3

Query Match 100.0%; Score 461; DB 3; Length 87;
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Db 61 RARKYLOQOMERFLFEDGTVEAOGYVP 87

RESULT 3
US-09-955-502-4

; Sequence 4, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4

; LENGTH: 86
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica

US-09-955-502-4

Query Match 96.2%; Score 443.5; DB 3; Length 86;

Best Local Similarity 98.9%; Pred. No. 2e-43; Indels 1; Gaps 1;
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Db 1 MSRIIVNCVKLRBAEGDPPYPGELGTRIMQOISKEAMBEWKQIOTRLVNERNLNLADA 60

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Db 61 RARKYLOQOMERFLFEDGTVEAOGYVP 86

RESULT 4
US-09-955-502-29

; Sequence 29, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29

; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia mallei

US-09-955-502-29

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Qy 61 RARKYLOQOMERFLFEDGTVEAOGYVP 87
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RESULT 5
US-09-955-502-30

; Sequence 30, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia pseudomallei

US-09-955-502-30

Query Match 65.1%; Score 300; DB 3; Length 87;
Best Local Similarity 57.5%; Pred. No. 8.1e-27;
Matches 50; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 5.92509 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502A-3
Perfect score: 461
Sequence: 1 MSRIYNCVKLRBAGLDFP.....QOMERFLFDGTVEAGGVF 87

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

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Published Applications_AA_New:*
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4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	290	62.9	88 6	US-10-467-657-968 Sequence 968, App
2	70.5	15.3	200 6	US-10-793-626-1186 Sequence 1186, App
3	70.5	15.3	200 6	US-10-793-626-2390 Sequence 2390, App
4	67	14.5	1320 7	US-11-098-686-10831 Sequence 10831, App
5	64.5	14.0	567 7	US-11-033-039-1279 Sequence 1279, App
6	64.5	14.0	805 7	US-11-108-539-2 Sequence 2, App1
7	62.5	13.6	483 7	US-11-137-465-40 Sequence 40, App1
8	61.5	13.3	832 7	US-11-098-686-10182 Sequence 10182, App
9	60	13.0	240 7	US-11-044-111-10 Sequence 10, App1
10	59.5	12.9	623 7	US-11-072-512-3378 Sequence 3378, App
11	59	12.8	226 7	US-11-072-512-3820 Sequence 3820, App
12	59	12.8	265 6	US-10-793-626-174 Sequence 174, App
13	59	12.8	371 7	US-11-072-512-3421 Sequence 3421, App
14	59	12.8	805 6	US-10-927-661-77 Sequence 77, App1
15	58.5	12.7	662 7	US-11-072-175-184 Sequence 184, App
16	58	12.6	919 6	US-10-821-234-951 Sequence 951, App
17	57.5	12.5	104 7	US-11-120-308-74 Sequence 74, App1
18	57.5	12.5	398 6	US-10-793-626-44 Sequence 44, App1
19	57.5	12.5	398 6	US-10-821-234-1523 Sequence 1523, App
20	57.5	12.5	897 6	US-10-821-234-1523 Sequence 1523, App
21	57	12.4	212 7	US-11-044-111-6 Sequence 6, App1
22	57	12.4	212 7	US-11-044-111-6 Sequence 6, App1
23	57	12.4	239 7	US-11-044-111-5 Sequence 5, App1
24	57	12.4	239 7	US-11-044-111-5 Sequence 5, App1
25	57	12.4	240 7	US-11-044-111-9 Sequence 9, App1

26	57	12.4	464 6	US-10-959-322-5 Sequence 5, App1
27	57	12.4	809 7	US-11-072-512-3367 Sequence 3367, App
28	57	12.4	1056 7	US-11-044-111-22 Sequence 22, App1
29	56	12.1	183 7	US-11-072-512-3180 Sequence 3180, App
30	56	12.1	702 7	US-11-072-512-2154 Sequence 2154, App
31	56	12.1	1076 6	US-10-467-657-7916 Sequence 7916, App
32	55.5	12.0	237 6	US-10-467-657-570 Sequence 570, App
33	55.5	12.0	497 7	US-11-010-239-85 Sequence 85, App1
34	55.5	12.0	522 7	US-11-072-512-1665 Sequence 1665, App
35	55.5	12.0	563 7	US-11-040-218-23 Sequence 23, App1
36	55.5	12.0	623 7	US-11-072-512-3210 Sequence 3210, App
37	55.5	12.0	3353 7	US-11-037-243-64 Sequence 64, App1
38	55	11.9	519 7	US-11-099-691-10 Sequence 10, App1
39	54.5	11.8	356 7	US-11-143-986-9 Sequence 9, App1
40	54.5	11.8	356 7	US-11-143-986-9 Sequence 9, App1
41	54.5	11.8	1275 6	US-10-724-598-49 Sequence 49, App1
42	54.5	11.8	1340 7	US-11-070-575-6 Sequence 6, App1
43	54.5	11.8	1344 7	US-11-091-643-20 Sequence 20, App1
44	54.5	11.8	1659 7	US-11-072-175-205 Sequence 205, App
45	54.5	11.8	2080 7	US-11-124-367A-364 Sequence 364, App
46	54.5	11.8	2542 7	US-11-124-367A-363 Sequence 363, App
47	54	11.7	321 7	US-11-098-686-10431 Sequence 10431, App
48	53.5	11.6	372 6	US-10-467-657-2318 Sequence 2318, App
49	53.5	11.6	599 7	US-11-109-157A-3 Sequence 3, App1
50	53.5	11.6	1373 7	US-11-098-686-11150 Sequence 11150, App
51	53.5	11.6	1686 7	US-11-109-157A-1 Sequence 1, App1
52	53.5	11.6	1686 7	US-11-109-157A-1 Sequence 1, App1
53	53.5	11.6	2250 6	US-10-922-222B-57 Sequence 57, App1
54	53.5	11.6	2630 7	US-11-186-731-2 Sequence 2, App1
55	53.5	11.6	4060 6	US-10-922-232B-55 Sequence 55, App1
56	53.5	11.6	7938 7	US-10-922-232B-56 Sequence 56, App1
57	53.5	11.6	7968 7	US-11-186-731-5 Sequence 5, App1
58	53	11.5	200 7	US-11-194-246-402 Sequence 402, App
59	53	11.5	240 7	US-11-007-282-8 Sequence 8, App1
60	53	11.5	240 7	US-11-007-282-13 Sequence 13, App1
61	53	11.5	240 7	US-11-007-282-14 Sequence 14, App1
62	53	11.5	258 7	US-11-007-282-6 Sequence 6, App1
63	53	11.5	342 7	US-11-156-084-25 Sequence 25, App1
64	53	11.5	342 7	US-11-156-084-44 Sequence 44, App1
65	53	11.5	369 7	US-11-156-084-45 Sequence 45, App1
66	53	11.5	384 7	US-11-098-686-10752 Sequence 10752, App
67	53	11.5	453 7	US-11-072-512-3394 Sequence 3394, App
68	53	11.5	618 6	US-10-454-437-396 Sequence 396, App
69	53	11.5	619 7	US-11-156-084-24 Sequence 24, App1
70	53	11.5	784 6	US-10-517-929-324 Sequence 324, App
71	52.5	11.4	143 6	US-10-793-626-1714 Sequence 1714, App
72	52.5	11.4	237 7	US-11-044-111-11 Sequence 11, App1
73	52.5	11.4	362 6	US-10-517-929-68 Sequence 68, App1
74	52.5	11.4	471 6	US-10-770-726-68 Sequence 68, App1
75	52.5	11.4	471 7	US-11-152-366-31 Sequence 31, App1

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FOMTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR APPLICATION NUMBER: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWinn9, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 62.9%; Score 290; DB 6; Length 88;
Best Local Similarity 60.9%; Pred. No. 3.5e-27;
Matches 53; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 1 MSRIIVCVKLRKAEGLDPPYPGELGTRIMQISKEAMEW-KQIQ-TRLVNNRLNLADARARY----- 60
DB 1 MARVVPCKVKNKRAEGMKFPPLPNELGKRIFENVSQKMAAMTIRHQTWLTINENSLADP 60

QY 61 RARKYLOOQMERFLPFDGTVAEQVTP 87
DB 61 RAREYLAQOMEQYFFGDGADAVGQVTP 87

RESULT 2
US-10-793-626-1186
Sequence 1186, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/10/793, 626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1186
LENGTH: 200
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1186

Query Match 15.3%; Score 70.5; DB 6; Length 200;
Best Local Similarity 26.3%; Pred. No. 0.38;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;

QY 17 LDFF-PYPGELGTRIMQISKEAMEW--KQIQ-TRLVNNRLNLADARARY----- 65
DB 109 MDIPLLYENEL-----QDTVDVWVWVYTSISIQIDRLMERNNLSLEDKARVYSQISIDK 163

QY 66 -----LQOQMERFLPFDGTVAEQ 83
DB 164 KSRMADHVINDLGDKLELKNLQKLEBEGYIQSE 198

RESULT 3
US-10-793-626-2390
Sequence 2390, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/10/793, 626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2390
LENGTH: 200
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-2390

Query Match 15.3%; Score 70.5; DB 6; Length 200;
Best Local Similarity 26.3%; Pred. No. 0.38;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;

QY 17 LDFF-PYPGELGTRIMQISKEAMEW--KQIQ-TRLVNNRLNLADARARY----- 65
DB 109 MDIPLLYENEL-----QDTVDVWVWVYTSISIQIDRLMERNNLSLEDKARVYSQISIDK 163

QY 66 -----LQOQMERFLPFDGTVAEQ 83
DB 164 KSRMADHVINDLGDKLELKNLQKLEBEGYIQSE 198

RESULT 4
US-11-098-686-10831
Sequence 10831, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098, 686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10831
LENGTH: 1320
TYPE: PRT
ORGANISM: Lawsonia intracellularis
US-11-098-686-10831

Query Match 14.5%; Score 67; DB 7; Length 1320;
Best Local Similarity 31.5%; Pred. No. 9.4;
Matches 23; Conservative 11; Mismatches 25; Indels 14; Gaps 3;

QY 5 VNCYKLRKAEGLDPPYPGELGTRIMQISKEAMEW-KQIQ-TRLVNNRLNLADARARY----- 61
DB 217 LNTLSLHKSKELEQOQYHKKRLDIWHQ-----WEEBRLIQTRLEHLPISAFPODGA 271

QY 62 ARXYLOOQMERFL 74
DB 272 AK-----MERAL 278

RESULT 5
US-11-033-039-1279
Sequence 1279, Application US/11033039
Publication No. US2006002947A1
GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPTOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033, 039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 81.9977 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502a-4

Perfect score: 454
Sequence: 1 MSRIYVCYKLRBAEGLDLP.....QQQMERFLPEDGYEAQGV 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_21:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003s:*
- 7: geneeqp2004s:*
- 8: geneeqp2005s:*
- 9: geneeqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	86	5	ABB78149 Amino aci
2	443.5	97.7	87	5	ABB78148 Amino aci
3	443.5	97.7	87	5	ABB78147 Amino aci
4	282.5	62.2	87	5	ABB78175 Amino aci
5	276.5	60.9	87	5	ABB78174 Amino aci
6	272.5	60.0	88	5	ABB78171 Amino aci
7	272.5	60.0	88	5	ABB78172 Amino aci
8	272.5	60.0	88	5	ABB78173 Amino aci
9	272.5	60.0	88	5	ABB78172 Amino aci
10	257.5	56.7	87	5	ABB78176 Amino aci
11	246	54.2	91	5	ABB78150 Amino aci
12	245.5	53.4	87	5	ABB78157 Amino aci
13	245.5	53.4	88	5	ABB78154 Amino aci
14	242	53.3	89	9	ABB78154 Amino aci
15	242	53.3	95	9	ABB78156 L. pneumo
16	241	53.1	91	5	ABB78158 Amino aci
17	241	53.1	91	5	ABB78163 Amino aci
18	241	53.1	91	5	ABB78157 Amino aci
19	241	53.1	91	5	ABB78156 Amino aci
20	238.5	52.5	87	5	ABB78152 Amino aci
21	235	51.8	88	5	ABB78160 Amino aci
22	235	51.8	90	5	ABB78155 Amino aci
23	235	51.8	91	5	ABB78161 Amino aci
24	235	51.8	91	5	ABB78159 Amino aci

25	235	51.8	91	5	ABB78162 Amino aci
26	233.5	51.4	87	5	ABB78151 Amino aci
27	229	50.4	107	7	ABO65445 Klebsiell
28	228	50.2	93	7	ADF05158 Bacteri
29	225.5	49.7	87	5	ABB78153 Amino aci
30	223.5	49.2	92	6	ADA34169 Acinetoba
31	223	49.1	88	5	ABB78178 Amino aci
32	222.5	49.0	87	5	ABB78170 Amino aci
33	222.5	49.0	122	7	ABO74609 Pseudomon
34	222	48.9	78	5	ABB78164 Amino aci
35	212	46.7	90	5	ABB78165 Amino aci
36	204.5	45.0	87	5	ABB78169 Amino aci
37	200.5	44.2	90	5	ABB78168 Amino aci
38	200	44.1	76	5	ABB78166 Amino aci
39	187.5	41.3	90	5	ABB78167 Amino aci
40	157.5	34.7	110	8	ADL05173 M. catarr
41	156.5	16.9	749	5	ABB54524 Lactococc
42	156.5	16.0	303	9	ABM94402 W. xanthu
43	156.5	15.7	207	6	ABM73508 Staphyloc
44	156.5	15.7	207	6	ADVL6859 Staphyloc
45	156.5	15.7	207	6	ADVL6859 Staphyloc
46	156.5	15.5	200	4	ADW94758 Prolifera
47	156.5	15.5	200	4	ADW94758 Prolifera
48	156.5	15.5	200	4	ADW94758 Prolifera
49	156.5	15.5	208	5	ADW94758 Prolifera
50	156.5	15.5	208	5	ADW94758 Prolifera
51	156.5	15.5	366	2	ADW94758 Prolifera
52	156.5	15.3	1233	8	ADW94758 Prolifera
53	156.5	15.2	1233	8	ADW94758 Prolifera
54	156.5	15.2	1233	8	ADW94758 Prolifera
55	156.5	15.2	1233	8	ADW94758 Prolifera
56	156.5	15.2	1233	8	ADW94758 Prolifera
57	156.5	15.2	1233	8	ADW94758 Prolifera
58	156.5	15.2	1233	8	ADW94758 Prolifera
59	156.5	15.2	1233	8	ADW94758 Prolifera
60	156.5	15.2	1233	8	ADW94758 Prolifera
61	156.5	15.2	1233	8	ADW94758 Prolifera
62	156.5	15.2	1233	8	ADW94758 Prolifera
63	156.5	15.2	1233	8	ADW94758 Prolifera
64	156.5	15.2	1233	8	ADW94758 Prolifera
65	156.5	15.2	1233	8	ADW94758 Prolifera
66	156.5	15.2	1233	8	ADW94758 Prolifera
67	156.5	15.2	1233	8	ADW94758 Prolifera
68	156.5	15.2	1233	8	ADW94758 Prolifera
69	156.5	15.2	1233	8	ADW94758 Prolifera
70	156.5	15.2	1233	8	ADW94758 Prolifera
71	156.5	15.2	1233	8	ADW94758 Prolifera
72	156.5	15.2	1233	8	ADW94758 Prolifera
73	156.5	15.2	1233	8	ADW94758 Prolifera
74	156.5	15.2	1233	8	ADW94758 Prolifera
75	156.5	15.2	1233	8	ADW94758 Prolifera

ALIGNMENTS

RESULT 1	ABB78149	standard; protein; 86 AA
ID	ABB78149	
XX	ABB78149	
AC	ABB78149	
XX	05-NOV-2002	(first entry)
DT	05-NOV-2002	(first entry)
XX	Amino acid sequence of a YggX homologue.	
DE	Amino acid sequence of a YggX homologue.	
XX	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX	hydroxyl radical; DNA damage; YggX homologue.	
OS	Bordetella bronchiseptica.	
XX	Bordetella bronchiseptica.	
PN	US2002072118-A1.	
XX	US2002072118-A1.	

PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 CC
 SQ Sequence 86 AA;
 XX
 Query Match 100.0%; Score 454; DB 5; Length 86;
 Best Local Similarity 100.0%; Pred. No. 9.8e-47;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRIYVCVGLKREAGLDPPYPGELGTRIWQISKEAMEBKQIQTRLVNNRNLNLADA 60
 DB 1 MSRIYVCVGLKREAGLDPPYPGELGTRIWQISKEAMEBKQIQTRLVNNRNLNLADA 60
 QY 61 RARKYLQOQMERFLPEDGTVEAGVVP 86
 DB 61 RARKYLQOQMERFLPEDGTVEAGVVP 86
 DB
 RESULT 2
 ABB78148
 ID ABB78148 standard; protein; 87 AA.
 XX
 AC ABB78148;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.
 XX
 KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.
 XX
 OS Bordetella pertussis.
 XX
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YggX reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YggX homologues
 CC
 SQ Sequence 87 AA;
 XX
 Query Match 97.7%; Score 443.5; DB 5; Length 87;
 Best Local Similarity 98.9%; Pred. No. 1.8e-45;
 Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MSRIYVCVGLKREAGLDPPYPGELGTRIWQISKEAMEBKQIQTRLVNNRNLNLADA 60
 DB 1 MSRIYVCVGLKREAGLDPPYPGELGTRIWQISKEAMEBKQIQTRLVNNRNLNLADA 60
 QY 61 RARKYLQOQMERFLPEDGTVEAGVVP 86
 DB 61 RARKYLQOQMERFLPEDGTVEAGVVP 87
 DB
 RESULT 3
 ABB78147
 ID ABB78147 standard; protein; 87 AA.
 XX
 AC ABB78147;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of a YggX homologue.
 XX
 KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar Typhimurium;
 KW hydroxyl radical; DNA damage; YggX homologue.
 XX
 OS Bordetella pertussis.
 XX
 PN US2002072118-A1.
 XX
 PD 13-JUN-2002.
 XX
 PF 18-SEP-2001; 2001US-00955502.
 XX
 PR 22-SEP-2000; 2000US-0234588P.
 XX
 PA (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 PI Downs D, Gralnick JA;
 XX
 DR WPI; 2002-589476/63.
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YggX protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 PS Example; Fig 1A; 16pp; English.
 XX
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YggX protein (a protein identified from *Salmonella*

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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:05:33 ; Search time 13.2758 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-4
Perfect score: 454
Sequence: 1 MSRLVNCVKLRKRBGLDFP.....OOOMERFLFEDGTVEAGVVP 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	272.5	60.0	88	2	H81014 conserved hypotet
2	241	53.1	91	2	H85954 hypothetical prote
3	241	53.1	91	2	A65082 hypothetical prote
4	238.5	52.5	90	2	P91108 hypothetical prote
5	235	51.8	90	2	C64013 conserved hypotet
6	235	51.8	91	2	AH0879 conserved hypotet
7	222.5	49.0	90	2	H83003 conserved hypotet
8	212	46.7	90	2	A10116 conserved hypotet
9	200	44.1	93	2	H84994 conserved hypotet
10	195	43.0	105	2	C82624 conserved hypotet
11	176.5	16.9	749	2	B86774 conserved hypotet
12	171.5	15.7	855	2	B89952 conserved hypotet
13	171.5	15.7	855	2	A45713 conserved hypotet
14	169	15.2	429	2	A82501 conserved hypotet
15	169	15.2	522	1	I58155 conserved hypotet
16	168.5	15.1	241	2	I58155 conserved hypotet
17	168.5	15.1	241	2	I58155 conserved hypotet
18	168	15.0	134	2	T37027 conserved hypotet
19	168	15.0	393	2	S03576 conserved hypotet
20	167.5	14.9	714	2	S77385 conserved hypotet
21	167	14.8	389	2	T14751 conserved hypotet
22	166.5	14.6	591	1	FOVMVM conserved hypotet
23	166	14.5	318	2	S77153 conserved hypotet
24	165.5	14.4	164	2	B75293 conserved hypotet
25	165	14.3	323	2	JT0755 conserved hypotet
26	165	14.3	323	2	A86184 conserved hypotet
27	165	14.3	837	2	B89583 conserved hypotet
28	165	14.3	1276	2	T09204 conserved hypotet
29	164.5	14.2	228	2	C26599 conserved hypotet

30	64.5	14.2	229	2	B31775	clathrin light cha
31	64.5	14.2	238	1	LRR7B2	clathrin light cha
32	64.5	14.2	393	2	T49257	protein kinase-lik
33	64.5	14.2	560	1	HMIW7	hemagglutinin prec
34	64.5	14.2	622	2	T23804	hypothetical prote
35	64.5	14.2	688	2	AG3124	hypothetical prote
36	64.5	14.2	706	2	B99163	ATP-dependent DNA
37	64.5	14.2	2291	1	A46147	ATP-dependent DNA
38	64	14.1	133	2	G75385	spectrin beta chain
39	64	14.1	451	2	B64312	signal recognition
40	64	14.1	1068	2	S73091	hypothetical prote
41	63.5	14.0	353	1	FOVGR	gag polypeptide
42	63.5	14.0	563	1	A45359	hemagglutinin prec
43	63.5	14.0	805	2	A46266	WD-repeat protein
44	63	13.9	506	2	T50211	hypothetical prote
45	63	13.9	563	2	T17316	hypothetical prote
46	63	13.9	569	2	T47358	hypothetical prote
47	62.5	13.8	165	1	XUBSW1	methylated-DNA-lpr
48	62.5	13.8	388	2	T38810	hypothetical prote
49	62.5	13.8	563	1	HMIW	hemagglutinin prec
50	62.5	13.8	694	2	A95866	probable transkeo
51	62.5	13.8	853	2	S58375	aryl hydrocarbon r
52	62.5	13.8	920	2	JC7313	aryl hydrocarbon r
53	62.5	13.8	1675	2	S70770	hypothetical prote
54	62	13.7	337	2	AG2423	hypothetical prote
55	62	13.7	416	2	C47017	probable transcrip
56	62	13.7	416	2	AF2017	RNA polymerase sig
57	62	13.7	432	2	B75638	hypothetical prote
58	62	13.7	559	2	AH1719	phorbolone ABC tran
59	62	13.7	989	2	T46183	zinc proteinase (E
60	61.5	13.5	121	2	C97906	hypothetical prote
61	61.5	13.5	283	4	FOHUR1	retrovirus-related
62	61.5	13.5	310	2	FE4311	hypothetical prote
63	61.5	13.5	320	2	S69547	transcription init
64	61.5	13.5	430	2	S75313	serine-tRNA ligase
65	61.5	13.5	897	2	G02529	dynein heavy chain
66	61.5	13.5	1464	2	T07050	hypothetical prote
67	61	13.4	143	2	D70003	general stress pro
68	61	13.4	320	2	S11879	ethylene-forming e
69	61	13.4	321	2	T02754	probable 1-antibio
70	61	13.4	372	2	B81952	probable type II r
71	61	13.4	558	2	AD1349	phorbolone ABC tran
72	61	13.4	865	2	B84718	hypothetical prote
73	61	13.4	1138	2	T24635	hypothetical prote
74	61	13.4	1291	2	T09273	probable tail-host
75	61	13.4	3685	1	A27605	dystrophin, muscle

ALIGNMENTS

RESULT 1
H81014 conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: H81014; F81958
R:Retelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massimiani, V.; Plaza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: H81014
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-88 <TR>
A:Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:G7227279; PIDN:
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holtroyd, S.; Jorgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-2
Perfect score: 461
Sequence: 1 MSRIWNCVKLKREAEGLDFP.....QOMERFLPEDGTBAQGVVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	62.9	88	H81014	conserved hypother
2	256	55.5	90	C84013	hypothetical prote
3	255	55.3	91	A85954	hypothetical prote
4	255	55.3	91	A65082	hypothetical prote
5	255	55.3	91	F91108	hypothetical prote
6	249	54.0	90	C82320	conserved hypother
7	249	54.0	91	A80879	conserved hypother
8	240	52.1	90	H83003	conserved hypother
9	226	49.0	90	A10116	conserved hypother
10	205	44.5	105	C82624	conserved hypother
11	200	43.4	93	E84994	hypothetical prote
12	76.5	16.6	207	E89952	conserved hypother
13	76.5	16.6	749	E86774	hypothetical prote
14	71.5	15.5	855	A45713	Env transmembrane
15	69	15.0	429	A82501	hypothetical prote
16	68.5	14.9	241	S19999	hypothetical prote
17	68	14.8	134	T37027	hypothetical prote
18	67.5	14.6	318	H82399	hypothetical prote
19	67.5	14.6	522	1 ISBYSS	protein disulfide-
20	67.5	14.6	714	S77385	nitrate reductase
21	67	14.5	389	T14751	hypothetical prote
22	67	14.5	678	A81130	penicillin-binding
23	66.5	14.4	591	1 FOMVM	gag polyprotein -
24	66	14.3	318	S77153	transcription init
25	66	14.3	1276	T09204	probable tail-host
26	65.5	14.2	164	E75293	hypothetical prote
27	65	14.1	238	1 LKRTB2	clathrin light cha
28	65	14.1	323	2 J70755	ethylene-forming e
29	65	14.1	323	2 A86184	hypothetical prote

30	65	14.1	393	2	S03576	DNA-directed RNA p
31	64.5	14.0	228	2	C26599	clathrin light cha
32	64.5	14.0	229	2	B31775	clathrin light cha
33	64.5	14.0	393	2	T49257	protein kinase-lik
34	64.5	14.0	560	1	HMIV77	hemagglutinin prec
35	64.5	14.0	622	2	T23804	hypothetical prote
36	64.5	14.0	805	2	A46266	spectrin beta chai
37	64.5	14.0	2291	1	A46147	aryl hydrocarbon r
38	64.5	14.0	3063	2	S55505	fatty-acid synthas
39	64	13.9	133	2	G75385	hypothetical prote
40	64	13.9	299	2	T29546	protein SPE-11 - C
41	64	13.9	451	2	E64312	signal recognition
42	64	13.9	1068	2	S73091	hypothetical prote
43	63.5	13.8	353	1	FOMVGR	gag polyprotein -
44	63.5	13.8	563	1	A45539	hemagglutinin prec
45	63.5	13.8	853	2	S58375	aryl hydrocarbon r
46	63.5	13.8	920	2	JC7313	aryl hydrocarbon r
47	63	13.7	506	2	T50211	WD-repeat protein
48	63	13.7	569	2	T47358	hypothetical prote
49	62.5	13.6	388	2	T38810	hypothetical prote
50	62.5	13.6	563	1	HMIVF	hemagglutinin prec
51	62.5	13.6	694	2	A95866	probable transketo
52	62.5	13.6	897	2	G02529	dynein heavy chain
53	62.5	13.6	1675	2	S70770	hypothetical prote
54	62	13.4	337	2	AG2423	hypothetical prote
55	62	13.4	416	2	C47017	probable transcrip
56	62	13.4	416	2	AF2017	RNA polymerase sig
57	62	13.4	563	2	T17316	hypothetical prote
58	62	13.4	989	2	T46183	zinc proteinase (E
59	62	13.4	1291	2	T09273	probable tail-host
60	61.5	13.3	188	2	C87216	retrovirus-related
61	61.5	13.3	283	4	FOHUB1	probable hemagglut
62	61.5	13.3	310	2	P64311	hypothetical prote
63	61.5	13.3	320	2	S69547	transcription init
64	61.5	13.3	1464	2	T07050	hypothetical prote
65	61.5	13.3	4644	1	A38905	dynein heavy chain
66	61	13.2	143	2	D70003	general stress pro
67	61	13.2	320	2	S11879	ethylene-forming e
68	61	13.2	321	2	T02754	probable 1-aminoc
69	61	13.2	372	2	B81952	probable type II r
70	61	13.2	504	1	O4RTD5	cycochrome P450 2D
71	61	13.2	678	2	AE1490	penicillin-binding
72	61	13.2	865	2	E84718	hypothetical prote
73	61	13.2	1138	2	T24635	hypothetical prote
74	61	13.2	1245	2	T18211	delta endotoxin -
75	60.5	13.1	138	2	T10309	hypothetical prote

ALIGNMENTS

RESULT 1

H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: H81014; F81958
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Xie, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; UID:20175755; PMID:10710307
A:Accession: H81014
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-88 <TET>
A:Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN
A:Experimental source: serogroup B, strain MC58
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagele, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 / Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-2

Perfect score: 461

Sequence: 1 MSRIYVCYKREAEGLDEP.....QOMERFLPEDGTVAQGYVP 87

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

1: Geneseq_21:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	87	5	ABB78148 Amino aci
2	461	100.0	87	5	ABB78147 Amino aci
3	443.5	96.2	86	5	ABB78149 Amino aci
4	300	65.1	87	5	ABB78175 Amino aci
5	294	63.8	87	5	ABB78174 Amino aci
6	290	62.9	88	5	ABB78171 Amino aci
7	290	62.9	88	5	ABB78172 Amino aci
8	290	62.9	88	5	ABB78173 Amino aci
9	290	62.9	88	5	ABB78174 Amino aci
10	275	59.7	87	5	ABB78176 Amino aci
11	260	56.4	87	5	ABB78177 Amino aci
12	260	56.4	87	5	ABB78150 Amino aci
13	256	55.5	87	5	ABB78152 Amino aci
14	256	55.5	88	5	ABB78154 Amino aci
15	255	55.3	91	5	ABB78158 Amino aci
16	255	55.3	91	5	ABB78157 Amino aci
17	255	55.3	91	5	ABB78156 Amino aci
18	251	54.4	87	5	ABB78151 Amino aci
19	249	54.0	88	5	ABB78160 Amino aci
20	249	54.0	89	9	ABB78157 Amino aci
21	249	54.0	90	5	ABB78155 Amino aci
22	249	54.0	91	5	ABB78161 Amino aci
23	249	54.0	91	5	ABB78159 Amino aci
24	249	54.0	91	5	ABB78162 Amino aci

ALIGNMENTS

RESULT 1	ABB78148	standard; protein; 87 AA.
ID	ABB78148;	
AC	05-NOV-2002	(first entry)
DT		
XX		
DR		Amino acid sequence of a YggX homologue.
XX		
KW		Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX		hydroxyl radical; DNA damage; YggX homologue.
OS		Bordetella pertussis.
XX		
PN		US2002072118-A1.
XX		

25	249	54.0	95	9	ABB38294	Aeb38294 L. pneumo
26	243	52.7	87	5	ABB78153	Abb78153 Amino aci
27	243	52.7	107	7	ABO65445	ABO65445 Klebsiell
28	242	52.5	91	5	ABB78163	Abb78163 Amino aci
29	242	52.5	93	7	ADF05158	Adf05158 Bacterial
30	240	52.1	87	5	ABB78170	Abb78170 Amino aci
31	240	52.1	122	7	ABO74609	ABO74609 Pseudomon
32	230.5	50.0	92	6	ADA34169	Ada34169 Acinetoba
33	230	49.9	88	5	ABB78178	Abb78178 Amino aci
34	226	49.0	90	5	ABB78165	Abb78165 Amino aci
35	222	48.2	78	5	ABB78164	Abb78164 Amino aci
36	222	48.2	87	5	ABB78169	Abb78169 Amino aci
37	218	47.3	90	5	ABB78168	Abb78168 Amino aci
38	200	43.4	76	5	ABB78166	Abb78166 Amino aci
39	197.5	42.8	90	5	ABB78167	Abb78167 Amino aci
40	164	35.6	110	8	ADJ05173	Adj05173 M. catarr
41	76.5	16.6	207	6	ABM73508	Abm73508 Staphyloc
42	76.5	16.6	207	9	ADV16859	Adv16859 Staphyloc
43	76.5	16.6	207	9	ADW94758	Adw94758 Prolifera
44	76.5	16.6	749	5	ABBS4524	Abbs4524 Lactococc
45	72.5	15.7	303	9	ABM94402	Abm94402 M. xanthu
46	70.5	15.3	200	4	AAg82648	Aag82648 S. epider
47	70.5	15.3	200	4	AAg82046	Aag82046 S. epider
48	70.5	15.3	208	5	ABP38940	Abp38940 Staphyloc
49	70.5	15.3	208	8	ADSO6726	Adso6726 Staphyloc
50	70.5	15.3	308	6	ABM70179	Abm70179 Photorhab
51	69.5	15.1	1233	8	ADO66727	Ado66727 Novel hum
52	69	15.0	124	9	ADX40209	Adx40209 HIV Rev p
53	69	15.0	527	6	ADB06106	Adb06106 A11olococ
54	69	15.0	528	6	ADB06108	Adb06108 A11olococ
55	68.5	14.9	720	5	AAE26857	Aae26857 Anabaena
56	68.5	14.9	720	7	ADF29270	Adf29270 Bacterial
57	68.5	14.9	720	7	ADG32479	Adg32479 Pasteurel
58	67.5	14.6	522	2	AAW69726	Aaw69726 Saccharom
59	67.5	14.6	522	2	ABE13006	Aeb13006 Yeast pro
60	67.5	14.6	522	2	ABE50108	Aeb50108 Yeast dis
61	67.5	14.6	526	2	AAK26174	Aak26174 Protein d
62	67.5	14.6	530	9	ABE13007	Aeb13007 Yeast alt
63	67.5	14.6	530	9	ABE50109	Aeb50109 Yeast dis
64	67.5	14.6	714	8	ADN20031	Adn20031 Bacterial
65	67	14.5	381	5	AAO20498	Aao20498 Human amy
66	67	14.5	389	4	AAW80170	Aaw80170 Human pro
67	67	14.5	579	6	ABR39276	AbR39276 Protein s
68	67	14.5	678	5	ABR47819	AbR47819 Listeria
69	66.5	14.4	591	2	AAV41141	Aav41141 Mouse mam
70	66.5	14.4	860	2	AAV41140	Aav41140 Mouse mam
71	66.5	14.4	1755	3	AAV41139	Aav41139 Mouse mam
72	66	14.3	229	3	AAW41703	Aaw41703 Human ORF
73	66	14.3	318	5	ABG77906	Abg77906 High leve
74	66	14.3	503	2	AAW85085	Aaw85085 Esterase
75	66	14.3	856	6	ABR39820	AbR39820 Human SCA

PD 13-JUN-2002.
 XX 18-SEP-2001; 2001US-00955502.
 XX 22-SEP-2000; 2000US-0234588P.
 PR
 XX
 XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX
 XX Downs D, Gralnick JA;
 PI
 XX WPI; 2002-589476/63.
 DR
 XX
 PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX
 XX Example; Fig 1A; 16pp; English.
 PS
 CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX
 XX Sequence 87 AA;
 SQ

Query Match 100.0%; Score 461; DB 5; Length 87;
 Best Local Similarity 100.0%; Pred. No. 3.1e-47;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNENRNLADA 60
 DB 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNENRNLADA 60

QY 61 RARKYLQOQMERFLFEDGTVEAAGYVP 87
 DB 61 RARKYLQOQMERFLFEDGTVEAAGYVP 87

RESULT 2
 ABB78147
 ID ABB78147 standard; protein; 87 AA.
 XX

AC ABB78147;
 XX

DT 05-NOV-2002 (first entry)
 XX

DE Amino acid sequence of a YgxB homologue.
 XX

XX Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YgxB homologue.
 XX

OS *Bordetella pertussis*.
 XX

PN US2002072118-A1.
 XX

PD 13-JUN-2002.
 XX

PF 18-SEP-2001; 2001US-00955502.
 XX

PR 22-SEP-2000; 2000US-0234588P.
 XX

XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX

PI Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.
 XX

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX

PS Example; Fig 1A; 16pp; English.
 XX

CC The specification describes a method for reducing superoxide damage to a
 CC cell. The method comprises engineering the cell to produce more than the
 CC native amount of YgxB protein (a protein identified from *Salmonella*
 CC *enterica* serovar Typhimurium) or its homolog, where the cells are
 CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
 CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX

SQ Sequence 87 AA;
 XX

Query Match 100.0%; Score 461; DB 5; Length 87;
 Best Local Similarity 100.0%; Pred. No. 3.1e-47;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNENRNLADA 60
 DB 1 MSRIYVCVLRKREAGLDPPYPGELGTRIMQOISKEAMEWKOIQTRLVNENRNLADA 60

QY 61 RARKYLQOQMERFLFEDGTVEAAGYVP 87
 DB 61 RARKYLQOQMERFLFEDGTVEAAGYVP 87

RESULT 3
 ABB78149
 ID ABB78149 standard; protein; 86 AA.
 XX

AC ABB78149;
 XX

DT 05-NOV-2002 (first entry)
 XX

DE Amino acid sequence of a YgxB homologue.
 XX

XX Superoxide damage; cell; YgxB; *Salmonella enterica* serovar Typhimurium;
 KM hydroxyl radical; DNA damage; YgxB homologue.
 XX

OS *Bordetella bronchiseptica*.
 XX

PN US2002072118-A1.
 XX

PD 13-JUN-2002.
 XX

PF 18-SEP-2001; 2001US-00955502.
 XX

PR 22-SEP-2000; 2000US-0234588P.
 XX

XX (DOWN/) DOWNS D.
 PA (GRAL/) GRALNICK J A.
 XX

PI Downs D, Gralnick JA;
 XX

DR WPI; 2002-589476/63.
 XX

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
 PT cell, comprises engineering the cell to produce more YgxB protein, a
 PT protein identified from *Salmonella enterica* Serovar Typhimurium.
 XX

PS Example; Fig 1A; 16pp; English.
 XX

CC The specification describes a method for reducing superoxide damage to a
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 CC clusters. The resulting decrease in free-iron levels generates fewer
 CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
 CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
 CC cell. ABB78147-78 represent YgxB homologues
 XX